



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:10 AM GMT

PDB ID : 3NZJ
Title : Crystal structure of yeast 20S proteasome in complex with ligand 2a
Authors : Groll, M.; Gallastegui, N.; Marechal, X.; Le Ravalec, V.; Basse, N.; Richy, N.;
Genin, E.; Huber, R.; Moroder, M.; Vidal, V.; Reboud-Ravaux, M.
Deposited on : 2010-07-16
Resolution : 2.40 Å(reported)

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

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

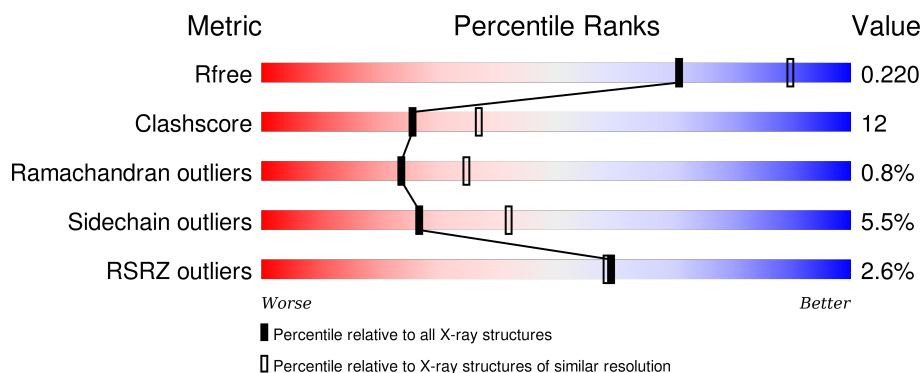
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	250	<div> <div>2%</div> <div>82% 17% •</div> </div>
1	O	250	<div> <div>2%</div> <div>80% 19% •</div> </div>
2	B	258	<div> <div>2%</div> <div>71% 19% • 5%</div> </div>
2	P	258	<div> <div>4%</div> <div>71% 20% • 5%</div> </div>
3	C	254	<div> <div>4%</div> <div>64% 27% • 5%</div> </div>

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Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	261	
8	V	261	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	287	
11	Y	287	
12	L	241	
12	Z	241	
13	1	266	
13	M	266	
14	2	215	
14	N	215	
15	3	5	
15	4	5	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
16	MES	K	212	-	-	-	X

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 51006 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
			1904	1201	321	379	3			
2	P	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			

- Molecule 3 is a protein called Proteasome component PRE6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			
3	Q	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	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
			1861	1162	314	378	7			
4	R	242	Total	C	N	O	S	0	0	0
			1861	1162	314	378	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
			1896	1205	330	357	4			
6	T	244	Total	C	N	O	S	0	0	0
			1896	1205	330	357	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
			1684	1061	293	323	7			
8	V	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	7			

- Molecule 9 is a protein called Proteasome 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			

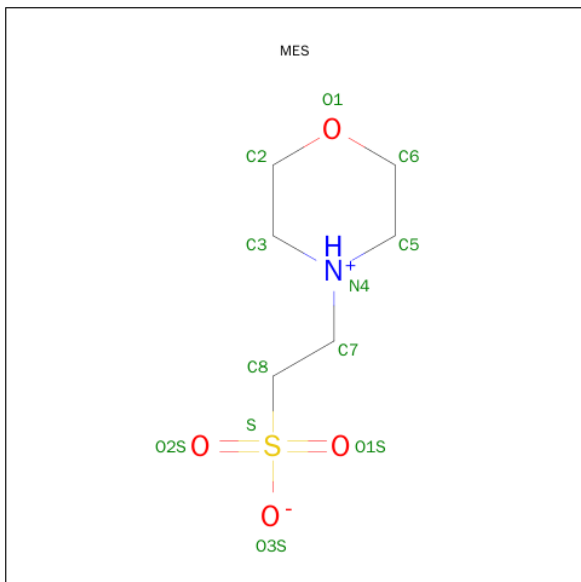
- Molecule 14 is a protein called Proteasome component PRE3.

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 a protein called TMC-95A mimic ligand 2a.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	3	5	Total	C	N	O	0	0	0
			54	42	5	7			
15	4	5	Total	C	N	O	0	0	0
			54	42	5	7			

- Molecule 16 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



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

- Molecule 17 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	58	Total	O	0	0
			58	58		
17	B	39	Total	O	0	0
			39	39		
17	C	43	Total	O	0	0
			43	43		
17	D	38	Total	O	0	0
			38	38		
17	E	22	Total	O	0	0
			22	22		
17	F	48	Total	O	0	0
			48	48		
17	G	62	Total	O	0	0
			62	62		
17	H	51	Total	O	0	0
			51	51		

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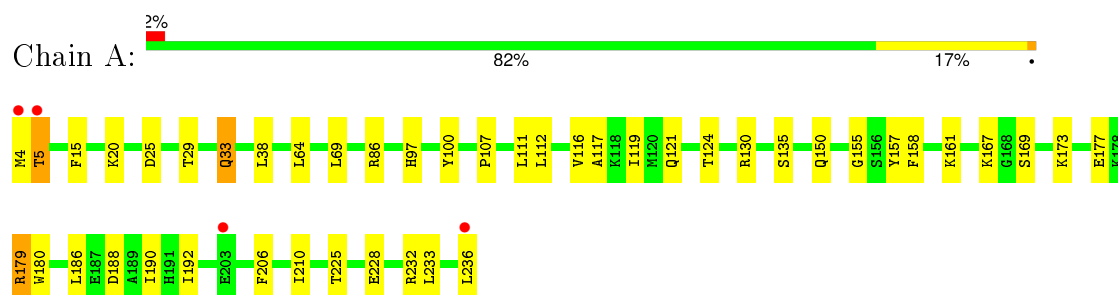
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	I	65	Total 65	O 65	0	0
17	J	52	Total 52	O 52	0	0
17	K	42	Total 42	O 42	0	0
17	L	57	Total 57	O 57	0	0
17	M	71	Total 71	O 71	0	0
17	N	61	Total 61	O 61	0	0
17	O	33	Total 33	O 33	0	0
17	P	30	Total 30	O 30	0	0
17	Q	26	Total 26	O 26	0	0
17	R	31	Total 31	O 31	0	0
17	S	19	Total 19	O 19	0	0
17	T	40	Total 40	O 40	0	0
17	U	61	Total 61	O 61	0	0
17	V	49	Total 49	O 49	0	0
17	W	61	Total 61	O 61	0	0
17	X	48	Total 48	O 48	0	0
17	Y	48	Total 48	O 48	0	0
17	Z	51	Total 51	O 51	0	0
17	1	70	Total 70	O 70	0	0
17	2	60	Total 60	O 60	0	0

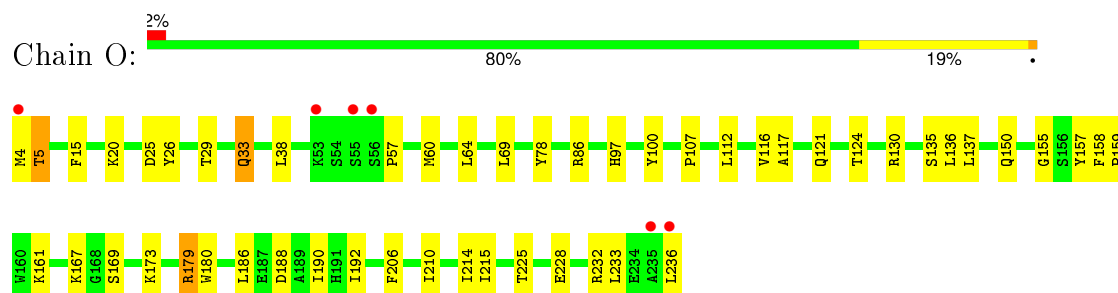
3 Residue-property plots [i](#)

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

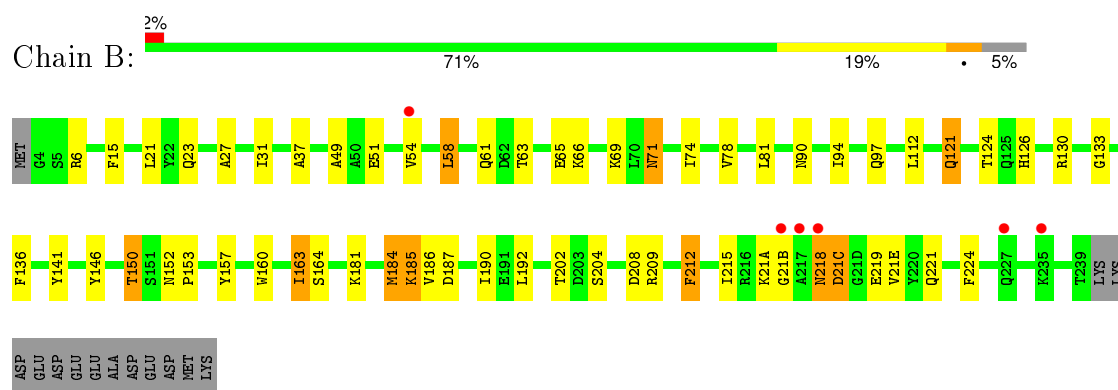
• Molecule 1: Proteasome component Y7



• Molecule 1: Proteasome component Y7

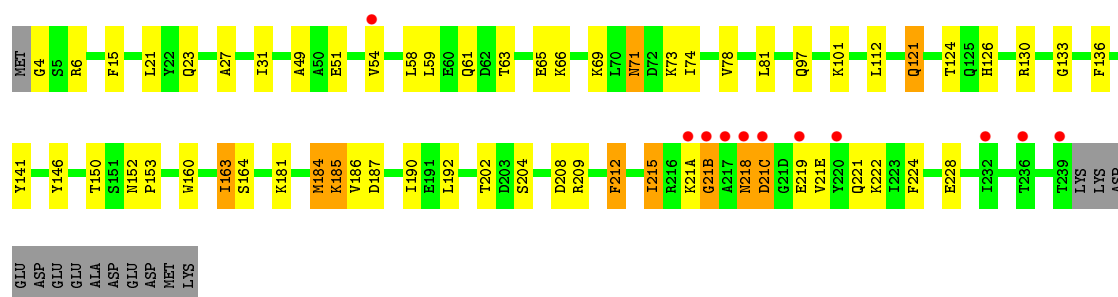


• Molecule 2: Proteasome component Y13

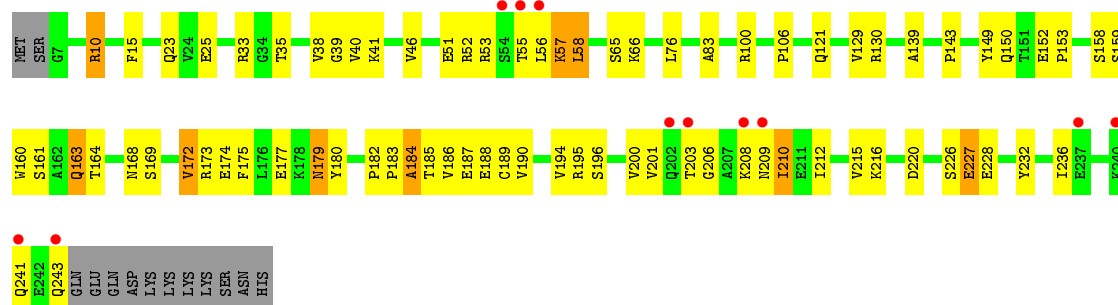


• Molecule 2: Proteasome component Y13

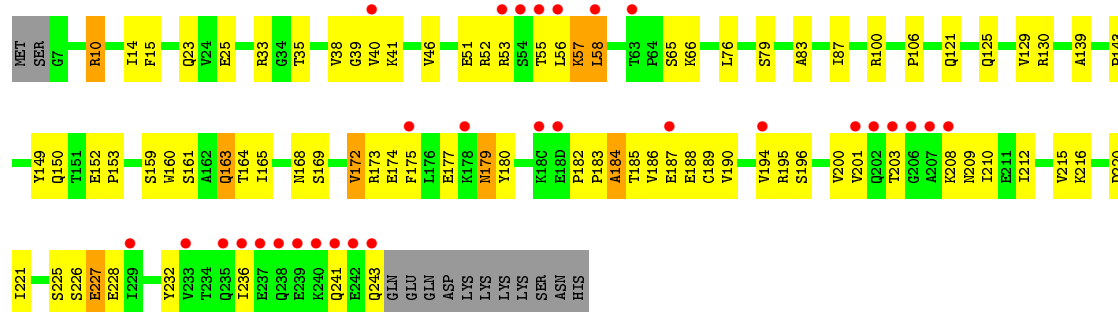




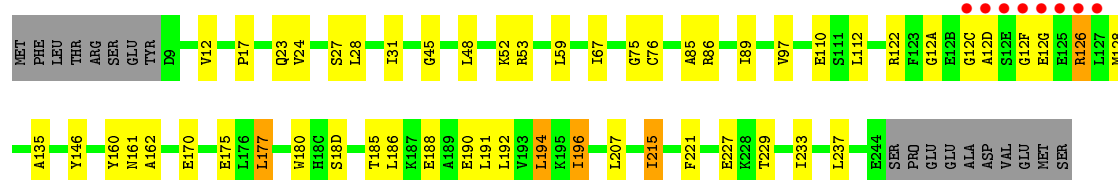
• Molecule 3: Proteasome component PRE6



• Molecule 3: Proteasome component PRE6

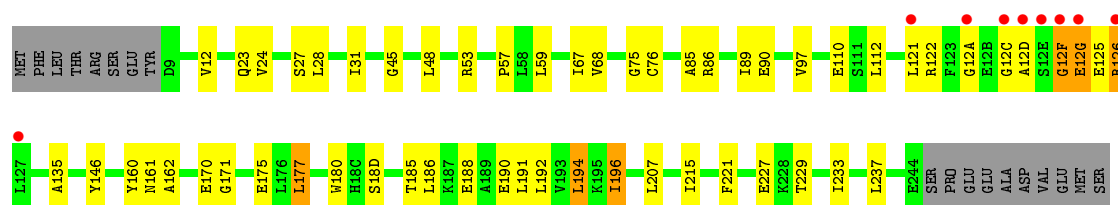


• Molecule 4: Proteasome component PUP2

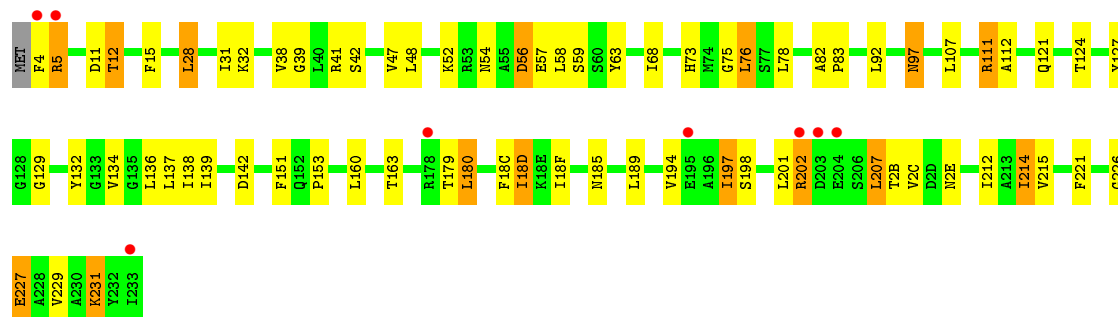


• Molecule 4: Proteasome component PUP2

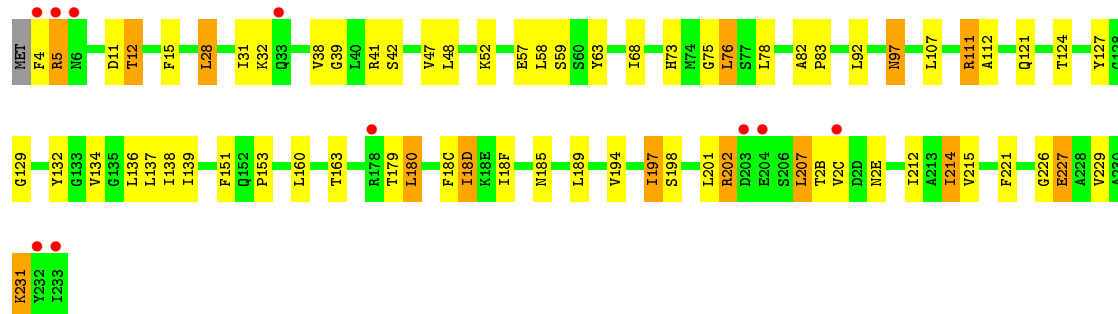




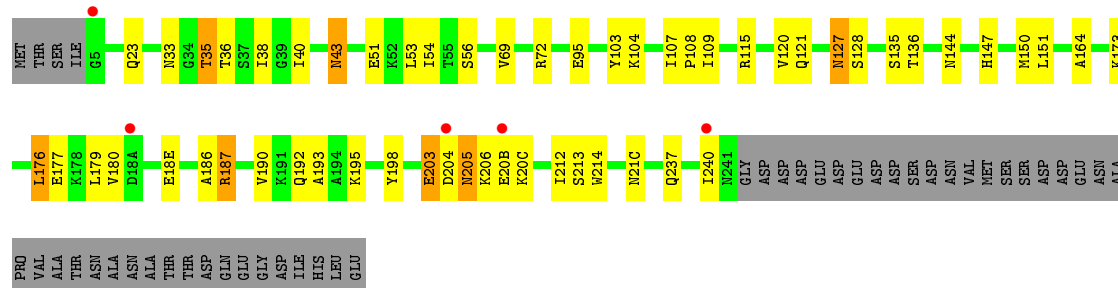
• Molecule 5: Proteasome component PRE5



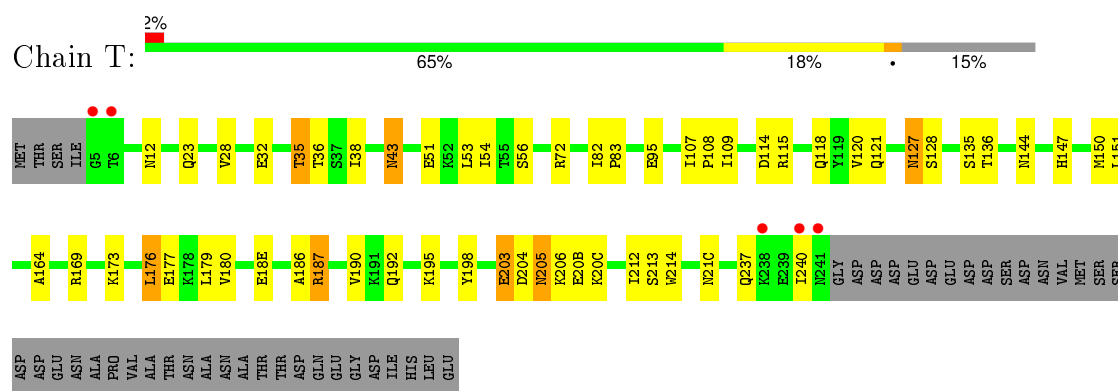
• Molecule 5: Proteasome component PRE5



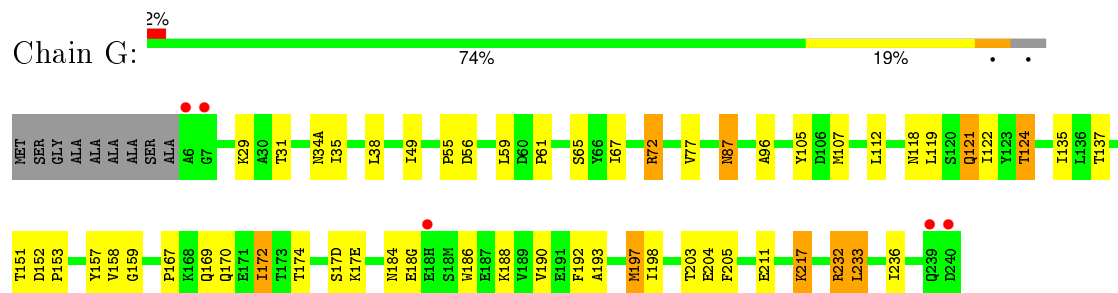
• Molecule 6: Proteasome component C1



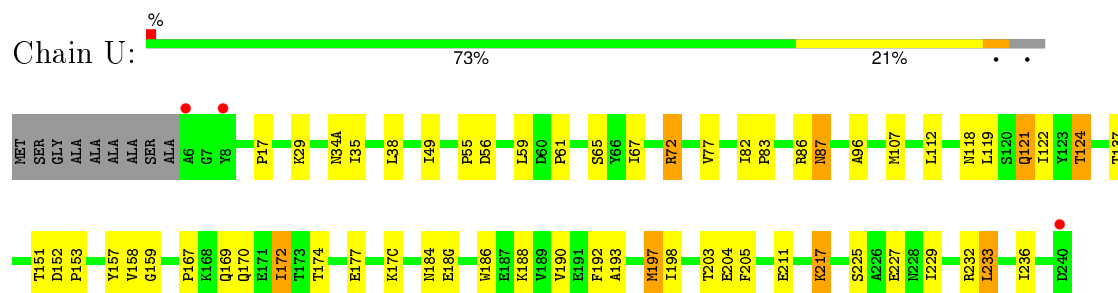
• Molecule 6: Proteasome component C1



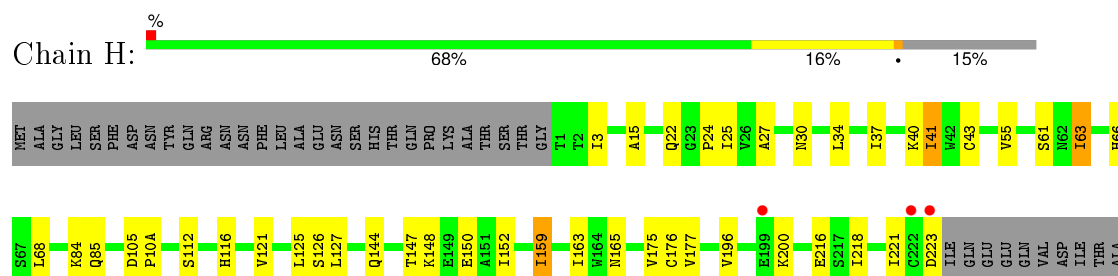
• Molecule 7: Proteasome component C7-alpha



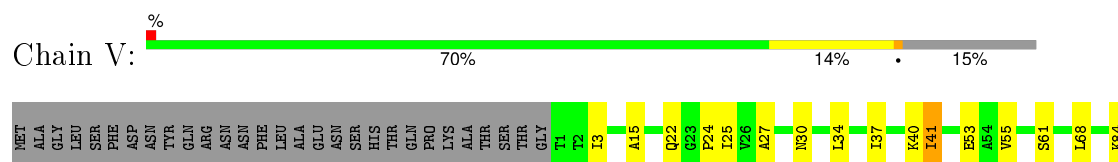
• Molecule 7: Proteasome component C7-alpha

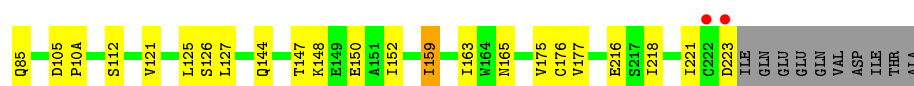


• Molecule 8: Proteasome component PUP1

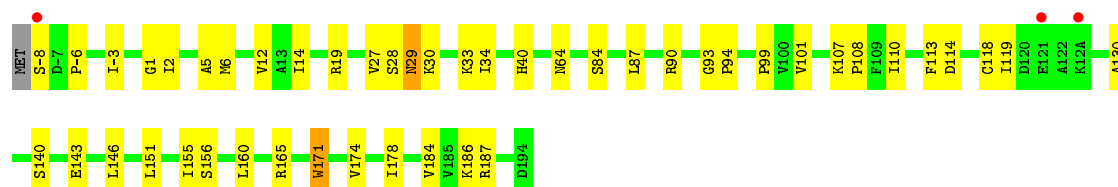


• Molecule 8: Proteasome component PUP1

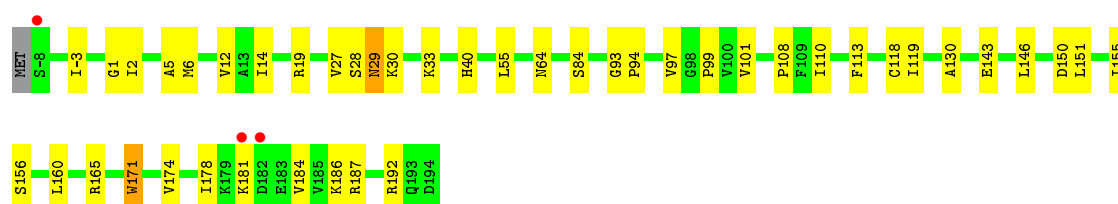
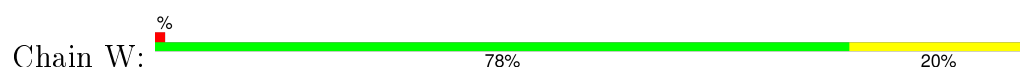




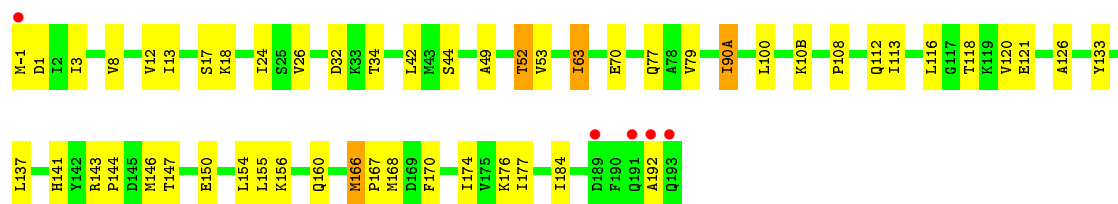
• Molecule 9: Proteasome component PUP3



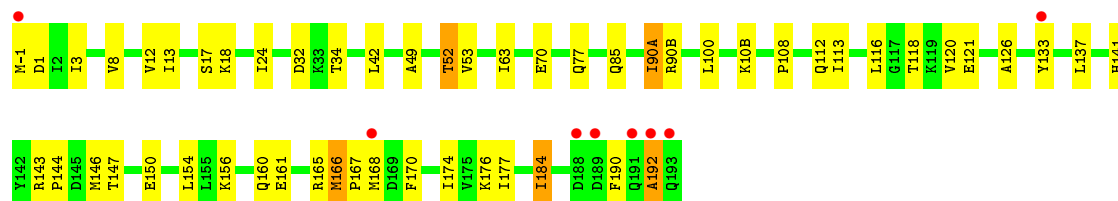
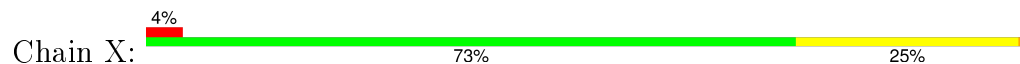
• Molecule 9: Proteasome component PUP3



• Molecule 10: Proteasome component C11



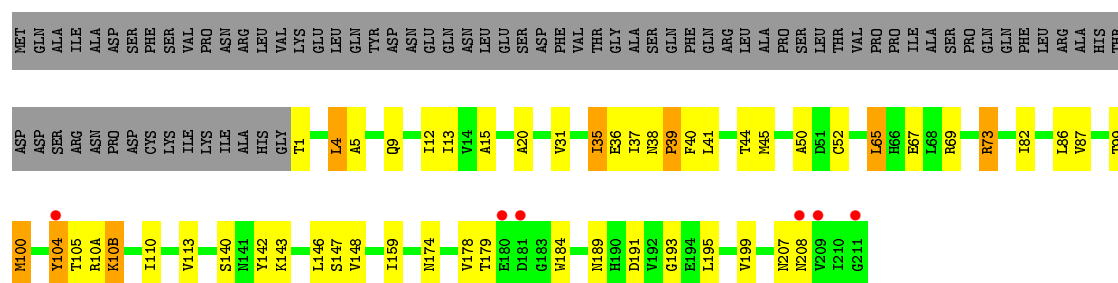
• Molecule 10: Proteasome component C11



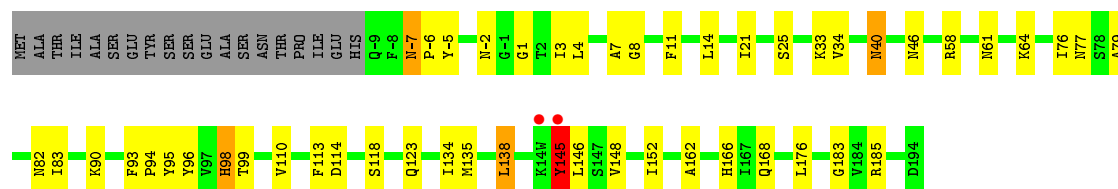
• Molecule 11: Proteasome component PRE2



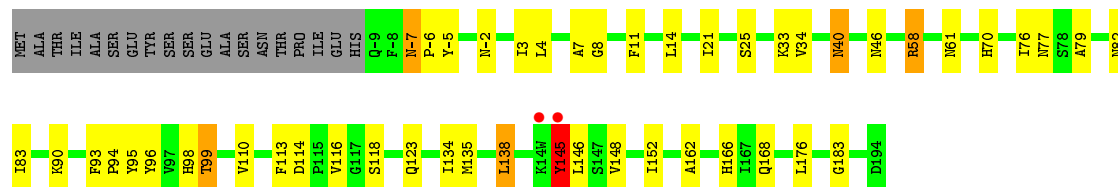
- Molecule 11: Proteasome component PRE2



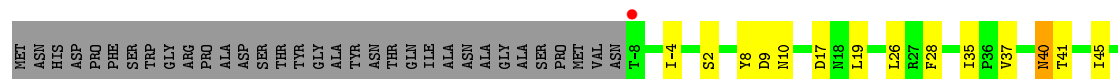
- Molecule 12: Proteasome component C5

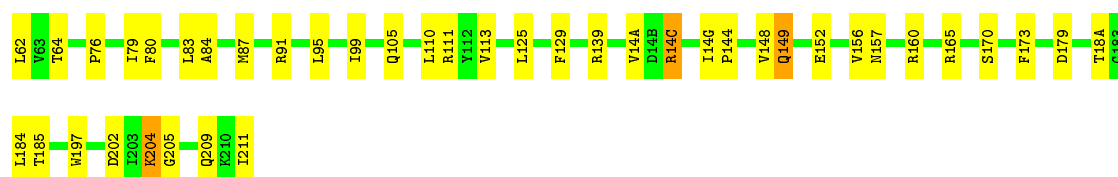


- Molecule 12: Proteasome component C5

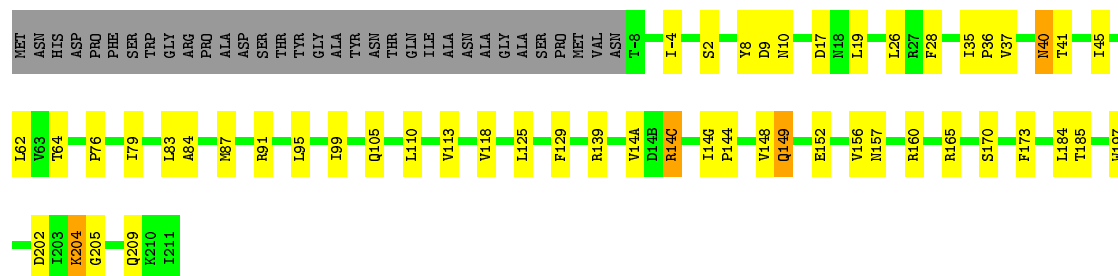


- Molecule 13: Proteasome component PRE4

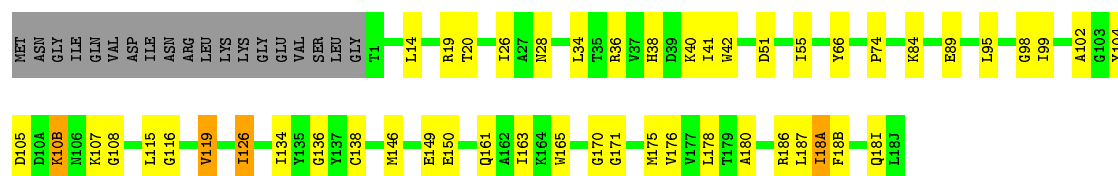




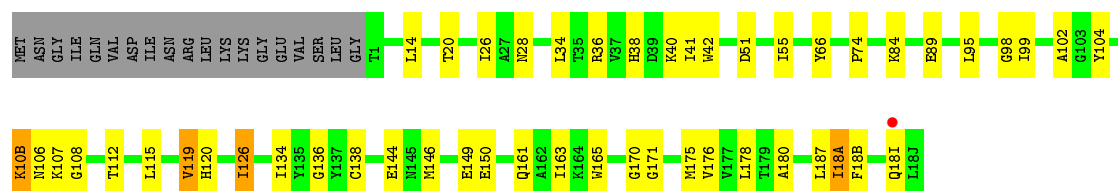
- Molecule 13: Proteasome component PRE4



- Molecule 14: Proteasome component PRE3



- Molecule 14: Proteasome component PRE3



- Molecule 15: TMC-95A mimic ligand 2a



- Molecule 15: TMC-95A mimic ligand 2a





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	136.48Å 301.13Å 145.37Å 90.00° 113.57° 90.00°	Depositor
Resolution (Å)	15.00 – 2.40 49.51 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.5 (15.00-2.40) 99.7 (49.51-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 2.39Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.233 , 0.249 0.220 , 0.220	Depositor DCC
R_{free} test set	20710 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	40.2	Xtriage
Anisotropy	0.786	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 40.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 415923 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	51006	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.28% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TY5, BOC, ABN, TRO, MES

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.39	0/1952	0.64	0/2642
1	O	0.39	0/1952	0.64	0/2642
2	B	0.38	0/1934	0.63	0/2618
2	P	0.39	0/1934	0.63	0/2618
3	C	0.37	0/1919	0.61	0/2598
3	Q	0.37	0/1919	0.61	0/2598
4	D	0.37	0/1886	0.63	1/2541 (0.0%)
4	R	0.37	0/1886	0.63	0/2541
5	E	0.37	0/1823	0.60	0/2463
5	S	0.37	0/1823	0.61	0/2463
6	F	0.38	0/1936	0.62	0/2614
6	T	0.40	0/1936	0.62	0/2614
7	G	0.43	0/1959	0.63	0/2652
7	U	0.42	0/1959	0.63	0/2652
8	H	0.41	1/1715 (0.1%)	0.67	0/2326
8	V	0.41	0/1715	0.68	0/2326
9	I	0.41	0/1611	0.67	0/2174
9	W	0.41	0/1611	0.68	0/2174
10	J	0.41	0/1613	0.65	0/2173
10	X	0.41	0/1613	0.66	0/2173
11	K	0.41	0/1681	0.67	0/2274
11	Y	0.41	0/1681	0.67	0/2274
12	L	0.42	0/1795	0.68	0/2420
12	Z	0.42	0/1795	0.67	0/2420
13	1	0.42	0/1855	0.68	1/2514 (0.0%)
13	M	0.41	0/1855	0.68	1/2514 (0.0%)
14	2	0.40	0/1541	0.64	0/2087
14	N	0.41	0/1541	0.64	0/2087
15	3	1.25	0/4	0.49	0/4
15	4	1.15	0/4	0.53	0/4
All	All	0.40	1/50448 (0.0%)	0.65	3/68200 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	O	0	1
12	L	0	1
12	Z	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	43	CYS	CB-SG	-5.11	1.73	1.81

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	1	95	LEU	N-CA-C	-5.74	95.49	111.00
13	M	95	LEU	N-CA-C	-5.60	95.88	111.00
4	D	128	MET	N-CA-C	-5.03	97.43	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	L	145	TYR	Sidechain
1	O	78	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	36	0
1	O	1915	0	1926	40	0
2	B	1904	0	1901	60	0
2	P	1904	0	1901	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1890	0	1900	73	0
3	Q	1890	0	1900	78	0
4	D	1861	0	1836	40	0
4	R	1861	0	1836	41	0
5	E	1795	0	1797	68	0
5	S	1795	0	1797	63	0
6	F	1896	0	1886	41	0
6	T	1896	0	1886	42	0
7	G	1921	0	1910	48	0
7	U	1921	0	1910	57	0
8	H	1684	0	1688	30	0
8	V	1684	0	1688	27	0
9	I	1581	0	1574	42	0
9	W	1581	0	1574	40	0
10	J	1585	0	1590	62	0
10	X	1585	0	1590	62	0
11	K	1644	0	1595	63	0
11	Y	1644	0	1595	62	0
12	L	1757	0	1711	39	0
12	Z	1757	0	1711	40	0
13	1	1824	0	1832	41	0
13	M	1824	0	1832	42	0
14	2	1512	0	1481	42	0
14	N	1512	0	1481	45	0
15	3	54	0	44	7	0
15	4	54	0	44	7	0
16	K	12	0	13	0	0
16	Y	12	0	13	0	0
17	1	70	0	0	1	0
17	2	60	0	0	1	0
17	A	58	0	0	0	0
17	B	39	0	0	1	0
17	C	43	0	0	1	0
17	D	38	0	0	1	0
17	E	22	0	0	1	0
17	F	48	0	0	2	0
17	G	62	0	0	0	0
17	H	51	0	0	3	0
17	I	65	0	0	2	0
17	J	52	0	0	1	0
17	K	42	0	0	3	0
17	L	57	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	M	71	0	0	2	0
17	N	61	0	0	2	0
17	O	33	0	0	0	0
17	P	30	0	0	2	0
17	Q	26	0	0	2	0
17	R	31	0	0	2	0
17	S	19	0	0	1	0
17	T	40	0	0	2	0
17	U	61	0	0	3	0
17	V	49	0	0	3	0
17	W	61	0	0	1	0
17	X	48	0	0	3	0
17	Y	48	0	0	2	0
17	Z	51	0	0	3	0
All	All	51006	0	49368	1238	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 12.

All (1238) 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:U:96:ALA:HA	7:U:107:MET:HE2	1.31	1.12
11:Y:10(B):LYS:H	11:Y:10(B):LYS:HD2	1.13	1.09
11:K:10(B):LYS:H	11:K:10(B):LYS:HD2	1.11	1.08
2:P:202:THR:HG22	2:P:204:SER:H	1.21	1.06
7:G:96:ALA:HA	7:G:107:MET:HE2	1.33	1.05
2:B:202:THR:HG22	2:B:204:SER:H	1.22	1.03
1:O:124:THR:HG22	2:P:130:ARG:HH21	1.26	0.99
13:M:157:ASN:HD22	13:M:160:ARG:HH11	1.09	0.99
13:1:157:ASN:HD22	13:1:160:ARG:HH11	1.11	0.99
2:B:15:PHE:H	3:C:23:GLN:HE22	1.04	0.95
10:J:133:TYR:HE1	17:X:876:HOH:O	1.49	0.95
12:L:4:LEU:HD11	12:L:138:LEU:HD21	1.47	0.94
10:J:133:TYR:HD1	17:Y:593:HOH:O	1.48	0.94
5:S:15:PHE:H	6:T:23:GLN:HE22	1.12	0.94
1:A:124:THR:HG22	2:B:130:ARG:HH21	1.34	0.92
12:Z:4:LEU:HD11	12:Z:138:LEU:HD21	1.50	0.92
3:Q:195:ARG:HG3	3:Q:236:ILE:HD13	1.53	0.91
3:C:195:ARG:HG3	3:C:236:ILE:HD13	1.52	0.91
6:T:95:GLU:HG2	6:T:115:ARG:HB3	1.51	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:65:SER:HB2	17:Q:303:HOH:O	1.69	0.91
7:U:67:ILE:HD12	7:U:211:GLU:HG2	1.52	0.90
14:2:107:LYS:HG2	14:2:108:GLY:H	1.36	0.90
6:F:95:GLU:HG2	6:F:115:ARG:HB3	1.55	0.89
5:E:12:THR:HG21	5:E:124:THR:HA	1.55	0.89
5:E:207:LEU:HD23	5:E:207:LEU:H	1.37	0.89
5:E:15:PHE:H	6:F:23:GLN:HE22	1.15	0.89
2:B:124:THR:HG22	3:C:130:ARG:HH21	1.37	0.89
5:S:207:LEU:HD23	5:S:207:LEU:H	1.37	0.88
11:Y:10(B):LYS:CD	11:Y:10(B):LYS:H	1.84	0.88
10:J:-1:MET:HG2	10:J:1:ASP:H	1.38	0.88
2:P:124:THR:HG22	3:Q:130:ARG:HH21	1.38	0.88
11:Y:40:PHE:HB3	11:Y:73:ARG:NH2	1.88	0.88
11:K:40:PHE:HB3	11:K:73:ARG:NH2	1.88	0.87
2:P:15:PHE:H	3:Q:23:GLN:HE22	1.20	0.86
13:M:157:ASN:HD22	13:M:160:ARG:NH1	1.73	0.86
11:K:10(B):LYS:H	11:K:10(B):LYS:CD	1.82	0.86
3:C:163:GLN:HE22	3:C:173:ARG:HE	1.20	0.86
14:N:107:LYS:HG2	14:N:108:GLY:H	1.38	0.86
13:1:157:ASN:HD22	13:1:160:ARG:NH1	1.74	0.86
1:O:15:PHE:H	2:P:23:GLN:HE22	1.22	0.85
3:C:185:THR:HG22	3:C:187:GLU:H	1.41	0.85
5:S:12:THR:HG21	5:S:124:THR:HA	1.57	0.85
3:Q:185:THR:HG22	3:Q:187:GLU:H	1.40	0.84
7:G:67:ILE:HD12	7:G:211:GLU:HG2	1.57	0.84
11:Y:40:PHE:HB3	11:Y:73:ARG:HH21	1.40	0.84
10:X:-1:MET:HG2	10:X:1:ASP:H	1.40	0.84
13:M:139:ARG:HH11	8:V:165:ASN:HD22	1.27	0.83
3:Q:163:GLN:HE22	3:Q:173:ARG:HE	1.21	0.83
2:P:61:GLN:OE1	2:P:208:ASP:HA	1.79	0.83
6:F:36:THR:HG22	6:F:51:GLU:OE2	1.78	0.82
11:K:40:PHE:HB3	11:K:73:ARG:HH21	1.39	0.82
11:K:207:ASN:ND2	10:X:144:PRO:HG3	1.94	0.82
11:K:10(B):LYS:N	11:K:10(B):LYS:HD2	1.94	0.82
1:O:124:THR:CG2	2:P:130:ARG:HH21	1.92	0.81
6:T:36:THR:HG22	6:T:51:GLU:OE2	1.80	0.81
11:K:180:GLU:HB3	17:K:924:HOH:O	1.80	0.81
11:K:208:ASN:ND2	9:W:29:ASN:HD21	1.79	0.81
1:O:130:ARG:HH21	7:U:124:THR:HG22	1.45	0.80
2:B:61:GLN:OE1	2:B:208:ASP:HA	1.80	0.80
4:R:97:VAL:HG21	11:Y:65:LEU:HD13	1.61	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Z:33:LYS:HD2	12:Z:46:ASN:HD22	1.46	0.80
1:A:124:THR:CG2	2:B:130:ARG:HH21	1.95	0.80
11:K:174:ASN:HD21	11:K:189:ASN:HD22	1.29	0.79
12:L:33:LYS:HD2	12:L:46:ASN:HD22	1.46	0.79
2:B:163:ILE:HG13	2:B:164:SER:N	1.98	0.79
5:S:48:LEU:HG	5:S:139:ILE:HD13	1.64	0.79
2:P:163:ILE:HG13	2:P:164:SER:N	1.98	0.79
2:B:124:THR:CG2	3:C:130:ARG:HH21	1.95	0.79
1:A:15:PHE:H	2:B:23:GLN:HE22	1.30	0.79
5:E:201:LEU:HD11	5:E:207:LEU:HD22	1.65	0.78
3:Q:185:THR:HB	3:Q:188:GLU:HG2	1.64	0.78
6:F:35:THR:HG21	6:F:51:GLU:O	1.84	0.78
13:M:157:ASN:ND2	13:M:160:ARG:HH11	1.81	0.77
6:T:35:THR:HG21	6:T:51:GLU:O	1.85	0.77
13:I:157:ASN:ND2	13:I:160:ARG:HH11	1.82	0.77
11:K:207:ASN:HD21	10:X:144:PRO:HG3	1.49	0.77
1:O:130:ARG:HH21	7:U:124:THR:CG2	1.98	0.77
12:Z:166:HIS:HD2	12:Z:168:GLN:H	1.32	0.77
3:C:185:THR:HB	3:C:188:GLU:HG2	1.65	0.77
1:A:130:ARG:HH21	7:G:124:THR:HG22	1.47	0.77
2:P:163:ILE:HG13	2:P:164:SER:H	1.50	0.77
11:Y:10(B):LYS:N	11:Y:10(B):LYS:HD2	1.96	0.77
12:L:114:ASP:HB2	12:L:118:SER:HB3	1.67	0.76
5:S:201:LEU:HD11	5:S:207:LEU:HD22	1.66	0.76
12:L:166:HIS:HD2	12:L:168:GLN:H	1.33	0.76
4:D:97:VAL:HG21	11:K:65:LEU:HD13	1.67	0.76
1:O:86:ARG:HE	7:U:118:ASN:HD21	1.31	0.76
11:Y:45:MET:HB2	15:4:5:ABN:H5	1.67	0.76
9:W:27:VAL:HG13	17:X:622:HOH:O	1.85	0.76
3:Q:163:GLN:HA	3:Q:163:GLN:HE21	1.51	0.76
11:K:4:LEU:HD12	11:K:159:ILE:HD11	1.66	0.76
7:U:217:LYS:HE3	7:U:217:LYS:HA	1.68	0.76
10:J:144:PRO:HG3	11:Y:207:ASN:ND2	2.01	0.76
8:H:165:ASN:HD22	13:I:139:ARG:HH11	1.31	0.75
3:Q:15:PHE:H	4:R:23:GLN:HE22	1.31	0.75
11:Y:174:ASN:HD21	11:Y:189:ASN:HD22	1.35	0.75
11:K:143:LYS:HB2	11:K:146:LEU:CD1	2.16	0.75
2:B:163:ILE:HG13	2:B:164:SER:H	1.48	0.75
5:E:18(C):PHE:HA	5:E:18(F):ILE:HG12	1.68	0.75
7:G:217:LYS:HA	7:G:217:LYS:HE3	1.69	0.75
3:C:65:SER:HB2	17:C:274:HOH:O	1.86	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:65:GLU:HG3	2:B:66:LYS:HG3	1.69	0.74
11:Y:143:LYS:HB2	11:Y:146:LEU:CD1	2.16	0.74
9:I:29:ASN:HD21	11:Y:208:ASN:ND2	1.85	0.74
3:C:163:GLN:HA	3:C:163:GLN:HE21	1.53	0.74
3:C:15:PHE:H	4:D:23:GLN:HE22	1.35	0.74
6:T:127:ASN:HD22	6:T:127:ASN:C	1.91	0.74
2:P:65:GLU:HG3	2:P:66:LYS:HG3	1.68	0.73
14:N:136:GLY:HA2	14:2:161:GLN:HE21	1.53	0.73
11:Y:4:LEU:HD12	11:Y:159:ILE:HD11	1.68	0.73
12:L:4:LEU:CD1	12:L:138:LEU:HD21	2.18	0.73
12:Z:114:ASP:HB2	12:Z:118:SER:HB3	1.69	0.73
1:A:86:ARG:HE	7:G:118:ASN:HD21	1.34	0.73
14:N:34:LEU:HD13	14:N:176:VAL:HG23	1.71	0.73
2:B:219:GLU:HG2	2:B:21(E):VAL:H	1.54	0.73
5:S:18(C):PHE:HA	5:S:18(F):ILE:HG12	1.68	0.73
10:J:144:PRO:HG3	11:Y:207:ASN:HD21	1.54	0.73
6:T:127:ASN:HD22	6:T:128:SER:N	1.87	0.73
1:A:177:GLU:HG2	2:B:58:LEU:HD22	1.71	0.73
5:S:207:LEU:HA	5:S:2(E):ASN:ND2	2.04	0.72
5:S:75:GLY:HA3	5:S:221:PHE:CE2	2.24	0.72
11:K:45:MET:HB2	15:3:5:ABN:H5	1.71	0.72
3:C:106:PRO:HG2	3:C:143:PRO:HG3	1.71	0.72
2:P:124:THR:CG2	3:Q:130:ARG:HH21	2.01	0.72
13:1:14(C):ARG:HG3	13:1:14(C):ARG:HH11	1.55	0.72
11:K:208:ASN:HB3	17:K:776:HOH:O	1.89	0.72
2:B:219:GLU:HG2	2:B:21(E):VAL:N	2.05	0.72
14:N:161:GLN:NE2	14:2:136:GLY:HA2	2.05	0.72
14:N:136:GLY:HA2	14:2:161:GLN:NE2	2.04	0.72
6:F:127:ASN:HD22	6:F:127:ASN:C	1.92	0.72
7:G:170:GLN:HE21	7:G:174:THR:HG23	1.55	0.72
4:R:207:LEU:CD2	4:R:233:ILE:HD12	2.20	0.72
9:W:192:ARG:HG3	17:W:201:HOH:O	1.89	0.71
7:G:18(G):GLU:HG2	7:G:188:LYS:HB2	1.72	0.71
2:P:126:HIS:HB3	3:Q:129:VAL:HG12	1.72	0.71
3:C:160:TRP:CE2	4:D:59:LEU:HD23	2.25	0.71
12:Z:4:LEU:CD1	12:Z:138:LEU:HD21	2.20	0.71
11:Y:99:THR:HG22	11:Y:113:VAL:O	1.89	0.71
2:P:219:GLU:HG2	2:P:21(E):VAL:H	1.54	0.71
13:M:14(C):ARG:HH11	13:M:14(C):ARG:HG3	1.55	0.71
7:U:18(G):GLU:HG2	7:U:188:LYS:HB2	1.73	0.71
5:E:207:LEU:HA	5:E:2(E):ASN:ND2	2.06	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:48:LEU:HG	5:E:139:ILE:HD13	1.71	0.71
10:X:90(A):ILE:O	10:X:90(A):ILE:HD13	1.90	0.71
7:U:170:GLN:HE21	7:U:174:THR:HG23	1.56	0.71
2:P:97:GLN:HE22	9:W:64:ASN:HD22	1.39	0.71
10:J:-1:MET:HG2	10:J:1:ASP:N	2.05	0.71
1:A:177:GLU:HG2	2:B:58:LEU:CD2	2.21	0.71
14:N:161:GLN:HE21	14:2:136:GLY:HA2	1.56	0.71
10:J:90(A):ILE:O	10:J:90(A):ILE:HD13	1.90	0.71
4:R:207:LEU:HD21	4:R:233:ILE:HD12	1.71	0.70
5:E:75:GLY:HA3	5:E:221:PHE:CE2	2.26	0.70
5:S:214:ILE:HG13	5:S:215:VAL:N	2.07	0.70
5:E:198:SER:HA	5:E:201:LEU:HG	1.74	0.70
2:P:121:GLN:O	2:P:124:THR:HB	1.89	0.70
12:L:98:HIS:HD2	17:L:199:HOH:O	1.73	0.70
4:R:177:LEU:HD22	5:S:58:LEU:HD13	1.73	0.70
2:B:202:THR:HG22	2:B:204:SER:N	2.04	0.70
6:F:127:ASN:HD22	6:F:128:SER:N	1.90	0.70
3:Q:106:PRO:HG2	3:Q:143:PRO:HG3	1.74	0.70
3:C:163:GLN:NE2	3:C:164:THR:H	1.90	0.69
7:U:227:GLU:HG2	17:U:1255:HOH:O	1.91	0.69
2:B:121:GLN:O	2:B:124:THR:HB	1.92	0.69
10:X:-1:MET:HG2	10:X:1:ASP:N	2.06	0.69
1:O:86:ARG:HH21	7:U:118:ASN:HD22	1.40	0.69
7:G:18(G):GLU:HG2	7:G:188:LYS:CB	2.21	0.69
1:A:130:ARG:HH21	7:G:124:THR:CG2	2.05	0.69
5:S:207:LEU:HA	5:S:2(E):ASN:HD22	1.57	0.69
3:C:106:PRO:HG2	3:C:143:PRO:CG	2.22	0.69
4:D:207:LEU:CD2	4:D:233:ILE:HD12	2.22	0.69
14:2:34:LEU:HD13	14:2:176:VAL:HG23	1.74	0.69
7:U:96:ALA:CA	7:U:107:MET:HE2	2.18	0.69
4:R:121:LEU:HB2	17:R:853:HOH:O	1.92	0.69
5:S:198:SER:HA	5:S:201:LEU:HG	1.75	0.68
6:T:237:GLN:O	6:T:240:ILE:HG22	1.93	0.68
2:P:219:GLU:HG2	2:P:21(E):VAL:N	2.05	0.68
7:U:18(G):GLU:HG2	7:U:188:LYS:CB	2.23	0.68
5:S:132:TYR:O	5:S:153:PRO:HB3	1.93	0.68
3:Q:160:TRP:CE2	4:R:59:LEU:HD23	2.27	0.68
11:Y:4:LEU:HD11	11:Y:15:ALA:HB3	1.74	0.68
3:C:232:TYR:O	3:C:236:ILE:HG13	1.92	0.68
3:Q:106:PRO:HG2	3:Q:143:PRO:CG	2.23	0.68
3:Q:55:THR:HG22	3:Q:56:LEU:HD22	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:177:LEU:HD22	5:E:58:LEU:HD13	1.75	0.68
11:K:99:THR:HG22	11:K:113:VAL:O	1.92	0.68
4:D:207:LEU:HD21	4:D:233:ILE:HD12	1.75	0.68
1:O:97:HIS:HD2	8:V:61:SER:OG	1.76	0.68
5:E:214:ILE:HG13	5:E:215:VAL:N	2.07	0.68
11:K:142:TYR:O	11:K:143:LYS:HD2	1.94	0.68
6:F:237:GLN:O	6:F:240:ILE:HG22	1.94	0.68
2:P:202:THR:HG22	2:P:204:SER:N	2.03	0.68
1:A:20:LYS:HE3	1:A:25:ASP:OD1	1.94	0.68
2:B:126:HIS:HB3	3:C:129:VAL:HG12	1.76	0.67
11:K:4:LEU:HD11	11:K:15:ALA:HB3	1.75	0.67
10:X:32:ASP:OD2	10:X:34:THR:HG22	1.95	0.67
3:Q:232:TYR:O	3:Q:236:ILE:HG13	1.94	0.67
5:E:207:LEU:HA	5:E:2(E):ASN:HD22	1.58	0.67
1:O:86:ARG:HE	7:U:118:ASN:ND2	1.93	0.67
11:K:207:ASN:HD21	10:X:144:PRO:CG	2.08	0.67
11:Y:142:TYR:O	11:Y:143:LYS:HD2	1.94	0.67
13:M:8:TYR:CE2	13:M:148:VAL:HG22	2.30	0.67
9:I:143:GLU:HG3	9:I:146:LEU:HD21	1.77	0.67
4:R:31:ILE:HD13	4:R:135:ALA:HB2	1.76	0.67
9:W:143:GLU:HG3	9:W:146:LEU:HD21	1.77	0.67
9:I:6:MET:HE3	9:I:155:ILE:HA	1.77	0.67
2:B:185:LYS:HE2	2:B:187:ASP:OD1	1.95	0.66
11:K:207:ASN:ND2	10:X:144:PRO:CG	2.58	0.66
10:J:10(B):LYS:HB2	10:J:10(B):LYS:NZ	2.11	0.66
14:2:107:LYS:HG2	14:2:108:GLY:N	2.09	0.66
3:Q:163:GLN:NE2	3:Q:164:THR:H	1.93	0.66
4:D:31:ILE:HD13	4:D:135:ALA:HB2	1.76	0.66
1:O:121:GLN:O	1:O:124:THR:HB	1.96	0.66
9:I:6:MET:HE3	9:I:155:ILE:HD12	1.76	0.66
10:J:32:ASP:OD2	10:J:34:THR:HG22	1.96	0.66
3:C:55:THR:HG22	3:C:56:LEU:HD22	1.78	0.66
7:G:96:ALA:CA	7:G:107:MET:HE2	2.19	0.65
10:X:10(B):LYS:NZ	10:X:10(B):LYS:HB2	2.10	0.65
13:1:8:TYR:CE2	13:1:148:VAL:HG22	2.31	0.65
1:A:121:GLN:O	1:A:124:THR:HB	1.95	0.65
11:K:38:ASN:O	11:K:40:PHE:N	2.30	0.65
14:N:107:LYS:HG2	14:N:108:GLY:N	2.10	0.65
1:O:20:LYS:HE3	1:O:25:ASP:OD1	1.95	0.65
10:J:156:LYS:O	10:J:160:GLN:HG3	1.97	0.65
9:W:6:MET:HE3	9:W:155:ILE:HA	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:1:40:ASN:HD22	13:1:40:ASN:H	1.44	0.65
13:M:40:ASN:H	13:M:40:ASN:HD22	1.44	0.65
2:B:97:GLN:HE22	9:I:64:ASN:HD22	1.43	0.64
5:E:132:TYR:O	5:E:153:PRO:HB3	1.96	0.64
2:B:160:TRP:CE2	2:B:163:ILE:HD13	2.33	0.64
5:E:201:LEU:HD11	5:E:207:LEU:CD2	2.27	0.64
7:G:121:GLN:O	7:G:124:THR:HB	1.97	0.64
11:Y:38:ASN:O	11:Y:40:PHE:N	2.31	0.64
1:A:86:ARG:HH21	7:G:118:ASN:HD22	1.44	0.64
9:I:90:ARG:HD2	17:I:1159:HOH:O	1.96	0.64
2:P:160:TRP:CE2	2:P:163:ILE:HD13	2.33	0.64
5:E:15:PHE:H	6:F:23:GLN:NE2	1.94	0.64
5:S:201:LEU:HD11	5:S:207:LEU:CD2	2.27	0.64
3:Q:185:THR:HG22	3:Q:187:GLU:N	2.12	0.64
10:J:144:PRO:CG	11:Y:207:ASN:HD21	2.11	0.64
3:C:186:VAL:O	3:C:190:VAL:HG23	1.98	0.63
11:K:12:ILE:HG21	11:K:110:ILE:HD11	1.80	0.63
4:R:186:LEU:O	4:R:190:GLU:HG3	1.98	0.63
9:W:6:MET:HE3	9:W:155:ILE:HD12	1.81	0.62
14:2:84:LYS:HG3	14:2:119:VAL:HG22	1.82	0.62
3:Q:186:VAL:O	3:Q:190:VAL:HG23	1.99	0.62
3:Q:190:VAL:O	3:Q:194:VAL:HG23	1.98	0.62
13:1:14(A):VAL:O	13:1:14(A):VAL:HG23	2.00	0.62
10:X:90(A):ILE:HG13	10:X:116:LEU:HD23	1.81	0.62
4:D:186:LEU:O	4:D:190:GLU:HG3	1.97	0.62
6:T:20(B):GLU:HG3	6:T:20(C):LYS:HG3	1.81	0.62
3:Q:195:ARG:CG	3:Q:236:ILE:HD13	2.27	0.62
3:Q:163:GLN:HE21	3:Q:163:GLN:CA	2.12	0.62
4:R:207:LEU:C	4:R:207:LEU:HD23	2.19	0.62
5:E:226:GLY:O	5:E:229:VAL:HG22	2.00	0.62
3:C:175:PHE:O	3:C:179:ASN:HB2	1.99	0.62
3:C:57:LYS:O	3:C:58:LEU:HB2	1.99	0.62
1:A:97:HIS:HD2	8:H:61:SER:OG	1.81	0.62
11:K:208:ASN:HD21	9:W:29:ASN:HD21	1.46	0.62
6:F:20(B):GLU:HG3	6:F:20(C):LYS:HG3	1.81	0.62
10:J:90(A):ILE:HG13	10:J:116:LEU:HD23	1.82	0.61
2:P:185:LYS:HE2	2:P:187:ASP:OD1	1.99	0.61
1:O:179:ARG:HH11	1:O:179:ARG:HB3	1.65	0.61
8:V:126:SER:O	8:V:127:LEU:HD23	2.00	0.61
4:D:12(D):ALA:HA	5:E:129:GLY:HA2	1.83	0.61
5:E:207:LEU:CD2	5:E:207:LEU:H	2.10	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:R:85:ALA:O	4:R:89:ILE:HG12	2.00	0.61
3:Q:175:PHE:O	3:Q:179:ASN:HB2	2.00	0.61
6:F:192:GLN:HE21	6:F:195:LYS:HE3	1.66	0.61
12:Z:96:TYR:CE1	15:4:2:TY5:H49	2.36	0.61
3:C:186:VAL:HG21	3:C:216:LYS:HE2	1.82	0.61
13:1:37:VAL:HG11	13:1:79:ILE:HD13	1.82	0.61
5:S:226:GLY:O	5:S:229:VAL:HG22	2.01	0.61
3:Q:186:VAL:HG21	3:Q:216:LYS:HE2	1.83	0.61
7:G:59:LEU:O	7:G:61:PRO:HD3	2.01	0.61
1:A:179:ARG:HB3	1:A:179:ARG:HH11	1.66	0.61
7:G:233:LEU:O	7:G:236:ILE:HG13	2.01	0.61
12:L:-7:ASN:HD22	12:L:-6:PRO:HD2	1.64	0.61
6:T:109:ILE:HD13	6:T:109:ILE:N	2.16	0.61
11:K:4:LEU:HD12	11:K:159:ILE:CD1	2.31	0.61
3:C:190:VAL:O	3:C:194:VAL:HG23	2.00	0.61
13:M:-4:ILE:HD13	14:N:115:LEU:HB3	1.83	0.61
10:X:156:LYS:O	10:X:160:GLN:HG3	2.00	0.61
8:H:126:SER:O	8:H:127:LEU:HD23	2.00	0.61
11:Y:12:ILE:HG21	11:Y:110:ILE:HD11	1.82	0.60
10:J:168:MET:HE1	10:X:167:PRO:CB	2.31	0.60
3:Q:57:LYS:O	3:Q:58:LEU:HB2	2.01	0.60
3:C:163:GLN:CA	3:C:163:GLN:HE21	2.14	0.60
10:J:144:PRO:CG	11:Y:207:ASN:ND2	2.63	0.60
5:E:38:VAL:HG23	5:E:197:ILE:HD12	1.83	0.60
14:2:18(A):ILE:HD13	14:2:18(B):PHE:N	2.17	0.60
5:E:18(D):ILE:O	5:E:18(D):ILE:HD13	2.01	0.60
10:J:133:TYR:CE1	17:X:876:HOH:O	2.37	0.60
4:D:229:THR:O	4:D:233:ILE:HG12	2.02	0.60
13:M:14(A):VAL:O	13:M:14(A):VAL:HG23	2.01	0.60
14:N:84:LYS:HG3	14:N:119:VAL:HG22	1.82	0.60
10:J:168:MET:HE1	10:X:167:PRO:HB2	1.83	0.60
11:Y:73:ARG:NH2	11:Y:104:TYR:O	2.34	0.60
2:B:112:LEU:C	2:B:112:LEU:HD23	2.22	0.60
14:N:126:ILE:HD13	14:N:126:ILE:H	1.66	0.60
5:S:207:LEU:H	5:S:207:LEU:CD2	2.10	0.60
14:N:18(A):ILE:HD13	14:N:18(B):PHE:N	2.17	0.60
8:H:218:ILE:N	8:H:218:ILE:HD12	2.17	0.60
3:C:195:ARG:CG	3:C:236:ILE:HD13	2.28	0.60
11:K:73:ARG:NH2	11:K:104:TYR:O	2.34	0.60
3:C:163:GLN:HE21	3:C:164:THR:H	1.50	0.60
10:J:112:GLN:NE2	10:J:126:ALA:H	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:233:LEU:O	7:U:236:ILE:HG13	2.01	0.60
4:D:85:ALA:O	4:D:89:ILE:HG12	2.02	0.60
3:C:41:LYS:HG2	3:C:161:SER:O	2.02	0.60
10:X:112:GLN:NE2	10:X:126:ALA:H	2.00	0.60
4:R:229:THR:O	4:R:233:ILE:HG12	2.02	0.59
4:D:207:LEU:HD23	4:D:207:LEU:C	2.21	0.59
14:2:126:ILE:H	14:2:126:ILE:HD13	1.66	0.59
14:N:36:ARG:HG3	14:N:42:TRP:CE2	2.37	0.59
5:S:38:VAL:HG23	5:S:197:ILE:HD12	1.84	0.59
11:Y:4:LEU:HD12	11:Y:159:ILE:CD1	2.32	0.59
5:S:15:PHE:H	6:T:23:GLN:NE2	1.93	0.59
14:2:36:ARG:HG3	14:2:42:TRP:CE2	2.37	0.59
6:T:192:GLN:HE21	6:T:195:LYS:HE3	1.67	0.59
8:V:218:ILE:HD12	8:V:218:ILE:N	2.18	0.59
5:S:18(D):ILE:HD13	5:S:18(D):ILE:O	2.02	0.59
10:X:52:THR:HG22	10:X:53:VAL:N	2.18	0.58
10:J:167:PRO:HB2	10:X:168:MET:HE1	1.85	0.58
10:J:52:THR:HG22	10:J:53:VAL:N	2.18	0.58
7:U:107:MET:CE	7:U:112:LEU:HD13	2.34	0.58
12:L:114:ASP:CB	12:L:118:SER:HB3	2.32	0.58
11:K:174:ASN:ND2	11:K:189:ASN:HD22	2.00	0.58
11:Y:1:THR:OG1	15:4:5:ABN:H2A	2.04	0.58
12:L:96:TYR:CE1	15:3:2:TY5:H49	2.38	0.58
6:F:109:ILE:HG21	6:F:147:HIS:HB2	1.86	0.58
1:A:188:ASP:O	1:A:192:ILE:HG12	2.04	0.58
10:J:167:PRO:CB	10:X:168:MET:HE1	2.34	0.58
14:N:146:MET:HE3	14:N:150:GLU:HB3	1.86	0.58
7:U:121:GLN:O	7:U:124:THR:HB	2.02	0.58
14:N:98:GLY:C	14:N:99:ILE:HD13	2.24	0.58
13:1:-4:ILE:HD13	14:2:115:LEU:HB3	1.86	0.58
12:Z:114:ASP:CB	12:Z:118:SER:HB3	2.33	0.58
11:Y:4:LEU:CD1	11:Y:15:ALA:HB3	2.34	0.57
2:P:185:LYS:HD3	2:P:186:VAL:N	2.19	0.57
14:N:55:ILE:HD11	14:N:95:LEU:HD13	1.86	0.57
1:A:86:ARG:HE	7:G:118:ASN:ND2	1.99	0.57
7:U:59:LEU:O	7:U:61:PRO:HD3	2.04	0.57
4:R:207:LEU:HD21	4:R:233:ILE:CD1	2.33	0.57
14:2:107:LYS:CG	14:2:108:GLY:H	2.14	0.57
3:C:185:THR:HG22	3:C:187:GLU:N	2.14	0.57
2:P:112:LEU:HD23	2:P:112:LEU:C	2.24	0.57
14:2:51:ASP:O	14:2:55:ILE:HD12	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:51:ASP:O	14:N:55:ILE:HD12	2.05	0.57
3:C:46:VAL:O	3:C:215:VAL:HG12	2.05	0.57
12:Z:-7:ASN:HD22	12:Z:-6:PRO:HD2	1.70	0.57
11:K:1:THR:OG1	15:3:5:ABN:H2A	2.04	0.57
10:J:13:ILE:N	10:J:13:ILE:HD12	2.20	0.57
6:F:69:VAL:HG12	17:F:319:HOH:O	2.04	0.57
2:B:185:LYS:HD3	2:B:186:VAL:N	2.19	0.57
3:Q:163:GLN:HE21	3:Q:164:THR:H	1.53	0.56
8:H:3:ILE:HD11	8:H:127:LEU:HB2	1.86	0.56
11:K:143:LYS:HB2	11:K:146:LEU:HD13	1.86	0.56
14:2:55:ILE:HD11	14:2:95:LEU:HD13	1.87	0.56
4:R:45:GLY:HA2	4:R:146:TYR:CE1	2.39	0.56
3:C:241:GLN:C	3:C:243:GLN:H	2.07	0.56
10:J:24:ILE:O	10:X:133:TYR:OH	2.20	0.56
3:C:168:ASN:HB2	3:C:200:VAL:HG11	1.86	0.56
3:Q:168:ASN:HB2	3:Q:200:VAL:HG11	1.85	0.56
9:I:29:ASN:HD21	11:Y:208:ASN:HD21	1.53	0.56
7:U:77:VAL:CG1	7:U:137:THR:HB	2.34	0.56
12:L:148:VAL:O	12:L:152:ILE:HG12	2.05	0.56
3:Q:241:GLN:C	3:Q:243:GLN:H	2.07	0.56
13:1:19:LEU:HD21	13:1:26:LEU:HD22	1.87	0.56
13:M:19:LEU:HD12	13:M:28:PHE:O	2.05	0.56
6:T:198:TYR:HE2	6:T:237:GLN:HE21	1.52	0.56
13:1:19:LEU:HD12	13:1:28:PHE:O	2.06	0.56
13:M:19:LEU:HB2	13:M:170:SER:HB2	1.88	0.56
12:Z:145:TYR:CD1	12:Z:146:LEU:N	2.74	0.56
11:K:10(B):LYS:CD	11:K:10(B):LYS:N	2.63	0.56
4:D:207:LEU:HD21	4:D:233:ILE:CD1	2.35	0.56
13:1:37:VAL:HG11	13:1:79:ILE:CD1	2.36	0.56
12:L:145:TYR:CD1	12:L:146:LEU:N	2.73	0.56
14:2:146:MET:HE3	14:2:150:GLU:HB3	1.88	0.56
14:2:161:GLN:HE22	14:2:165:TRP:HE1	1.54	0.55
9:I:113:PHE:HA	9:I:118:CYS:O	2.05	0.55
5:E:76:LEU:O	5:E:76:LEU:HD23	2.07	0.55
1:O:60:MET:HE1	17:U:400:HOH:O	2.06	0.55
11:Y:143:LYS:HB2	11:Y:146:LEU:HD13	1.86	0.55
11:K:12:ILE:HB	11:K:178:VAL:HB	1.89	0.55
8:V:3:ILE:HD11	8:V:127:LEU:HB2	1.87	0.55
11:K:140:SER:OG	10:X:137:LEU:HD21	2.07	0.55
7:U:172:ILE:HD13	7:U:197:MET:CE	2.37	0.55
14:N:105:ASP:HB2	17:N:775:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:35:THR:HG23	6:T:51:GLU:HB3	1.88	0.55
8:V:34:LEU:HB2	17:V:578:HOH:O	2.06	0.55
13:M:37:VAL:HG11	13:M:79:ILE:HD13	1.88	0.55
4:D:45:GLY:HA2	4:D:146:TYR:CE1	2.41	0.55
6:T:147:HIS:HD2	17:T:282:HOH:O	1.88	0.55
11:Y:12:ILE:HB	11:Y:178:VAL:HB	1.89	0.55
4:D:175:GLU:HB3	4:D:196:ILE:HD13	1.89	0.55
3:Q:46:VAL:O	3:Q:215:VAL:HG12	2.07	0.55
2:P:152:ASN:HB2	2:P:153:PRO:HD2	1.89	0.55
10:J:133:TYR:OH	10:X:24:ILE:O	2.24	0.55
6:F:198:TYR:HE2	6:F:237:GLN:HE21	1.54	0.55
7:G:77:VAL:CG1	7:G:137:THR:HB	2.37	0.55
10:X:13:ILE:N	10:X:13:ILE:HD12	2.22	0.55
14:2:98:GLY:C	14:2:99:ILE:HD13	2.27	0.55
5:E:78:LEU:HD12	5:E:78:LEU:C	2.27	0.55
9:W:178:ILE:HG23	9:W:184:VAL:HG22	1.89	0.55
11:K:4:LEU:CD1	11:K:15:ALA:HB3	2.36	0.55
10:J:10(B):LYS:HB2	10:J:10(B):LYS:HZ2	1.70	0.55
14:N:14:LEU:HD11	14:N:102:ALA:HB3	1.89	0.55
4:D:75:GLY:HA3	4:D:221:PHE:CD2	2.42	0.55
5:S:2(B):THR:H	5:S:2(E):ASN:HD22	1.54	0.55
13:1:148:VAL:HG23	17:1:182:HOH:O	2.07	0.54
6:T:109:ILE:HG21	6:T:147:HIS:HB2	1.89	0.54
13:1:19:LEU:HB2	13:1:170:SER:HB2	1.89	0.54
5:S:76:LEU:O	5:S:76:LEU:HD23	2.07	0.54
1:O:4:MET:SD	1:O:5:THR:N	2.67	0.54
4:D:122:ARG:HG2	4:D:122:ARG:HH11	1.72	0.54
14:2:14:LEU:HD11	14:2:102:ALA:HB3	1.89	0.54
12:L:96:TYR:CD1	15:3:2:TY5:H49	2.42	0.54
3:Q:33:ARG:HB2	3:Q:33:ARG:NH1	2.23	0.54
5:E:2(B):THR:H	5:E:2(E):ASN:HD22	1.54	0.54
3:Q:172:VAL:HG23	3:Q:196:SER:HB2	1.89	0.54
6:T:127:ASN:ND2	6:T:127:ASN:C	2.61	0.54
14:2:84:LYS:HG3	14:2:119:VAL:CG2	2.38	0.54
6:T:187:ARG:HG3	6:T:187:ARG:HH11	1.72	0.54
10:X:52:THR:CG2	10:X:53:VAL:N	2.71	0.54
7:G:172:ILE:HD13	7:G:197:MET:CE	2.37	0.54
6:F:187:ARG:HG3	6:F:187:ARG:HH11	1.72	0.54
9:I:12:VAL:HG23	9:I:178:ILE:HB	1.88	0.54
12:L:123:GLN:HG3	12:L:145:TYR:OH	2.08	0.54
8:V:221:ILE:HD12	9:W:40:HIS:HA	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:V:148:LYS:O	8:V:152:ILE:HG12	2.08	0.54
3:Q:195:ARG:HG3	3:Q:236:ILE:CD1	2.34	0.54
11:Y:31:VAL:HG11	15:4:5:ABN:H3	1.90	0.54
14:N:161:GLN:HE22	14:N:165:TRP:HE1	1.54	0.54
1:O:188:ASP:O	1:O:192:ILE:HG12	2.07	0.54
2:P:121:GLN:HG3	3:Q:83:ALA:HB1	1.89	0.54
12:Z:96:TYR:CD1	15:4:2:TY5:H49	2.43	0.54
2:B:181:LYS:O	2:B:184:MET:HG3	2.08	0.54
10:J:141:HIS:HB2	10:J:154:LEU:HD11	1.90	0.54
17:V:1181:HOH:O	9:W:150:ASP:HA	2.06	0.54
7:G:107:MET:CE	7:G:112:LEU:HD13	2.37	0.54
14:N:176:VAL:HG12	14:N:178:LEU:CD1	2.38	0.54
4:R:162:ALA:HB3	5:S:58:LEU:HD23	1.89	0.54
14:2:176:VAL:HG12	14:2:178:LEU:CD1	2.37	0.54
5:E:31:ILE:HD11	5:E:153:PRO:HG2	1.90	0.54
3:Q:41:LYS:HG2	3:Q:161:SER:O	2.07	0.54
12:Z:99:THR:CG2	17:Z:231:HOH:O	2.56	0.54
4:R:75:GLY:HA3	4:R:221:PHE:CD2	2.44	0.54
1:A:206:PHE:CE1	1:A:210:ILE:HD11	2.43	0.54
11:K:40:PHE:CB	11:K:73:ARG:NH2	2.66	0.53
6:F:35:THR:HG23	6:F:51:GLU:HB3	1.89	0.53
4:R:160:TYR:CE2	5:S:59:SER:HB3	2.43	0.53
11:K:208:ASN:O	9:W:30:LYS:NZ	2.41	0.53
1:O:159:PRO:O	2:P:59:LEU:HD12	2.08	0.53
5:E:73:HIS:HE1	5:E:107:LEU:O	1.92	0.53
9:W:113:PHE:HA	9:W:118:CYS:O	2.07	0.53
7:U:152:ASP:HB2	7:U:153:PRO:CD	2.38	0.53
5:S:78:LEU:HD12	5:S:78:LEU:C	2.29	0.53
3:C:195:ARG:HG3	3:C:236:ILE:CD1	2.33	0.53
11:K:31:VAL:HG11	15:3:5:ABN:H3	1.90	0.53
3:Q:216:LYS:HB2	3:Q:220:ASP:HB3	1.91	0.53
11:K:31:VAL:HG11	15:3:5:ABN:C3	2.39	0.53
6:F:109:ILE:HD13	6:F:109:ILE:N	2.22	0.53
12:Z:148:VAL:O	12:Z:152:ILE:HG12	2.09	0.53
14:2:10(B):LYS:C	14:2:10(B):LYS:HD3	2.29	0.53
10:J:133:TYR:CE2	10:J:166:MET:HG2	2.43	0.53
11:Y:174:ASN:ND2	11:Y:189:ASN:HD22	2.04	0.53
4:D:194:LEU:HG	4:D:233:ILE:HD13	1.91	0.53
4:D:192:LEU:O	4:D:196:ILE:HG13	2.09	0.53
9:W:12:VAL:HG23	9:W:178:ILE:HB	1.90	0.53
5:S:73:HIS:HE1	5:S:107:LEU:O	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:52:THR:CG2	10:J:53:VAL:N	2.70	0.53
4:R:45:GLY:HA2	4:R:146:TYR:CD1	2.43	0.53
9:I:99:PRO:HB2	9:I:113:PHE:CD2	2.43	0.53
13:M:19:LEU:HD21	13:M:26:LEU:HD22	1.90	0.53
7:G:152:ASP:HB2	7:G:153:PRO:CD	2.39	0.53
6:F:173:LYS:O	6:F:177:GLU:HG3	2.09	0.53
11:Y:143:LYS:HB2	11:Y:146:LEU:HD11	1.89	0.53
7:U:198:ILE:HG23	7:U:203:THR:O	2.08	0.53
5:S:160:LEU:HD13	5:S:163:THR:HB	1.91	0.53
5:E:160:LEU:HD13	5:E:163:THR:HB	1.91	0.53
1:A:4:MET:SD	1:A:5:THR:N	2.67	0.53
7:G:198:ILE:HG23	7:G:203:THR:O	2.07	0.53
8:V:175:VAL:HG12	8:V:176:CYS:N	2.24	0.53
3:C:216:LYS:HB2	3:C:220:ASP:HB3	1.90	0.53
12:Z:123:GLN:HG3	12:Z:145:TYR:OH	2.09	0.53
9:I:178:ILE:HG23	9:I:184:VAL:HG22	1.91	0.53
6:T:203:GLU:O	6:T:206:LYS:HD2	2.09	0.53
2:P:215:ILE:HD13	2:P:221:GLN:HG2	1.91	0.53
10:X:141:HIS:HB2	10:X:154:LEU:HD11	1.89	0.53
10:J:42:LEU:HB2	10:J:184:ILE:HD13	1.91	0.53
2:B:51:GLU:OE2	2:B:202:THR:HG23	2.10	0.52
11:Y:31:VAL:HG11	15:4:5:ABN:C3	2.39	0.52
11:Y:45:MET:CB	15:4:5:ABN:H5	2.36	0.52
5:S:52:LYS:HB3	5:S:63:TYR:HB3	1.90	0.52
3:C:33:ARG:HB2	3:C:33:ARG:NH1	2.25	0.52
13:M:41:THR:OG1	13:M:76:PRO:HG3	2.09	0.52
11:K:143:LYS:HB2	11:K:146:LEU:HD11	1.90	0.52
12:L:185:ARG:NH1	17:L:1161:HOH:O	2.35	0.52
14:N:10(B):LYS:HD3	14:N:10(B):LYS:C	2.29	0.52
7:U:107:MET:HE3	7:U:112:LEU:HD13	1.90	0.52
5:E:194:VAL:O	5:E:197:ILE:HG22	2.09	0.52
9:W:99:PRO:HB2	9:W:113:PHE:CD2	2.44	0.52
5:E:207:LEU:HD23	5:E:207:LEU:N	2.17	0.52
2:B:121:GLN:HG3	3:C:83:ALA:HB1	1.92	0.52
11:Y:40:PHE:CB	11:Y:73:ARG:NH2	2.66	0.52
5:S:31:ILE:HD11	5:S:153:PRO:HG2	1.91	0.52
10:J:147:THR:OG1	10:J:150:GLU:HG3	2.10	0.52
7:U:34(A):ASN:HD22	7:U:167:PRO:HG2	1.74	0.52
13:1:149:GLN:NE2	13:1:149:GLN:H	2.07	0.52
3:C:57:LYS:HD2	3:C:58:LEU:N	2.24	0.52
14:N:84:LYS:HG3	14:N:119:VAL:CG2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:169:SER:HA	3:C:172:VAL:CG1	2.40	0.52
2:B:152:ASN:HB2	2:B:153:PRO:HD2	1.91	0.52
8:H:105:ASP:HB2	8:H:10(A):PRO:CD	2.39	0.52
3:Q:173:ARG:O	3:Q:177:GLU:HG3	2.10	0.52
7:G:18(G):GLU:HG2	7:G:188:LYS:HB3	1.90	0.52
11:K:180:GLU:N	17:K:924:HOH:O	2.42	0.52
1:O:206:PHE:CE1	1:O:210:ILE:HD11	2.45	0.52
14:N:34:LEU:CD1	14:N:176:VAL:HG23	2.39	0.51
13:1:40:ASN:HD22	13:1:40:ASN:N	2.05	0.51
3:Q:57:LYS:HD2	3:Q:58:LEU:N	2.25	0.51
3:Q:46:VAL:HB	3:Q:215:VAL:CG1	2.40	0.51
3:C:227:GLU:OE1	3:C:227:GLU:N	2.41	0.51
12:L:40:ASN:HD21	12:L:183:GLY:HA2	1.75	0.51
13:M:197:TRP:CH2	14:2:171:GLY:HA2	2.45	0.51
3:C:52:ARG:HB2	3:C:209:ASN:HA	1.91	0.51
4:R:194:LEU:HG	4:R:233:ILE:HD13	1.92	0.51
2:P:152:ASN:HB2	2:P:153:PRO:CD	2.40	0.51
10:X:18:LYS:HD3	10:X:174:ILE:HG13	1.92	0.51
10:X:133:TYR:CE2	10:X:166:MET:HG2	2.44	0.51
3:C:172:VAL:HG23	3:C:196:SER:HB2	1.92	0.51
2:P:97:GLN:NE2	9:W:64:ASN:HD22	2.05	0.51
9:I:6:MET:CE	9:I:155:ILE:HA	2.41	0.51
11:Y:179:THR:HB	17:Y:812:HOH:O	2.10	0.51
14:2:34:LEU:CD1	14:2:176:VAL:HG23	2.41	0.51
2:P:101:LYS:NZ	10:X:85:GLN:NE2	2.57	0.51
4:R:122:ARG:HH11	4:R:122:ARG:HG2	1.75	0.51
10:J:168:MET:CE	10:X:168:MET:CE	2.89	0.51
3:C:41:LYS:HD3	3:C:161:SER:HA	1.93	0.51
17:T:284:HOH:O	7:U:86:ARG:HD2	2.10	0.51
3:Q:52:ARG:HB2	3:Q:209:ASN:HA	1.90	0.51
3:Q:227:GLU:N	3:Q:227:GLU:OE1	2.43	0.51
3:C:40:VAL:HG23	3:C:189:CYS:SG	2.51	0.51
7:G:107:MET:HE1	7:G:112:LEU:HD13	1.93	0.51
7:U:18(G):GLU:HG2	7:U:188:LYS:HB3	1.93	0.51
12:Z:90:LYS:HD3	12:Z:95:TYR:CE1	2.45	0.51
7:G:96:ALA:HA	7:G:107:MET:CE	2.23	0.51
12:Z:134:ILE:HD11	12:Z:162:ALA:HB2	1.92	0.51
2:B:218:ASN:O	2:B:21(C):ASP:HB2	2.11	0.51
6:T:192:GLN:HE21	6:T:195:LYS:CE	2.24	0.51
6:T:179:LEU:HD11	6:T:192:GLN:HG3	1.92	0.51
8:V:53:GLU:HB2	17:V:1327:HOH:O	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:67:ILE:HG22	4:D:221:PHE:HZ	1.75	0.51
2:B:152:ASN:HB2	2:B:153:PRO:CD	2.41	0.51
4:R:12(D):ALA:HB3	4:R:126:ARG:HD3	1.93	0.51
2:P:27:ALA:O	2:P:31:ILE:HG12	2.11	0.51
11:K:4:LEU:HD13	11:K:15:ALA:O	2.11	0.51
4:R:67:ILE:HG22	4:R:221:PHE:HZ	1.75	0.51
6:T:173:LYS:O	6:T:177:GLU:HG3	2.11	0.51
9:I:27:VAL:HG13	17:J:898:HOH:O	2.10	0.51
3:Q:169:SER:HA	3:Q:172:VAL:CG1	2.41	0.50
14:N:99:ILE:HD13	14:N:99:ILE:N	2.26	0.50
4:D:45:GLY:HA2	4:D:146:TYR:CD1	2.46	0.50
5:E:107:LEU:HD11	5:E:111:ARG:HG2	1.92	0.50
3:Q:40:VAL:HG23	3:Q:189:CYS:SG	2.51	0.50
13:M:17:ASP:HA	13:M:173:PHE:CB	2.41	0.50
5:S:227:GLU:CD	5:S:227:GLU:H	2.13	0.50
1:O:57:PRO:HG2	7:U:177:GLU:HG2	1.92	0.50
13:M:149:GLN:NE2	13:M:149:GLN:H	2.10	0.50
2:P:51:GLU:OE2	2:P:202:THR:HG23	2.11	0.50
14:2:176:VAL:HG12	14:2:178:LEU:HD13	1.94	0.50
4:D:12(D):ALA:HB3	4:D:126:ARG:HD3	1.92	0.50
6:F:179:LEU:HD11	6:F:192:GLN:HG3	1.93	0.50
5:E:52:LYS:HB3	5:E:63:TYR:HB3	1.92	0.50
12:Z:40:ASN:HD21	12:Z:183:GLY:HA2	1.76	0.50
12:L:90:LYS:HD3	12:L:95:TYR:CE1	2.45	0.50
7:G:72:ARG:NH1	7:G:72:ARG:HB2	2.27	0.50
7:U:96:ALA:HA	7:U:107:MET:CE	2.22	0.50
12:Z:93:PHE:N	12:Z:94:PRO:HD3	2.26	0.50
8:H:148:LYS:O	8:H:152:ILE:HG12	2.11	0.50
6:F:192:GLN:HE21	6:F:195:LYS:CE	2.23	0.50
2:P:4:GLY:HA3	5:S:127:TYR:CE1	2.47	0.50
8:H:41:ILE:HD13	8:H:41:ILE:N	2.27	0.50
2:P:218:ASN:O	2:P:21(C):ASP:HB2	2.11	0.50
2:P:21:LEU:HD13	2:P:124:THR:HG23	1.94	0.50
7:G:77:VAL:HG12	7:G:137:THR:HB	1.93	0.50
7:G:34(A):ASN:HD22	7:G:167:PRO:HG2	1.76	0.50
12:L:21:ILE:HD12	12:L:21:ILE:C	2.30	0.50
10:J:18:LYS:HD3	10:J:174:ILE:HG13	1.93	0.50
7:U:77:VAL:HG12	7:U:137:THR:HB	1.92	0.50
9:W:6:MET:CE	9:W:155:ILE:HA	2.41	0.50
13:M:37:VAL:HG11	13:M:79:ILE:CD1	2.42	0.50
3:Q:46:VAL:HG11	3:Q:139:ALA:HB1	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:227:GLU:CD	3:C:227:GLU:H	2.15	0.50
13:1:76:PRO:HD2	13:1:105:GLN:OE1	2.12	0.50
5:E:227:GLU:CD	5:E:227:GLU:H	2.14	0.50
11:K:40:PHE:CB	11:K:73:ARG:HH21	2.18	0.50
10:X:52:THR:HG22	10:X:53:VAL:HG23	1.93	0.50
1:O:33:GLN:HA	1:O:33:GLN:HE21	1.77	0.50
5:S:92:LEU:HD11	5:S:112:ALA:HB1	1.93	0.50
5:E:18(C):PHE:HA	5:E:18(F):ILE:CG1	2.39	0.49
5:S:194:VAL:O	5:S:197:ILE:HG22	2.12	0.49
12:L:93:PHE:N	12:L:94:PRO:HD3	2.27	0.49
2:P:181:LYS:O	2:P:184:MET:HG3	2.11	0.49
3:C:152:GLU:HB2	3:C:153:PRO:HD2	1.94	0.49
13:1:17:ASP:HA	13:1:173:PHE:CB	2.42	0.49
1:O:179:ARG:HB3	1:O:179:ARG:NH1	2.26	0.49
10:J:52:THR:HG22	10:J:53:VAL:H	1.77	0.49
3:C:46:VAL:HB	3:C:215:VAL:CG1	2.41	0.49
12:Z:90:LYS:HD3	12:Z:95:TYR:CZ	2.47	0.49
11:Y:4:LEU:HD13	11:Y:15:ALA:O	2.12	0.49
8:H:105:ASP:HB2	8:H:10(A):PRO:HD2	1.94	0.49
1:A:33:GLN:HA	1:A:33:GLN:HE21	1.77	0.49
17:R:886:HOH:O	12:Z:70:HIS:HE1	1.95	0.49
14:2:134:ILE:HD12	14:2:138:CYS:SG	2.51	0.49
7:U:72:ARG:HB2	7:U:72:ARG:NH1	2.27	0.49
4:R:53:ARG:HG2	4:R:53:ARG:O	2.12	0.49
6:T:95:GLU:CG	6:T:115:ARG:HB3	2.35	0.49
5:S:207:LEU:N	5:S:207:LEU:HD23	2.17	0.49
12:Z:21:ILE:HD12	12:Z:21:ILE:C	2.33	0.49
9:W:84:SER:OG	9:W:119:ILE:HD11	2.11	0.49
6:T:186:ALA:O	6:T:190:VAL:HG23	2.12	0.49
7:G:87:ASN:HD22	7:G:87:ASN:C	2.16	0.49
5:E:12:THR:CG2	5:E:124:THR:HA	2.35	0.49
5:S:107:LEU:HD11	5:S:111:ARG:HG2	1.94	0.49
12:L:90:LYS:HD3	12:L:95:TYR:CZ	2.47	0.49
8:H:175:VAL:HG12	8:H:176:CYS:N	2.26	0.49
10:X:147:THR:OG1	10:X:150:GLU:HG3	2.12	0.49
7:U:118:ASN:O	7:U:122:ILE:HD12	2.12	0.49
7:G:170:GLN:NE2	7:G:174:THR:HG23	2.27	0.49
3:C:226:SER:HB2	3:C:227:GLU:OE1	2.12	0.49
3:Q:227:GLU:H	3:Q:227:GLU:CD	2.15	0.49
13:1:41:THR:OG1	13:1:76:PRO:HG3	2.12	0.49
4:D:112:LEU:C	4:D:112:LEU:HD13	2.33	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:5:ALA:HB2	9:W:14:ILE:CD1	2.42	0.49
14:N:107:LYS:CG	14:N:108:GLY:H	2.14	0.49
6:F:203:GLU:O	6:F:206:LYS:HD2	2.11	0.49
10:J:113:ILE:HA	10:J:118:THR:O	2.13	0.49
1:A:161:LYS:HD3	1:A:180:TRP:CZ3	2.47	0.49
14:2:163:ILE:HG23	14:2:170:GLY:HA2	1.95	0.49
11:K:36:GLU:HG2	11:K:184:TRP:CZ2	2.48	0.49
2:B:78:VAL:HG22	2:B:136:PHE:CE2	2.48	0.49
5:E:92:LEU:HD11	5:E:112:ALA:HB1	1.95	0.49
8:V:41:ILE:HD13	8:V:41:ILE:N	2.27	0.49
9:I:84:SER:OG	9:I:119:ILE:HD11	2.13	0.49
12:L:1:GLY:N	17:L:755:HOH:O	2.45	0.49
2:B:21:LEU:HD13	2:B:124:THR:HG23	1.94	0.48
6:F:127:ASN:ND2	6:F:127:ASN:C	2.61	0.48
9:W:101:VAL:O	9:W:110:ILE:HA	2.13	0.48
6:T:35:THR:CG2	6:T:51:GLU:O	2.60	0.48
11:Y:142:TYR:C	11:Y:143:LYS:HD2	2.34	0.48
11:Y:4:LEU:C	11:Y:4:LEU:HD22	2.33	0.48
11:K:12:ILE:CG2	11:K:110:ILE:HD11	2.42	0.48
10:J:52:THR:HG22	10:J:53:VAL:HG23	1.94	0.48
12:L:134:ILE:HD11	12:L:162:ALA:HB2	1.95	0.48
5:S:136:LEU:HB2	5:S:151:PHE:HB3	1.95	0.48
4:R:185:THR:OG1	4:R:188:GLU:HG3	2.13	0.48
2:P:78:VAL:HG22	2:P:136:PHE:CE2	2.47	0.48
11:K:45:MET:CB	15:3:5:ABN:H5	2.41	0.48
7:G:197:MET:HG2	7:G:205:PHE:CE1	2.49	0.48
3:Q:226:SER:HB2	3:Q:227:GLU:OE1	2.13	0.48
14:2:40:LYS:C	14:2:41:ILE:HD13	2.34	0.48
12:L:79:ALA:O	12:L:83:ILE:HG13	2.13	0.48
1:A:232:ARG:HG3	1:A:232:ARG:HH11	1.77	0.48
11:K:86:LEU:HD13	11:K:86:LEU:C	2.33	0.48
11:Y:10(B):LYS:CD	11:Y:10(B):LYS:N	2.65	0.48
3:C:163:GLN:HE21	3:C:164:THR:N	2.11	0.48
13:M:139:ARG:HH11	8:V:165:ASN:ND2	2.03	0.48
12:L:-7:ASN:HD22	12:L:-6:PRO:CD	2.25	0.48
12:Z:79:ALA:O	12:Z:83:ILE:HG13	2.14	0.48
5:S:231:LYS:HD2	5:S:231:LYS:H	1.77	0.48
3:C:173:ARG:O	3:C:177:GLU:HG3	2.14	0.48
3:Q:163:GLN:HA	3:Q:163:GLN:NE2	2.24	0.48
3:C:201:VAL:HG21	3:C:210:ILE:HD11	1.95	0.48
6:F:186:ALA:O	6:F:190:VAL:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:97:ASN:HD21	12:L:61:ASN:HD21	1.62	0.48
11:K:142:TYR:C	11:K:143:LYS:HD2	2.33	0.48
13:1:14(C):ARG:CG	13:1:14(C):ARG:HH11	2.26	0.48
6:F:53:LEU:HD13	6:F:20(C):LYS:HD2	1.96	0.48
14:N:171:GLY:HA2	13:1:197:TRP:CH2	2.49	0.48
11:K:4:LEU:C	11:K:4:LEU:HD22	2.34	0.48
3:Q:41:LYS:HD3	3:Q:161:SER:HA	1.95	0.48
1:O:161:LYS:HD3	1:O:180:TRP:CZ3	2.49	0.48
5:S:12:THR:CG2	5:S:124:THR:HA	2.36	0.48
7:G:186:TRP:O	7:G:190:VAL:HG23	2.13	0.48
13:M:84:ALA:HA	13:M:113:VAL:HG21	1.96	0.48
5:E:231:LYS:HD2	5:E:231:LYS:H	1.78	0.48
5:S:15:PHE:N	6:T:23:GLN:HE22	1.95	0.48
3:C:163:GLN:HA	3:C:163:GLN:NE2	2.25	0.48
13:M:40:ASN:HD22	13:M:40:ASN:N	2.05	0.48
13:M:76:PRO:HD2	13:M:105:GLN:OE1	2.14	0.48
11:Y:36:GLU:HG2	11:Y:184:TRP:CZ2	2.49	0.48
3:Q:152:GLU:HB2	3:Q:153:PRO:HD2	1.94	0.48
7:G:118:ASN:O	7:G:122:ILE:HD12	2.13	0.47
9:I:30:LYS:NZ	11:Y:208:ASN:O	2.46	0.47
3:Q:160:TRP:CZ2	4:R:59:LEU:HD23	2.49	0.47
9:I:114:ASP:HB2	17:I:851:HOH:O	2.14	0.47
7:U:49:ILE:HD12	7:U:193:ALA:CB	2.44	0.47
7:U:186:TRP:O	7:U:190:VAL:HG23	2.15	0.47
2:P:63:THR:HG22	2:P:63:THR:O	2.14	0.47
4:D:185:THR:OG1	4:D:188:GLU:HG3	2.14	0.47
10:X:90(A):ILE:HG13	10:X:116:LEU:CD2	2.45	0.47
10:X:52:THR:HG22	10:X:53:VAL:H	1.78	0.47
14:2:175:MET:HB2	14:2:187:LEU:HB2	1.95	0.47
13:M:110:LEU:HG	13:M:125:LEU:HD12	1.96	0.47
6:T:72:ARG:HD2	13:1:64:THR:OG1	2.14	0.47
7:U:87:ASN:HD22	7:U:87:ASN:C	2.17	0.47
9:I:1:GLY:HA3	9:I:33:LYS:HE2	1.96	0.47
10:X:10(B):LYS:HB2	10:X:10(B):LYS:HZ2	1.77	0.47
1:A:179:ARG:HB3	1:A:179:ARG:NH1	2.27	0.47
11:Y:12:ILE:CG2	11:Y:110:ILE:HD11	2.44	0.47
4:R:192:LEU:O	4:R:196:ILE:HG13	2.15	0.47
4:D:160:TYR:CE2	5:E:59:SER:HB3	2.50	0.47
10:J:168:MET:CE	10:X:168:MET:HE3	2.44	0.47
8:V:105:ASP:HB2	8:V:10(A):PRO:CD	2.44	0.47
1:O:232:ARG:HH11	1:O:232:ARG:HG3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:176:VAL:HG12	14:N:178:LEU:HD13	1.96	0.47
5:E:2(C):VAL:O	5:E:226:GLY:HA2	2.14	0.47
8:H:34:LEU:HB2	17:H:540:HOH:O	2.13	0.47
5:E:142:ASP:HB2	17:M:885:HOH:O	2.15	0.47
1:A:112:LEU:O	1:A:116:VAL:HG23	2.15	0.47
11:Y:86:LEU:C	11:Y:86:LEU:HD13	2.35	0.47
2:B:63:THR:HG22	2:B:63:THR:O	2.15	0.47
4:R:24:VAL:O	4:R:27:SER:HB3	2.15	0.47
11:Y:195:LEU:O	11:Y:199:VAL:HG23	2.15	0.47
10:X:113:ILE:HA	10:X:118:THR:O	2.15	0.47
1:A:225:THR:OG1	1:A:228:GLU:HG3	2.15	0.47
9:I:101:VAL:O	9:I:110:ILE:HA	2.15	0.47
14:N:40:LYS:O	14:N:41:ILE:HD13	2.15	0.47
12:L:113:PHE:CD1	12:L:113:PHE:N	2.82	0.47
5:S:180:LEU:HA	5:S:18(C):PHE:CE2	2.50	0.47
6:T:53:LEU:HD13	6:T:20(C):LYS:HD2	1.96	0.47
6:F:192:GLN:NE2	6:F:195:LYS:HE3	2.30	0.47
3:C:46:VAL:HG11	3:C:139:ALA:HB1	1.97	0.47
5:E:111:ARG:HG2	5:E:111:ARG:HH11	1.80	0.47
2:B:27:ALA:O	2:B:31:ILE:HG12	2.15	0.47
3:C:182:PRO:O	3:C:184:ALA:N	2.48	0.47
12:L:135:MET:CE	9:W:165:ARG:NH2	2.78	0.47
10:J:133:TYR:CZ	10:J:166:MET:HG2	2.50	0.47
2:B:185:LYS:CD	2:B:187:ASP:H	2.28	0.47
13:1:184:LEU:HD23	13:1:185:THR:N	2.30	0.47
13:1:35:ILE:N	13:1:35:ILE:HD12	2.29	0.47
10:J:137:LEU:HD21	11:Y:140:SER:OG	2.14	0.47
7:U:192:PHE:CD1	7:U:192:PHE:C	2.87	0.47
5:E:28:LEU:HA	5:E:31:ILE:HD12	1.97	0.46
9:W:12:VAL:HG13	9:W:108:PRO:HB3	1.97	0.46
14:N:175:MET:HB2	14:N:187:LEU:HB2	1.96	0.46
1:A:150:GLN:O	1:A:157:TYR:HA	2.14	0.46
6:F:33:ASN:HB2	17:F:1331:HOH:O	2.15	0.46
14:N:163:ILE:HG23	14:N:170:GLY:HA2	1.98	0.46
17:P:462:HOH:O	3:Q:87:ILE:HD11	2.16	0.46
3:Q:149:TYR:CE1	3:Q:159:SER:HB3	2.50	0.46
5:S:18(C):PHE:HA	5:S:18(F):ILE:CG1	2.40	0.46
13:M:14(C):ARG:CG	13:M:14(C):ARG:HH11	2.26	0.46
2:B:49:ALA:HB2	2:B:212:PHE:CE1	2.50	0.46
2:P:160:TRP:CD2	2:P:163:ILE:HD13	2.50	0.46
2:B:141:TYR:CD1	2:B:21(E):VAL:HG21	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:134:VAL:O	5:S:153:PRO:HG3	2.15	0.46
12:L:-7:ASN:ND2	12:L:-5:TYR:H	2.13	0.46
14:2:40:LYS:O	14:2:41:ILE:HD13	2.15	0.46
13:M:35:ILE:N	13:M:35:ILE:HD12	2.30	0.46
3:C:160:TRP:CZ2	4:D:59:LEU:HD23	2.49	0.46
5:E:31:ILE:HD11	5:E:153:PRO:CG	2.45	0.46
8:V:40:LYS:C	8:V:41:ILE:HD13	2.36	0.46
13:1:84:ALA:HA	13:1:113:VAL:HG21	1.97	0.46
14:N:26:ILE:HG13	13:1:165:ARG:C	2.35	0.46
2:B:71:ASN:HA	2:B:71:ASN:HD22	1.53	0.46
8:H:40:LYS:C	8:H:41:ILE:HD13	2.36	0.46
4:D:24:VAL:O	4:D:27:SER:HB3	2.15	0.46
7:G:192:PHE:CD1	7:G:192:PHE:C	2.87	0.46
5:E:15:PHE:HB2	6:F:23:GLN:HE22	1.80	0.46
10:J:90(A):ILE:HG13	10:J:116:LEU:CD2	2.45	0.46
12:Z:-7:ASN:ND2	12:Z:-5:TYR:H	2.14	0.46
7:U:203:THR:HG22	7:U:204:GLU:N	2.31	0.46
1:O:150:GLN:O	1:O:157:TYR:HA	2.16	0.46
11:K:20:ALA:HB2	11:K:31:VAL:HG21	1.97	0.46
5:E:38:VAL:HG12	5:E:39:GLY:N	2.31	0.46
3:Q:182:PRO:O	3:Q:184:ALA:N	2.49	0.46
1:A:177:GLU:HG2	2:B:58:LEU:HD21	1.97	0.46
2:P:141:TYR:CD1	2:P:21(E):VAL:HG21	2.51	0.46
5:S:31:ILE:HD11	5:S:153:PRO:CG	2.46	0.46
5:S:2(C):VAL:O	5:S:226:GLY:HA2	2.16	0.46
6:T:192:GLN:NE2	6:T:195:LYS:HE3	2.30	0.46
1:O:225:THR:OG1	1:O:228:GLU:HG3	2.16	0.46
7:G:105:TYR:OH	8:H:66:HIS:HE1	1.99	0.46
11:Y:38:ASN:OD1	11:Y:38:ASN:C	2.53	0.46
13:1:83:LEU:O	13:1:87:MET:HG2	2.15	0.46
5:S:97:ASN:HD21	12:Z:61:ASN:HD21	1.63	0.46
10:J:168:MET:HE2	10:X:168:MET:HE2	1.98	0.46
10:X:34:THR:HG21	10:X:176:LYS:NZ	2.30	0.46
14:N:126:ILE:HD13	14:N:126:ILE:N	2.32	0.46
14:2:36:ARG:HG3	14:2:42:TRP:CZ2	2.51	0.46
10:J:13:ILE:HG21	10:J:155:LEU:HD12	1.99	0.46
7:G:203:THR:HG22	7:G:204:GLU:N	2.31	0.46
12:L:7:ALA:HB2	12:L:110:VAL:HG23	1.97	0.46
7:G:49:ILE:HD12	7:G:193:ALA:CB	2.46	0.46
2:B:15:PHE:H	3:C:23:GLN:NE2	1.90	0.45
3:C:228:GLU:O	3:C:232:TYR:HD1	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:186:VAL:O	2:B:190:ILE:HG13	2.16	0.45
2:P:186:VAL:O	2:P:190:ILE:HG13	2.15	0.45
14:2:99:ILE:N	14:2:99:ILE:HD13	2.30	0.45
2:B:71:ASN:HB3	2:B:74:ILE:H	1.81	0.45
5:S:41:ARG:NH1	5:S:42:SER:O	2.48	0.45
7:U:17(C):LYS:HE3	7:U:17(C):LYS:HB2	1.78	0.45
7:U:67:ILE:HD12	7:U:211:GLU:CG	2.36	0.45
9:I:12:VAL:CG2	9:I:178:ILE:HB	2.46	0.45
1:O:112:LEU:O	1:O:116:VAL:HG23	2.16	0.45
3:Q:38:VAL:HG22	3:Q:39:GLY:N	2.32	0.45
9:W:1:GLY:HA3	9:W:33:LYS:HE2	1.99	0.45
8:H:24:PRO:HG2	8:H:25:ILE:HD12	1.98	0.45
3:C:38:VAL:HG22	3:C:39:GLY:N	2.31	0.45
12:Z:113:PHE:CD1	12:Z:113:PHE:N	2.84	0.45
11:Y:40:PHE:CB	11:Y:73:ARG:HH21	2.19	0.45
7:G:55:PRO:HG2	7:G:56:ASP:H	1.81	0.45
7:U:38:LEU:HD23	7:U:197:MET:HE3	1.99	0.45
10:X:12:VAL:HG23	10:X:108:PRO:HB2	1.99	0.45
2:B:181:LYS:HG3	2:B:184:MET:HG3	1.99	0.45
2:P:6:ARG:HG2	3:Q:10:ARG:HH21	1.81	0.45
13:I:110:LEU:HG	13:I:125:LEU:HD12	1.98	0.45
10:X:3:ILE:HG22	10:X:100:LEU:CD1	2.47	0.45
9:I:174:VAL:HG21	9:I:186:LYS:HE3	1.98	0.45
5:E:47:VAL:HG22	5:E:214:ILE:HD12	1.97	0.45
8:H:15:ALA:C	8:H:159:ILE:HD11	2.37	0.45
9:I:5:ALA:HB2	9:I:14:ILE:CD1	2.46	0.45
3:C:158:SER:HB2	4:D:59:LEU:HD21	1.98	0.45
3:Q:152:GLU:HB2	3:Q:153:PRO:CD	2.46	0.45
12:L:34:VAL:HG12	12:L:176:LEU:HD22	1.97	0.45
4:D:53:ARG:HG2	4:D:53:ARG:O	2.15	0.45
3:Q:177:GLU:OE2	4:R:57:PRO:HD2	2.17	0.45
3:C:152:GLU:HB2	3:C:153:PRO:CD	2.46	0.45
4:R:175:GLU:HB3	4:R:196:ILE:HD13	1.99	0.45
2:B:81:LEU:HD23	2:B:133:GLY:HA3	1.97	0.45
11:K:195:LEU:O	11:K:199:VAL:HG23	2.17	0.45
2:P:81:LEU:HD23	2:P:133:GLY:HA3	1.97	0.45
6:F:107:ILE:HA	6:F:108:PRO:HD3	1.78	0.45
6:F:72:ARG:HD2	13:M:64:THR:OG1	2.16	0.45
5:E:136:LEU:HB2	5:E:151:PHE:HB3	1.97	0.45
4:D:162:ALA:HB3	5:E:58:LEU:HD23	1.99	0.45
9:W:174:VAL:HG21	9:W:186:LYS:HE3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:8:SER:O	9:I:6:PRO:HD3	2.17	0.45
5:E:82:ALA:HB3	5:E:83:PRO:HD3	1.98	0.45
8:V:25:ILE:HD12	8:V:25:ILE:N	2.32	0.45
5:E:76:LEU:C	5:E:76:LEU:HD23	2.37	0.45
14:N:66:TYR:CD2	14:N:74:PRO:HB3	2.52	0.45
2:P:71:ASN:HB3	2:P:74:ILE:H	1.82	0.45
3:Q:201:VAL:HG21	3:Q:210:ILE:HD11	1.98	0.45
12:Z:34:VAL:HG12	12:Z:176:LEU:HD22	1.98	0.45
12:Z:58:ARG:HH11	12:Z:58:ARG:HG2	1.82	0.45
10:J:133:TYR:OH	10:X:24:ILE:HG13	2.16	0.45
12:L:166:HIS:CD2	12:L:168:GLN:H	2.23	0.45
5:E:180:LEU:HA	5:E:18(C):PHE:CE2	2.52	0.45
13:M:148:VAL:HG23	17:M:502:HOH:O	2.15	0.45
13:M:152:GLU:O	13:M:156:VAL:HG23	2.17	0.45
13:M:83:LEU:O	13:M:87:MET:HG2	2.17	0.45
4:D:17:PRO:HD2	17:D:1171:HOH:O	2.15	0.45
6:F:192:GLN:NE2	6:F:195:LYS:CE	2.80	0.45
12:Z:-7:ASN:HD22	12:Z:-6:PRO:CD	2.29	0.45
10:J:12:VAL:C	10:J:13:ILE:HD12	2.37	0.45
9:I:12:VAL:HG13	9:I:108:PRO:HB3	1.99	0.45
14:N:134:ILE:HD12	14:N:138:CYS:SG	2.57	0.45
8:V:15:ALA:C	8:V:159:ILE:HD11	2.38	0.45
13:M:14(G):ILE:HB	13:M:144:PRO:CD	2.47	0.45
10:J:24:ILE:HG13	10:X:133:TYR:OH	2.17	0.44
10:J:34:THR:HG21	10:J:176:LYS:NZ	2.32	0.44
2:P:6:ARG:HG2	3:Q:10:ARG:NH2	2.32	0.44
8:H:84:LYS:HG3	8:H:85:GLN:N	2.32	0.44
2:B:202:THR:CG2	2:B:204:SER:HB2	2.47	0.44
10:X:133:TYR:CZ	10:X:166:MET:HG2	2.53	0.44
12:Z:166:HIS:CD2	12:Z:168:GLN:H	2.23	0.44
5:S:47:VAL:HG22	5:S:214:ILE:HD12	1.99	0.44
7:U:55:PRO:HG2	7:U:56:ASP:H	1.81	0.44
5:S:111:ARG:HH11	5:S:111:ARG:HG2	1.80	0.44
9:I:5:ALA:HB2	9:I:14:ILE:HD12	1.99	0.44
10:J:143:ARG:HB2	10:J:146:MET:HG3	1.99	0.44
13:M:205:GLY:HA3	13:M:209:GLN:HB3	1.99	0.44
4:D:227:GLU:OE2	4:D:227:GLU:N	2.47	0.44
2:P:202:THR:CG2	2:P:204:SER:HB2	2.48	0.44
5:S:201:LEU:O	5:S:202:ARG:HB2	2.17	0.44
2:B:160:TRP:CD2	2:B:163:ILE:HD13	2.51	0.44
11:K:4:LEU:CD1	11:K:159:ILE:HD11	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Z:114:ASP:HB3	12:Z:118:SER:H	1.82	0.44
13:M:40:ASN:ND2	13:M:40:ASN:H	2.14	0.44
2:P:185:LYS:CD	2:P:187:ASP:H	2.30	0.44
14:N:36:ARG:HG3	14:N:42:TRP:CZ2	2.52	0.44
6:T:192:GLN:NE2	6:T:195:LYS:CE	2.80	0.44
13:1:9:ASP:OD1	13:1:10:ASN:N	2.50	0.44
8:H:63:ILE:HD13	8:H:63:ILE:HA	1.81	0.44
11:K:45:MET:HB3	11:K:52:CYS:HB3	1.99	0.44
10:J:13:ILE:N	10:J:13:ILE:CD1	2.81	0.44
6:T:176:LEU:O	6:T:180:VAL:HG23	2.17	0.44
12:Z:7:ALA:HB2	12:Z:110:VAL:HG23	1.98	0.44
4:D:12:VAL:CG2	4:D:12(A):GLY:HA2	2.48	0.44
2:B:51:GLU:OE2	2:B:209:ARG:NH2	2.47	0.44
3:Q:228:GLU:O	3:Q:232:TYR:HD1	2.00	0.44
14:2:126:ILE:N	14:2:126:ILE:HD13	2.30	0.44
5:S:38:VAL:HG12	5:S:39:GLY:N	2.31	0.44
14:N:40:LYS:C	14:N:41:ILE:HD13	2.38	0.44
9:I:165:ARG:NH2	12:Z:135:MET:CE	2.81	0.44
7:G:158:VAL:HG22	7:G:159:GLY:N	2.32	0.44
7:U:151:THR:HG22	7:U:157:TYR:HB2	1.99	0.44
4:D:161:ASN:HB3	4:D:180:TRP:CE2	2.53	0.44
5:E:15:PHE:HB2	6:F:23:GLN:NE2	2.33	0.44
7:U:197:MET:HG2	7:U:205:PHE:CE1	2.52	0.44
5:S:68:ILE:HB	5:S:76:LEU:CD2	2.48	0.44
4:R:12(D):ALA:HA	5:S:129:GLY:HA2	1.99	0.44
9:W:5:ALA:HB2	9:W:14:ILE:HD12	1.99	0.44
13:1:14(G):ILE:HB	13:1:144:PRO:CD	2.48	0.44
13:M:211:ILE:HD11	17:2:193:HOH:O	2.18	0.44
3:C:76:LEU:HD23	3:C:76:LEU:C	2.38	0.44
10:X:166:MET:HA	10:X:167:PRO:HD3	1.76	0.44
10:J:168:MET:HG2	10:X:168:MET:CE	2.48	0.44
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	2.00	0.44
8:H:25:ILE:N	8:H:25:ILE:HD12	2.32	0.44
8:V:24:PRO:HG2	8:V:25:ILE:HD12	1.99	0.44
14:N:186:ARG:HD3	17:N:933:HOH:O	2.16	0.44
8:H:216:GLU:HG3	9:I:187:ARG:HG2	1.99	0.44
5:S:2(B):THR:OG1	5:S:2(E):ASN:HB3	2.18	0.44
7:U:170:GLN:NE2	7:U:174:THR:HG23	2.27	0.44
13:1:40:ASN:ND2	13:1:40:ASN:H	2.13	0.44
5:E:134:VAL:O	5:E:153:PRO:HG3	2.17	0.44
5:S:227:GLU:N	5:S:227:GLU:CD	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:84:SER:CB	9:W:119:ILE:HD11	2.48	0.44
8:H:221:ILE:HD12	9:I:40:HIS:HA	2.00	0.44
10:J:3:ILE:HG22	10:J:100:LEU:CD1	2.48	0.44
14:2:66:TYR:CD2	14:2:74:PRO:HB3	2.53	0.44
6:T:38:ILE:HG22	6:T:164:ALA:CB	2.48	0.44
11:K:147:SER:O	11:K:148:VAL:C	2.55	0.44
10:J:168:MET:CE	10:X:168:MET:HG2	2.48	0.44
3:C:164:THR:HG21	3:C:172:VAL:HG13	2.00	0.44
7:G:65:SER:HA	7:G:211:GLU:OE2	2.18	0.44
5:S:28:LEU:HA	5:S:31:ILE:HD12	2.00	0.44
13:M:184:LEU:HD23	13:M:185:THR:N	2.32	0.44
4:R:112:LEU:C	4:R:112:LEU:HD13	2.39	0.44
1:O:124:THR:HG22	2:P:130:ARG:NH2	2.10	0.43
11:K:38:ASN:OD1	11:K:38:ASN:C	2.55	0.43
7:G:87:ASN:ND2	7:G:87:ASN:C	2.72	0.43
6:T:136:THR:O	6:T:150:MET:HA	2.18	0.43
7:G:151:THR:HG22	7:G:157:TYR:HB2	1.99	0.43
9:I:28:SER:HB2	10:J:120:VAL:HG21	2.00	0.43
8:H:116:HIS:HE1	17:H:762:HOH:O	2.00	0.43
1:A:69:LEU:HD23	1:A:69:LEU:C	2.38	0.43
13:M:45:ILE:HG12	13:M:99:ILE:HG12	2.00	0.43
5:E:201:LEU:O	5:E:202:ARG:HB2	2.18	0.43
2:B:97:GLN:NE2	9:I:64:ASN:HD22	2.14	0.43
6:F:176:LEU:O	6:F:180:VAL:HG23	2.17	0.43
6:F:212:ILE:HG22	6:F:213:SER:N	2.34	0.43
14:N:161:GLN:NE2	14:N:165:TRP:HE1	2.16	0.43
10:J:12:VAL:HG23	10:J:108:PRO:HB2	2.00	0.43
4:R:12:VAL:CG2	4:R:12(A):GLY:HA2	2.48	0.43
4:R:86:ARG:HD3	4:R:86:ARG:HA	1.87	0.43
11:Y:45:MET:HB3	11:Y:52:CYS:HB3	2.00	0.43
11:Y:4:LEU:CD1	11:Y:159:ILE:HD11	2.42	0.43
14:N:14:LEU:O	14:N:175:MET:HA	2.18	0.43
1:O:100:TYR:CG	1:O:107:PRO:HB3	2.53	0.43
4:R:161:ASN:HB3	4:R:180:TRP:CE2	2.54	0.43
5:E:15:PHE:N	6:F:23:GLN:HE22	1.97	0.43
14:2:14:LEU:O	14:2:175:MET:HA	2.18	0.43
17:S:656:HOH:O	6:T:12:ASN:HB2	2.18	0.43
4:R:90:GLU:OE1	11:Y:69:ARG:HD2	2.18	0.43
3:Q:163:GLN:HE21	3:Q:164:THR:N	2.14	0.43
5:S:76:LEU:HA	5:S:137:LEU:O	2.19	0.43
12:Z:99:THR:HG22	17:Z:231:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:69:LYS:HG3	2:P:221:GLN:OE1	2.19	0.43
7:U:34(A):ASN:HA	7:U:167:PRO:HG2	2.01	0.43
6:T:212:ILE:HG22	6:T:213:SER:N	2.34	0.43
2:P:121:GLN:CG	3:Q:83:ALA:HB1	2.49	0.43
2:P:101:LYS:HZ1	10:X:85:GLN:NE2	2.16	0.43
8:V:105:ASP:HB2	8:V:10(A):PRO:HD2	1.99	0.43
10:X:17:SER:HB2	10:X:170:PHE:HB2	2.00	0.43
11:Y:67:GLU:HG2	11:Y:73:ARG:HA	2.01	0.43
5:E:227:GLU:CD	5:E:227:GLU:N	2.71	0.43
10:X:146:MET:HE3	10:X:150:GLU:HB3	2.01	0.43
14:2:38:HIS:HB3	14:2:41:ILE:HG12	2.00	0.43
14:N:38:HIS:HB3	14:N:41:ILE:HG12	1.99	0.43
13:1:35:ILE:HA	13:1:36:PRO:HD3	1.86	0.43
5:E:41:ARG:NH1	5:E:42:SER:O	2.50	0.43
2:B:6:ARG:HB2	5:E:127:TYR:OH	2.18	0.43
13:M:202:ASP:O	13:M:204:LYS:HD3	2.18	0.43
3:C:35:THR:HB	3:C:51:GLU:HG3	2.00	0.43
6:T:35:THR:CG2	6:T:36:THR:N	2.82	0.43
1:A:177:GLU:CG	2:B:58:LEU:CD2	2.94	0.43
3:C:161:SER:HB3	3:C:180:TYR:CE1	2.54	0.43
11:Y:5:ALA:HA	11:Y:13:ILE:O	2.18	0.43
14:N:104:TYR:OH	14:N:180:ALA:HB2	2.19	0.43
10:J:17:SER:HB2	10:J:170:PHE:HB2	2.01	0.43
13:1:205:GLY:HA3	13:1:209:GLN:HB3	2.00	0.43
7:G:17(D):SER:O	7:G:17(E):LYS:HB2	2.19	0.43
3:C:149:TYR:CE1	3:C:159:SER:HB3	2.54	0.43
3:Q:79:SER:OG	3:Q:165:ILE:HG13	2.19	0.43
4:R:227:GLU:OE2	4:R:227:GLU:N	2.48	0.43
5:E:214:ILE:HG13	5:E:215:VAL:H	1.81	0.42
5:E:31:ILE:HD11	5:E:153:PRO:CD	2.49	0.42
12:Z:-2:ASN:HA	12:Z:21:ILE:O	2.19	0.42
14:N:26:ILE:HG13	13:1:165:ARG:O	2.19	0.42
9:I:28:SER:CB	10:J:120:VAL:HG21	2.49	0.42
13:1:202:ASP:O	13:1:204:LYS:HD3	2.19	0.42
2:B:90:ASN:O	2:B:94:ILE:HG12	2.18	0.42
1:O:233:LEU:O	1:O:236:LEU:HB2	2.19	0.42
13:M:9:ASP:OD1	13:M:10:ASN:N	2.51	0.42
5:S:179:THR:HG22	5:S:179:THR:O	2.18	0.42
2:P:202:THR:HG21	2:P:204:SER:HB2	2.01	0.42
9:I:155:ILE:HG23	9:I:156:SER:N	2.34	0.42
13:1:40:ASN:ND2	13:1:40:ASN:N	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:76:LEU:HD23	5:S:76:LEU:C	2.39	0.42
7:U:87:ASN:ND2	7:U:87:ASN:C	2.72	0.42
8:H:159:ILE:HG22	8:H:163:ILE:HD12	2.00	0.42
13:1:45:ILE:HG12	13:1:99:ILE:HG12	2.01	0.42
1:A:186:LEU:O	1:A:190:ILE:HG13	2.19	0.42
1:A:100:TYR:CG	1:A:107:PRO:HB3	2.53	0.42
11:Y:147:SER:O	11:Y:148:VAL:C	2.57	0.42
7:U:65:SER:HA	7:U:211:GLU:OE2	2.19	0.42
5:E:2(B):THR:OG1	5:E:2(E):ASN:HB3	2.20	0.42
5:S:31:ILE:HD11	5:S:153:PRO:CD	2.49	0.42
11:K:99:THR:CG2	11:K:113:VAL:HB	2.50	0.42
11:K:36:GLU:O	11:K:37:ILE:C	2.57	0.42
4:D:170:GLU:N	4:D:170:GLU:OE1	2.49	0.42
6:F:43:ASN:N	6:F:43:ASN:HD22	2.17	0.42
9:W:6:MET:HB3	9:W:151:LEU:HD11	2.00	0.42
12:Z:99:THR:HG23	17:Z:231:HOH:O	2.18	0.42
12:Z:90:LYS:HE3	12:Z:93:PHE:O	2.20	0.42
7:U:225:SER:O	7:U:229:ILE:HG13	2.19	0.42
9:W:55:LEU:CD1	9:W:97:VAL:HG21	2.50	0.42
3:Q:168:ASN:O	3:Q:172:VAL:HG12	2.20	0.42
1:A:169:SER:O	1:A:173:LYS:HG3	2.19	0.42
9:I:6:MET:HB3	9:I:151:LEU:HD11	2.00	0.42
9:W:12:VAL:CG2	9:W:178:ILE:HB	2.49	0.42
8:V:152:ILE:HD11	8:V:177:VAL:CG2	2.49	0.42
12:Z:40:ASN:HA	12:Z:40:ASN:HD22	1.69	0.42
10:X:143:ARG:HB2	10:X:146:MET:HG3	2.00	0.42
12:L:135:MET:HE3	9:W:165:ARG:NH2	2.33	0.42
2:B:6:ARG:HG3	2:B:6:ARG:HH11	1.84	0.42
6:F:38:ILE:HG22	6:F:164:ALA:CB	2.50	0.42
10:X:42:LEU:HB2	10:X:184:ILE:HD13	2.01	0.42
10:J:63:ILE:HD11	10:J:79:VAL:HG13	2.00	0.42
17:E:1080:HOH:O	12:L:64:LYS:HE3	2.19	0.42
5:E:179:THR:O	5:E:179:THR:HG22	2.19	0.42
14:2:20:THR:OG1	14:2:28:ASN:HB3	2.20	0.42
6:F:35:THR:CG2	6:F:51:GLU:O	2.60	0.42
14:2:161:GLN:NE2	14:2:165:TRP:HE1	2.15	0.42
1:O:29:THR:O	1:O:33:GLN:HG2	2.20	0.42
2:P:181:LYS:HG3	2:P:184:MET:HG3	2.00	0.42
11:Y:35:ILE:HD11	11:Y:37:ILE:HD13	2.02	0.42
6:T:82:ILE:HB	6:T:83:PRO:HD3	2.01	0.42
12:L:76:ILE:HG23	12:L:77:ASN:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:136:THR:O	6:F:150:MET:HA	2.20	0.42
1:A:38:LEU:HD12	1:A:38:LEU:C	2.40	0.42
1:O:38:LEU:HD12	1:O:38:LEU:C	2.40	0.42
2:B:202:THR:HG21	2:B:204:SER:HB2	2.01	0.42
9:W:119:ILE:N	9:W:119:ILE:HD12	2.34	0.42
9:I:14:ILE:HG13	9:I:34:ILE:HD13	2.00	0.42
10:J:63:ILE:CD1	10:J:79:VAL:HG13	2.49	0.42
4:R:170:GLU:OE1	4:R:170:GLU:N	2.48	0.42
1:O:214:ILE:C	1:O:215:ILE:HD13	2.40	0.42
2:P:49:ALA:HB2	2:P:212:PHE:CE1	2.54	0.42
7:U:29:LYS:HD2	7:U:29:LYS:HA	1.85	0.42
12:L:114:ASP:HB3	12:L:118:SER:H	1.84	0.42
10:X:112:GLN:HE22	10:X:126:ALA:H	1.66	0.42
11:Y:36:GLU:O	11:Y:37:ILE:C	2.57	0.42
7:U:49:ILE:HD12	7:U:193:ALA:HB1	2.02	0.42
9:W:19:ARG:HB2	9:W:171:TRP:HB2	2.02	0.42
9:I:2:ILE:HG21	9:I:130:ALA:HB3	2.01	0.42
2:B:150:THR:O	2:B:157:TYR:HA	2.20	0.42
8:V:84:LYS:HG3	8:V:85:GLN:N	2.34	0.42
1:O:69:LEU:HD23	1:O:69:LEU:C	2.40	0.42
6:T:43:ASN:HD22	6:T:43:ASN:N	2.18	0.42
7:U:107:MET:HE1	7:U:112:LEU:HD13	2.00	0.42
5:E:76:LEU:HA	5:E:137:LEU:O	2.19	0.42
3:Q:161:SER:HB3	3:Q:180:TYR:CE1	2.55	0.42
7:G:34(A):ASN:HA	7:G:167:PRO:HG2	2.02	0.42
5:S:82:ALA:HB3	5:S:83:PRO:HD3	2.01	0.42
5:E:54:ASN:ND2	5:E:56:ASP:O	2.53	0.42
11:K:44:THR:OG1	11:K:100:MET:HB2	2.19	0.42
12:Z:8:GLY:HA3	12:Z:11:PHE:CE2	2.55	0.42
11:K:5:ALA:HA	11:K:13:ILE:O	2.20	0.42
2:B:224:PHE:HD2	2:B:224:PHE:H	1.67	0.42
8:H:165:ASN:ND2	13:I:139:ARG:HH11	2.08	0.42
5:S:214:ILE:HG13	5:S:215:VAL:H	1.83	0.42
9:I:107:LYS:HA	9:I:108:PRO:HD3	1.86	0.42
8:V:175:VAL:CG1	8:V:176:CYS:N	2.83	0.42
3:Q:159:SER:HB2	17:Q:1140:HOH:O	2.20	0.42
1:A:233:LEU:O	1:A:236:LEU:HB2	2.20	0.42
5:E:4:PHE:CG	5:E:5:ARG:N	2.88	0.42
8:V:147:THR:OG1	8:V:150:GLU:HG3	2.20	0.42
7:G:31:THR:HG21	7:G:135:ILE:HG13	2.02	0.42
3:Q:164:THR:HG21	3:Q:172:VAL:HG13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:97:HIS:CD2	8:V:61:SER:OG	2.63	0.41
13:M:40:ASN:ND2	13:M:40:ASN:N	2.67	0.41
10:J:112:GLN:HE22	10:J:126:ALA:H	1.66	0.41
9:I:87:LEU:HD11	9:I:99:PRO:HG2	2.01	0.41
10:X:12:VAL:C	10:X:13:ILE:HD12	2.41	0.41
3:Q:35:THR:HB	3:Q:51:GLU:HG3	2.02	0.41
8:V:216:GLU:HG3	9:W:187:ARG:HG2	2.01	0.41
8:H:22:GLN:HG3	8:H:27:ALA:HB2	2.02	0.41
11:Y:44:THR:OG1	11:Y:100:MET:HB2	2.20	0.41
2:P:6:ARG:HG3	2:P:6:ARG:HH11	1.85	0.41
8:H:41:ILE:N	8:H:41:ILE:CD1	2.83	0.41
12:L:-2:ASN:HA	12:L:21:ILE:O	2.19	0.41
10:J:18:LYS:CG	10:J:174:ILE:HG13	2.49	0.41
2:P:78:VAL:HG22	2:P:136:PHE:HE2	1.85	0.41
2:B:6:ARG:HG2	3:C:10:ARG:HH21	1.85	0.41
11:Y:191:ASP:OD2	11:Y:193:GLY:N	2.53	0.41
2:B:69:LYS:HG3	2:B:221:GLN:OE1	2.20	0.41
3:Q:76:LEU:HD23	3:Q:76:LEU:C	2.40	0.41
5:E:138:ILE:N	5:E:138:ILE:HD12	2.36	0.41
11:Y:10(A):ARG:HH11	11:Y:10(A):ARG:HG2	1.85	0.41
3:Q:33:ARG:HH11	3:Q:33:ARG:CB	2.33	0.41
10:X:18:LYS:CG	10:X:174:ILE:HG13	2.51	0.41
11:Y:50:ALA:CB	12:Z:116:VAL:HG23	2.50	0.41
13:1:152:GLU:O	13:1:156:VAL:HG23	2.20	0.41
1:O:186:LEU:O	1:O:190:ILE:HG13	2.20	0.41
13:M:165:ARG:C	14:2:26:ILE:HG13	2.41	0.41
4:D:86:ARG:HD3	4:D:86:ARG:HA	1.87	0.41
11:K:67:GLU:HG2	11:K:73:ARG:HA	2.01	0.41
6:F:35:THR:CG2	6:F:36:THR:N	2.81	0.41
1:O:130:ARG:NH2	7:U:124:THR:HG22	2.23	0.41
2:B:185:LYS:HD3	2:B:187:ASP:H	1.85	0.41
7:U:82:ILE:CG2	7:U:83:PRO:HD3	2.50	0.41
6:T:28:VAL:O	6:T:32:GLU:HG3	2.19	0.41
2:P:146:TYR:OH	2:P:21(A):LYS:HB2	2.19	0.41
2:P:51:GLU:OE2	2:P:209:ARG:NH2	2.48	0.41
1:A:173:LYS:O	1:A:177:GLU:HG3	2.20	0.41
7:G:72:ARG:HB2	7:G:72:ARG:HH11	1.85	0.41
5:E:97:ASN:ND2	12:L:61:ASN:HD21	2.18	0.41
14:N:19:ARG:NE	14:N:26:ILE:HD13	2.35	0.41
2:P:71:ASN:HB3	2:P:73:LYS:H	1.86	0.41
4:R:170:GLU:HG2	4:R:171:GLY:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:2:ILE:HG21	9:W:130:ALA:HB3	2.03	0.41
10:X:190:PHE:C	10:X:192:ALA:H	2.24	0.41
6:F:120:VAL:HG21	6:F:151:LEU:HD21	2.02	0.41
3:Q:125:GLN:HG3	3:Q:125:GLN:O	2.20	0.41
10:J:166:MET:HA	10:J:167:PRO:HD3	1.76	0.41
14:2:106:ASN:O	14:2:107:LYS:HB3	2.21	0.41
3:C:100:ARG:NH1	3:C:106:PRO:HB3	2.35	0.41
4:R:68:VAL:HG21	4:R:89:ILE:HD12	2.02	0.41
7:G:56:ASP:HB3	7:G:59:LEU:HG	2.03	0.41
1:A:29:THR:O	1:A:33:GLN:HG2	2.21	0.41
13:M:179:ASP:HB3	13:M:18(A):THR:OG1	2.19	0.41
9:W:93:GLY:N	9:W:94:PRO:CD	2.83	0.41
4:D:215:ILE:O	4:D:215:ILE:HD13	2.20	0.41
13:M:-4:ILE:HD12	14:N:116:GLY:HA2	2.02	0.41
9:I:119:ILE:HD12	9:I:119:ILE:N	2.36	0.41
9:I:84:SER:CB	9:I:119:ILE:HD11	2.50	0.41
2:B:224:PHE:CD2	2:B:224:PHE:N	2.89	0.41
7:U:158:VAL:HG22	7:U:159:GLY:N	2.35	0.41
1:O:169:SER:O	1:O:173:LYS:HG3	2.21	0.41
6:T:107:ILE:HA	6:T:108:PRO:HD3	1.76	0.41
10:J:168:MET:HG2	10:X:168:MET:HE3	2.02	0.41
3:C:175:PHE:CZ	3:C:195:ARG:HB3	2.55	0.41
3:C:163:GLN:CA	3:C:163:GLN:NE2	2.83	0.41
12:L:33:LYS:HD2	12:L:46:ASN:ND2	2.25	0.41
2:P:97:GLN:NE2	17:P:299:HOH:O	2.50	0.41
13:1:113:VAL:HA	13:1:118:VAL:O	2.21	0.41
10:X:3:ILE:HD13	10:X:3:ILE:HA	1.94	0.41
11:K:13:ILE:HD12	11:K:152:LEU:HD23	2.02	0.41
1:O:117:ALA:HB1	1:O:155:GLY:O	2.20	0.41
5:S:4:PHE:CG	5:S:5:ARG:N	2.88	0.41
8:V:22:GLN:HG3	8:V:27:ALA:HB2	2.02	0.41
14:2:104:TYR:OH	14:2:180:ALA:HB2	2.20	0.41
11:K:10(A):ARG:HB3	11:K:10(B):LYS:HE3	2.02	0.41
3:C:168:ASN:O	3:C:172:VAL:HG12	2.21	0.41
9:W:155:ILE:HG23	9:W:156:SER:N	2.35	0.41
8:H:152:ILE:HD11	8:H:177:VAL:CG2	2.51	0.41
10:J:44:SER:OG	10:J:100:LEU:HB2	2.21	0.41
14:2:112:THR:HG22	14:2:120:HIS:HB2	2.03	0.41
12:L:8:GLY:HA3	12:L:11:PHE:CE2	2.56	0.41
2:B:146:TYR:OH	2:B:21(A):LYS:HB2	2.21	0.41
9:I:19:ARG:HB2	9:I:171:TRP:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:196:VAL:HG23	17:H:520:HOH:O	2.20	0.41
10:X:161:GLU:OE2	10:X:161:GLU:HA	2.21	0.41
7:G:38:LEU:C	7:G:38:LEU:HD12	2.42	0.41
10:X:90(B):ARG:HG2	10:X:90(B):ARG:HH11	1.85	0.41
4:R:12(F):GLY:O	4:R:12(G):GLU:HB2	2.20	0.41
8:V:112:SER:HB3	8:V:125:LEU:HD13	2.03	0.41
2:P:222:LYS:NZ	2:P:228:GLU:OE2	2.53	0.41
7:U:56:ASP:HB3	7:U:59:LEU:HG	2.02	0.41
3:Q:241:GLN:C	3:Q:243:GLN:N	2.74	0.41
17:B:565:HOH:O	3:C:33:ARG:HD2	2.20	0.41
6:T:38:ILE:HG22	6:T:164:ALA:HB2	2.03	0.41
1:A:117:ALA:HB1	1:A:155:GLY:O	2.20	0.41
9:W:181:LYS:HE3	9:W:181:LYS:HB3	1.93	0.41
11:K:37:ILE:HB	11:K:41:LEU:HB3	2.03	0.40
1:O:136:LEU:O	1:O:150:GLN:HA	2.22	0.40
4:R:12(G):GLU:HG2	4:R:125:GLU:H	1.86	0.40
6:T:120:VAL:HG21	6:T:151:LEU:HD21	2.02	0.40
8:H:147:THR:OG1	8:H:150:GLU:HG3	2.21	0.40
13:M:80:PHE:CE1	13:M:111:ARG:HD3	2.56	0.40
12:Z:76:ILE:HG23	12:Z:77:ASN:N	2.35	0.40
2:P:224:PHE:H	2:P:224:PHE:HD2	1.67	0.40
3:Q:100:ARG:NH1	3:Q:106:PRO:HB3	2.35	0.40
3:Q:215:VAL:HG23	3:Q:221:ILE:HG13	2.03	0.40
2:P:224:PHE:N	2:P:224:PHE:CD2	2.89	0.40
6:F:103:TYR:O	6:F:104:LYS:HB3	2.22	0.40
7:G:232:ARG:NE	7:G:232:ARG:HA	2.36	0.40
11:Y:105:THR:HB	11:Y:10(B):LYS:CD	2.51	0.40
10:J:24:ILE:CG1	10:X:133:TYR:OH	2.69	0.40
3:Q:175:PHE:CZ	3:Q:195:ARG:HB3	2.56	0.40
3:C:168:ASN:CB	3:C:200:VAL:HG11	2.51	0.40
3:Q:163:GLN:NE2	3:Q:163:GLN:CA	2.82	0.40
3:C:158:SER:CB	4:D:59:LEU:HD21	2.52	0.40
4:D:59:LEU:C	4:D:59:LEU:HD13	2.41	0.40
4:D:177:LEU:CD2	5:E:58:LEU:HD13	2.48	0.40
3:Q:58:LEU:HD12	3:Q:58:LEU:HA	1.91	0.40
5:E:68:ILE:HB	5:E:76:LEU:CD2	2.50	0.40
3:C:33:ARG:CB	3:C:33:ARG:HH11	2.34	0.40
8:V:159:ILE:HG22	8:V:163:ILE:HD12	2.03	0.40
7:U:82:ILE:HG22	7:U:83:PRO:HD3	2.03	0.40
6:T:114:ASP:O	6:T:118:GLN:HG2	2.21	0.40
8:H:200:LYS:HE3	9:I:140:SER:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:28:SER:CB	10:X:120:VAL:HG21	2.51	0.40
8:H:112:SER:HB3	8:H:125:LEU:HD13	2.02	0.40
5:S:138:ILE:HD12	5:S:138:ILE:N	2.36	0.40
7:G:29:LYS:HD2	7:G:29:LYS:HA	1.85	0.40
11:K:10(A):ARG:HG2	11:K:10(A):ARG:HH11	1.86	0.40
3:Q:225:SER:OG	3:Q:228:GLU:HG3	2.22	0.40
11:K:208:ASN:HD21	9:W:29:ASN:ND2	2.17	0.40
2:B:37:ALA:O	2:B:164:SER:HA	2.22	0.40
10:X:137:LEU:HD23	10:X:137:LEU:HA	1.94	0.40
12:L:90:LYS:HE3	12:L:93:PHE:O	2.22	0.40
7:U:72:ARG:HB2	7:U:72:ARG:HH11	1.85	0.40
11:Y:37:ILE:HB	11:Y:41:LEU:HB3	2.03	0.40
2:P:21(A):LYS:O	2:P:21(B):GLY:C	2.60	0.40
9:W:28:SER:HB2	10:X:120:VAL:HG21	2.04	0.40
11:K:16:VAL:HG21	11:K:34:VAL:HG23	2.03	0.40
9:I:93:GLY:N	9:I:94:PRO:CD	2.84	0.40
6:F:40:ILE:HD12	6:F:193:ALA:HB2	2.02	0.40
14:N:20:THR:OG1	14:N:28:ASN:HB3	2.21	0.40
7:U:35:ILE:HD11	17:U:1201:HOH:O	2.21	0.40
1:O:137:LEU:HA	1:O:137:LEU:HD23	1.91	0.40
11:Y:10(A):ARG:HB3	11:Y:10(B):LYS:HE3	2.04	0.40
3:Q:168:ASN:CB	3:Q:200:VAL:HG11	2.51	0.40
3:C:241:GLN:C	3:C:243:GLN:N	2.74	0.40
3:C:206:GLY:HA3	3:C:209:ASN:HB2	2.04	0.40
2:P:6:ARG:HB2	5:S:127:TYR:OH	2.22	0.40
2:P:71:ASN:HA	2:P:71:ASN:HD22	1.53	0.40
9:I:165:ARG:NH2	12:Z:135:MET:HE3	2.36	0.40
1:O:26:TYR:CD1	7:U:17:PRO:HA	2.56	0.40
1:A:111:LEU:HA	1:A:111:LEU:HD23	1.85	0.40
10:J:26:VAL:HG23	10:X:165:ARG: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%)	236 (95%)	10 (4%)	2 (1%)	24	35
1	O	248/250 (99%)	236 (95%)	10 (4%)	2 (1%)	24	35
2	B	242/258 (94%)	222 (92%)	16 (7%)	4 (2%)	11	14
2	P	242/258 (94%)	224 (93%)	14 (6%)	4 (2%)	11	14
3	C	239/254 (94%)	224 (94%)	9 (4%)	6 (2%)	7	7
3	Q	239/254 (94%)	222 (93%)	11 (5%)	6 (2%)	7	7
4	D	240/260 (92%)	228 (95%)	8 (3%)	4 (2%)	11	14
4	R	240/260 (92%)	228 (95%)	8 (3%)	4 (2%)	11	14
5	E	231/234 (99%)	213 (92%)	15 (6%)	3 (1%)	15	21
5	S	231/234 (99%)	213 (92%)	15 (6%)	3 (1%)	15	21
6	F	242/288 (84%)	234 (97%)	7 (3%)	1 (0%)	39	56
6	T	242/288 (84%)	233 (96%)	8 (3%)	1 (0%)	39	56
7	G	241/252 (96%)	232 (96%)	9 (4%)	0	100	100
7	U	241/252 (96%)	232 (96%)	9 (4%)	0	100	100
8	H	220/261 (84%)	209 (95%)	11 (5%)	0	100	100
8	V	220/261 (84%)	210 (96%)	10 (4%)	0	100	100
9	I	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
9	W	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
10	J	196/198 (99%)	187 (95%)	6 (3%)	3 (2%)	13	17
10	X	196/198 (99%)	187 (95%)	6 (3%)	3 (2%)	13	17
11	K	210/287 (73%)	204 (97%)	5 (2%)	1 (0%)	34	48
11	Y	210/287 (73%)	204 (97%)	5 (2%)	1 (0%)	34	48
12	L	220/241 (91%)	214 (97%)	6 (3%)	0	100	100
12	Z	220/241 (91%)	214 (97%)	6 (3%)	0	100	100
13	1	231/266 (87%)	220 (95%)	10 (4%)	1 (0%)	39	56
13	M	231/266 (87%)	220 (95%)	10 (4%)	1 (0%)	39	56
14	2	194/215 (90%)	184 (95%)	10 (5%)	0	100	100
14	N	194/215 (90%)	185 (95%)	9 (5%)	0	100	100
15	3	1/5 (20%)	1 (100%)	0	0	100	100
15	4	1/5 (20%)	1 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	6314/6948 (91%)	6009 (95%)	255 (4%)	50 (1%)	24	35

All (50) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	21(C)	ASP
3	C	58	LEU
4	D	12(G)	GLU
11	K	39	PRO
2	P	21(C)	ASP
3	Q	58	LEU
4	R	12(G)	GLU
11	Y	39	PRO
1	A	5	THR
2	B	54	VAL
2	B	21(B)	GLY
3	C	203	THR
4	D	18(D)	SER
5	E	5	ARG
5	E	202	ARG
10	J	192	ALA
1	O	5	THR
2	P	54	VAL
2	P	21(B)	GLY
3	Q	203	THR
4	R	18(D)	SER
5	S	5	ARG
5	S	202	ARG
10	X	192	ALA
1	A	167	LYS
2	B	184	MET
3	C	183	PRO
4	D	12(C)	GLY
4	D	12(F)	GLY
6	F	205	ASN
1	O	167	LYS
3	Q	183	PRO
3	Q	184	ALA
4	R	12(C)	GLY
4	R	12(F)	GLY
6	T	205	ASN
3	C	179	ASN

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Mol	Chain	Res	Type
3	C	184	ALA
5	E	180	LEU
2	P	184	MET
3	Q	179	ASN
5	S	180	LEU
3	C	53	ARG
10	J	49	ALA
13	M	2	SER
3	Q	53	ARG
13	1	2	SER
10	X	49	ALA
10	J	8	VAL
10	X	8	VAL

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%)	50	71
1	O	209/209 (100%)	204 (98%)	5 (2%)	57	76
2	B	203/216 (94%)	193 (95%)	10 (5%)	31	48
2	P	203/216 (94%)	193 (95%)	10 (5%)	31	48
3	C	213/226 (94%)	200 (94%)	13 (6%)	23	36
3	Q	213/226 (94%)	200 (94%)	13 (6%)	23	36
4	D	198/215 (92%)	186 (94%)	12 (6%)	23	36
4	R	198/215 (92%)	187 (94%)	11 (6%)	26	41
5	E	192/193 (100%)	173 (90%)	19 (10%)	10	14
5	S	192/193 (100%)	174 (91%)	18 (9%)	11	16
6	F	201/239 (84%)	185 (92%)	16 (8%)	15	23
6	T	201/239 (84%)	184 (92%)	17 (8%)	13	20
7	G	207/210 (99%)	194 (94%)	13 (6%)	22	35
7	U	207/210 (99%)	195 (94%)	12 (6%)	25	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	181/214 (85%)	171 (94%)	10 (6%)	27	42
8	V	181/214 (85%)	172 (95%)	9 (5%)	30	48
9	I	172/173 (99%)	168 (98%)	4 (2%)	58	78
9	W	172/173 (99%)	168 (98%)	4 (2%)	58	78
10	J	175/175 (100%)	167 (95%)	8 (5%)	33	51
10	X	175/175 (100%)	166 (95%)	9 (5%)	29	46
11	K	169/235 (72%)	158 (94%)	11 (6%)	21	33
11	Y	169/235 (72%)	158 (94%)	11 (6%)	21	33
12	L	185/201 (92%)	174 (94%)	11 (6%)	24	38
12	Z	185/201 (92%)	174 (94%)	11 (6%)	24	38
13	1	199/224 (89%)	192 (96%)	7 (4%)	43	64
13	M	199/224 (89%)	192 (96%)	7 (4%)	43	64
14	2	162/178 (91%)	154 (95%)	8 (5%)	31	48
14	N	162/178 (91%)	155 (96%)	7 (4%)	35	55
All	All	5332/5816 (92%)	5040 (94%)	292 (6%)	27	42

All (292) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	64	LEU
1	A	119	ILE
1	A	135	SER
1	A	158	PHE
1	A	179	ARG
2	B	58	LEU
2	B	71	ASN
2	B	121	GLN
2	B	150	THR
2	B	163	ILE
2	B	185	LYS
2	B	192	LEU
2	B	212	PHE
2	B	215	ILE
2	B	218	ASN
3	C	10	ARG
3	C	25	GLU

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Mol	Chain	Res	Type
3	C	57	LYS
3	C	66	LYS
3	C	121	GLN
3	C	150	GLN
3	C	163	GLN
3	C	172	VAL
3	C	174	GLU
3	C	208	LYS
3	C	210	ILE
3	C	212	ILE
3	C	227	GLU
4	D	28	LEU
4	D	48	LEU
4	D	52	LYS
4	D	76	CYS
4	D	110	GLU
4	D	126	ARG
4	D	177	LEU
4	D	191	LEU
4	D	194	LEU
4	D	196	ILE
4	D	215	ILE
4	D	237	LEU
5	E	11	ASP
5	E	12	THR
5	E	28	LEU
5	E	32	LYS
5	E	56	ASP
5	E	57	GLU
5	E	76	LEU
5	E	97	ASN
5	E	111	ARG
5	E	121	GLN
5	E	18(D)	ILE
5	E	185	ASN
5	E	189	LEU
5	E	197	ILE
5	E	207	LEU
5	E	212	ILE
5	E	214	ILE
5	E	227	GLU
5	E	231	LYS

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Mol	Chain	Res	Type
6	F	35	THR
6	F	43	ASN
6	F	54	ILE
6	F	56	SER
6	F	121	GLN
6	F	127	ASN
6	F	135	SER
6	F	144	ASN
6	F	176	LEU
6	F	18(E)	GLU
6	F	187	ARG
6	F	203	GLU
6	F	204	ASP
6	F	205	ASN
6	F	214	TRP
6	F	21(C)	ASN
7	G	35	ILE
7	G	72	ARG
7	G	87	ASN
7	G	119	LEU
7	G	121	GLN
7	G	124	THR
7	G	169	GLN
7	G	172	ILE
7	G	184	ASN
7	G	197	MET
7	G	217	LYS
7	G	232	ARG
7	G	233	LEU
8	H	30	ASN
8	H	37	ILE
8	H	41	ILE
8	H	55	VAL
8	H	63	ILE
8	H	68	LEU
8	H	121	VAL
8	H	144	GLN
8	H	159	ILE
8	H	223	ASP
9	I	-3	ILE
9	I	29	ASN
9	I	160	LEU

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Mol	Chain	Res	Type
9	I	171	TRP
10	J	52	THR
10	J	63	ILE
10	J	70	GLU
10	J	77	GLN
10	J	90(A)	ILE
10	J	121	GLU
10	J	166	MET
10	J	177	ILE
11	K	4	LEU
11	K	9	GLN
11	K	35	ILE
11	K	39	PRO
11	K	65	LEU
11	K	73	ARG
11	K	82	ILE
11	K	87	VAL
11	K	100	MET
11	K	104	TYR
11	K	10(B)	LYS
12	L	-7	ASN
12	L	3	ILE
12	L	14	LEU
12	L	25	SER
12	L	40	ASN
12	L	58	ARG
12	L	82	ASN
12	L	98	HIS
12	L	99	THR
12	L	138	LEU
12	L	145	TYR
13	M	40	ASN
13	M	62	LEU
13	M	91	ARG
13	M	129	PHE
13	M	14(C)	ARG
13	M	149	GLN
13	M	204	LYS
14	N	89	GLU
14	N	10(B)	LYS
14	N	119	VAL
14	N	126	ILE

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Mol	Chain	Res	Type
14	N	149	GLU
14	N	18(A)	ILE
14	N	18(I)	GLN
1	O	33	GLN
1	O	64	LEU
1	O	135	SER
1	O	158	PHE
1	O	179	ARG
2	P	58	LEU
2	P	71	ASN
2	P	121	GLN
2	P	150	THR
2	P	163	ILE
2	P	185	LYS
2	P	192	LEU
2	P	212	PHE
2	P	215	ILE
2	P	218	ASN
3	Q	10	ARG
3	Q	14	ILE
3	Q	25	GLU
3	Q	57	LYS
3	Q	66	LYS
3	Q	121	GLN
3	Q	150	GLN
3	Q	163	GLN
3	Q	172	VAL
3	Q	174	GLU
3	Q	208	LYS
3	Q	212	ILE
3	Q	227	GLU
4	R	28	LEU
4	R	48	LEU
4	R	76	CYS
4	R	110	GLU
4	R	126	ARG
4	R	177	LEU
4	R	191	LEU
4	R	194	LEU
4	R	196	ILE
4	R	215	ILE
4	R	237	LEU

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Mol	Chain	Res	Type
5	S	11	ASP
5	S	12	THR
5	S	28	LEU
5	S	32	LYS
5	S	57	GLU
5	S	76	LEU
5	S	97	ASN
5	S	111	ARG
5	S	121	GLN
5	S	18(D)	ILE
5	S	185	ASN
5	S	189	LEU
5	S	197	ILE
5	S	207	LEU
5	S	212	ILE
5	S	214	ILE
5	S	227	GLU
5	S	231	LYS
6	T	35	THR
6	T	43	ASN
6	T	54	ILE
6	T	56	SER
6	T	121	GLN
6	T	127	ASN
6	T	135	SER
6	T	144	ASN
6	T	169	ARG
6	T	176	LEU
6	T	18(E)	GLU
6	T	187	ARG
6	T	203	GLU
6	T	204	ASP
6	T	205	ASN
6	T	214	TRP
6	T	21(C)	ASN
7	U	72	ARG
7	U	87	ASN
7	U	119	LEU
7	U	121	GLN
7	U	124	THR
7	U	169	GLN
7	U	172	ILE

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Mol	Chain	Res	Type
7	U	184	ASN
7	U	197	MET
7	U	217	LYS
7	U	232	ARG
7	U	233	LEU
8	V	30	ASN
8	V	37	ILE
8	V	41	ILE
8	V	55	VAL
8	V	68	LEU
8	V	121	VAL
8	V	144	GLN
8	V	159	ILE
8	V	223	ASP
9	W	-3	ILE
9	W	29	ASN
9	W	160	LEU
9	W	171	TRP
10	X	52	THR
10	X	63	ILE
10	X	70	GLU
10	X	77	GLN
10	X	90(A)	ILE
10	X	121	GLU
10	X	166	MET
10	X	177	ILE
10	X	184	ILE
11	Y	4	LEU
11	Y	9	GLN
11	Y	35	ILE
11	Y	39	PRO
11	Y	65	LEU
11	Y	73	ARG
11	Y	82	ILE
11	Y	87	VAL
11	Y	100	MET
11	Y	104	TYR
11	Y	10(B)	LYS
12	Z	-7	ASN
12	Z	3	ILE
12	Z	14	LEU
12	Z	25	SER

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Mol	Chain	Res	Type
12	Z	40	ASN
12	Z	58	ARG
12	Z	82	ASN
12	Z	98	HIS
12	Z	99	THR
12	Z	138	LEU
12	Z	145	TYR
13	1	40	ASN
13	1	62	LEU
13	1	91	ARG
13	1	129	PHE
13	1	14(C)	ARG
13	1	149	GLN
13	1	204	LYS
14	2	89	GLU
14	2	10(B)	LYS
14	2	119	VAL
14	2	126	ILE
14	2	144	GLU
14	2	149	GLU
14	2	18(A)	ILE
14	2	18(I)	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (185) such sidechains are listed below:

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

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Mol	Chain	Res	Type
3	C	163	GLN
3	C	238	GLN
3	C	243	GLN
4	D	23	GLN
4	D	108	ASN
4	D	147	GLN
4	D	161	ASN
4	D	199	GLN
4	D	226	ASN
5	E	7	ASN
5	E	33	GLN
5	E	64	GLN
5	E	73	HIS
5	E	104	ASN
5	E	121	GLN
5	E	123	ASN
5	E	125	GLN
5	E	170	GLN
5	E	185	ASN
5	E	199	GLN
5	E	2(E)	ASN
6	F	23	GLN
6	F	43	ASN
6	F	90	ASN
6	F	121	GLN
6	F	127	ASN
6	F	192	GLN
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	170	GLN
7	G	178	ASN
7	G	184	ASN
7	G	228	ASN
8	H	30	ASN
8	H	66	HIS
8	H	114	HIS
8	H	144	GLN
8	H	165	ASN

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Mol	Chain	Res	Type
8	H	172	ASN
8	H	190	ASN
9	I	81	GLN
10	J	36	GLN
10	J	54	GLN
10	J	77	GLN
10	J	85	GLN
10	J	112	GLN
10	J	141	HIS
10	J	186	GLN
11	K	85	ASN
11	K	174	ASN
11	K	207	ASN
11	K	208	ASN
12	L	-9	GLN
12	L	-7	ASN
12	L	40	ASN
12	L	46	ASN
12	L	61	ASN
12	L	67	HIS
12	L	70	HIS
12	L	70(A)	ASN
12	L	82	ASN
12	L	14(B)	ASN
12	L	1(I)	ASN
12	L	166	HIS
13	M	10	ASN
13	M	40	ASN
13	M	89	GLN
13	M	93	ASN
13	M	149	GLN
13	M	157	ASN
13	M	172	ASN
13	M	191	GLN
14	N	157	HIS
14	N	161	GLN
1	O	33	GLN
1	O	97	HIS
2	P	23	GLN
2	P	71	ASN
2	P	97	GLN
2	P	121	GLN

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Mol	Chain	Res	Type
2	P	125	GLN
2	P	156	ASN
2	P	177	GLN
2	P	218	ASN
3	Q	23	GLN
3	Q	82	ASN
3	Q	121	GLN
3	Q	125	GLN
3	Q	150	GLN
3	Q	163	GLN
3	Q	243	GLN
4	R	23	GLN
4	R	108	ASN
4	R	114	GLN
4	R	147	GLN
4	R	161	ASN
4	R	199	GLN
4	R	226	ASN
5	S	7	ASN
5	S	64	GLN
5	S	73	HIS
5	S	104	ASN
5	S	121	GLN
5	S	123	ASN
5	S	125	GLN
5	S	170	GLN
5	S	185	ASN
5	S	199	GLN
5	S	2(E)	ASN
6	T	23	GLN
6	T	43	ASN
6	T	90	ASN
6	T	121	GLN
6	T	127	ASN
6	T	192	GLN
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	170	GLN

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Mol	Chain	Res	Type
7	U	178	ASN
7	U	184	ASN
7	U	228	ASN
8	V	30	ASN
8	V	66	HIS
8	V	144	GLN
8	V	165	ASN
8	V	172	ASN
8	V	190	ASN
9	W	81	GLN
10	X	36	GLN
10	X	54	GLN
10	X	85	GLN
10	X	112	GLN
10	X	141	HIS
10	X	186	GLN
11	Y	85	ASN
11	Y	174	ASN
11	Y	207	ASN
11	Y	208	ASN
12	Z	-9	GLN
12	Z	-7	ASN
12	Z	40	ASN
12	Z	46	ASN
12	Z	61	ASN
12	Z	67	HIS
12	Z	70	HIS
12	Z	70(A)	ASN
12	Z	82	ASN
12	Z	85	HIS
12	Z	14(B)	ASN
12	Z	1(I)	ASN
12	Z	166	HIS
13	1	10	ASN
13	1	40	ASN
13	1	89	GLN
13	1	93	ASN
13	1	149	GLN
13	1	157	ASN
13	1	172	ASN
13	1	191	GLN
14	2	157	HIS

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Mol	Chain	Res	Type
14	2	161	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
15	TY5	3	2	15	19,20,21	1.66	3 (15%)	22,25,27	1.22	3 (13%)
15	TRO	3	4	15	13,16,17	3.04	5 (38%)	11,22,24	2.15	2 (18%)
15	TY5	4	2	15	19,20,21	1.65	3 (15%)	22,25,27	1.19	3 (13%)
15	TRO	4	4	15	13,16,17	3.03	5 (38%)	11,22,24	2.12	2 (18%)

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	TY5	3	2	15	-	0/9/11/13	0/2/2/2
15	TRO	3	4	15	-	0/2/6/8	0/2/2/2
15	TY5	4	2	15	-	0/9/11/13	0/2/2/2
15	TRO	4	4	15	-	0/2/6/8	0/2/2/2

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	4	2	TY5	CD1-CG	2.02	1.43	1.38
15	4	4	TRO	CZ3-CH2	2.06	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	3	2	TY5	CE2-CD2	2.10	1.42	1.38
15	3	2	TY5	CD1-CG	2.12	1.43	1.38
15	4	2	TY5	CE2-CD2	2.14	1.42	1.38
15	3	4	TRO	CZ3-CH2	2.37	1.44	1.38
15	3	2	TY5	CE2-CZ	2.46	1.43	1.38
15	4	2	TY5	CE2-CZ	2.49	1.43	1.38
15	4	4	TRO	CH2-CZ2	2.55	1.42	1.36
15	3	4	TRO	CH2-CZ2	2.88	1.43	1.36
15	3	4	TRO	CZ3-CE3	2.94	1.43	1.36
15	4	4	TRO	CZ3-CE3	3.17	1.43	1.36
15	3	4	TRO	CB-CG	6.02	1.59	1.51
15	4	4	TRO	CB-CG	6.48	1.59	1.51
15	4	4	TRO	CG-CD2	7.07	1.54	1.41
15	3	4	TRO	CG-CD2	7.44	1.55	1.41

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	3	4	TRO	CB-CG-CD1	-5.12	112.84	124.01
15	4	4	TRO	CB-CG-CD1	-5.08	112.94	124.01
15	3	4	TRO	O-C-CA	-2.99	117.71	125.49
15	4	4	TRO	O-C-CA	-2.99	117.71	125.49
15	3	2	TY5	O-C-CA	-2.58	118.77	125.49
15	4	2	TY5	O-C-CA	-2.49	119.01	125.49
15	4	2	TY5	OH-C49-C50	2.08	115.46	109.21
15	3	2	TY5	OH-C49-C50	2.19	115.79	109.21
15	4	2	TY5	C49-OH-CZ	3.30	126.56	117.70
15	3	2	TY5	C49-OH-CZ	3.48	127.04	117.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	3	2	TY5	2	0
15	4	2	TY5	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates 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	$\# Z > 2$
16	MES	K	212	-	11,12,12	1.78	2 (18%)	14,16,16	2.44	4 (28%)
16	MES	Y	212	-	11,12,12	1.78	1 (9%)	14,16,16	2.51	4 (28%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	MES	K	212	-	-	0/6/14/14	0/1/1/1
16	MES	Y	212	-	-	0/6/14/14	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	K	212	MES	O1-C6	-4.30	1.24	1.42
16	Y	212	MES	O1-C6	-4.29	1.24	1.42
16	K	212	MES	O2S-S	2.06	1.51	1.45

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Y	212	MES	O2S-S-C8	-6.46	101.39	106.91
16	K	212	MES	O2S-S-C8	-5.73	102.01	106.91
16	Y	212	MES	C7-N4-C3	3.15	119.34	111.27
16	K	212	MES	O3S-S-O1S	3.21	119.07	111.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Y	212	MES	O3S-S-O1S	3.29	119.27	111.61
16	K	212	MES	C7-N4-C3	3.58	120.44	111.27
16	K	212	MES	O1-C6-C5	4.41	121.94	111.84
16	Y	212	MES	O1-C6-C5	4.52	122.19	111.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	250/250 (100%)	-0.29	4 (1%) 74 74	35, 49, 79, 105	0
1	O	250/250 (100%)	-0.21	6 (2%) 62 61	37, 51, 81, 104	0
2	B	244/258 (94%)	-0.13	6 (2%) 61 60	36, 53, 91, 117	0
2	P	244/258 (94%)	-0.03	11 (4%) 37 38	37, 54, 93, 117	0
3	C	241/254 (94%)	-0.02	11 (4%) 36 37	39, 56, 110, 125	0
3	Q	241/254 (94%)	0.29	30 (12%) 5 5	39, 59, 111, 125	0
4	D	242/260 (93%)	-0.07	8 (3%) 50 50	39, 57, 92, 123	0
4	R	242/260 (93%)	-0.07	9 (3%) 45 46	40, 58, 91, 123	0
5	E	233/234 (99%)	-0.04	8 (3%) 49 49	42, 59, 86, 111	0
5	S	233/234 (99%)	-0.02	10 (4%) 39 40	42, 60, 87, 111	0
6	F	244/288 (84%)	-0.21	5 (2%) 68 68	36, 52, 90, 106	0
6	T	244/288 (84%)	-0.18	5 (2%) 68 68	36, 53, 91, 107	0
7	G	243/252 (96%)	-0.31	5 (2%) 67 66	34, 48, 76, 115	0
7	U	243/252 (96%)	-0.35	3 (1%) 81 81	35, 48, 75, 115	0
8	H	222/261 (85%)	-0.32	3 (1%) 78 77	35, 47, 69, 97	0
8	V	222/261 (85%)	-0.36	2 (0%) 85 85	35, 48, 69, 97	0
9	I	204/205 (99%)	-0.30	3 (1%) 76 75	34, 47, 67, 82	0
9	W	204/205 (99%)	-0.20	3 (1%) 76 75	36, 48, 68, 82	0
10	J	198/198 (100%)	-0.27	5 (2%) 61 60	34, 48, 66, 124	0
10	X	198/198 (100%)	-0.35	8 (4%) 42 43	36, 49, 66, 125	0
11	K	212/287 (73%)	-0.20	8 (3%) 44 45	33, 48, 75, 85	0
11	Y	212/287 (73%)	-0.17	6 (2%) 56 55	35, 49, 76, 86	0
12	L	222/241 (92%)	-0.36	2 (0%) 85 85	34, 47, 70, 96	0
12	Z	222/241 (92%)	-0.35	2 (0%) 85 85	35, 47, 69, 96	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1	233/266 (87%)	-0.53	0 100 100	34, 46, 61, 68	0
13	M	233/266 (87%)	-0.44	1 (0%) 93 93	32, 46, 62, 66	0
14	2	196/215 (91%)	-0.38	1 (0%) 91 91	33, 44, 67, 80	0
14	N	196/215 (91%)	-0.48	0 100 100	34, 44, 67, 80	0
15	3	1/5 (20%)	-0.16	0 100 100	52, 52, 52, 52	0
15	4	1/5 (20%)	-0.19	0 100 100	55, 55, 55, 55	0
All	All	6370/6948 (91%)	-0.22	165 (2%) 59 58	32, 50, 83, 125	0

All (165) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	12(D)	ALA	13.8
4	D	12(E)	SER	11.1
4	R	12(F)	GLY	11.1
10	J	192	ALA	9.3
3	Q	56	LEU	9.0
3	C	55	THR	8.9
7	U	6	ALA	8.9
4	R	12(D)	ALA	8.2
10	X	193	GLN	8.0
4	D	12(F)	GLY	8.0
2	P	217	ALA	7.2
2	B	218	ASN	7.2
7	G	6	ALA	7.2
12	L	145	TYR	7.2
4	R	12(E)	SER	7.0
3	Q	203	THR	6.7
1	A	4	MET	6.6
3	C	56	LEU	6.6
10	J	193	GLN	6.3
2	P	218	ASN	6.1
7	U	240	ASP	6.1
5	S	4	PHE	5.9
10	X	192	ALA	5.9
4	R	12(C)	GLY	5.6
4	D	12(G)	GLU	5.4
5	S	233	ILE	5.3
5	E	4	PHE	5.3
4	D	12(C)	GLY	5.2
3	Q	236	ILE	5.2

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Mol	Chain	Res	Type	RSRZ
5	S	203	ASP	5.2
1	O	4	MET	5.0
3	Q	240	LYS	4.9
6	T	240	ILE	4.8
9	W	-8	SER	4.7
3	Q	55	THR	4.7
12	Z	145	TYR	4.6
3	Q	242	GLU	4.6
5	E	203	ASP	4.5
1	O	236	LEU	4.5
1	O	235	ALA	4.5
4	R	126	ARG	4.4
2	B	217	ALA	4.4
12	Z	14(W)	LYS	4.3
2	P	54	VAL	4.3
10	X	189	ASP	4.2
3	C	240	LYS	4.2
5	S	5	ARG	4.2
5	E	233	ILE	4.1
1	O	55	SER	4.1
12	L	14(W)	LYS	4.1
13	M	-8	THR	4.1
4	D	126	ARG	4.1
6	F	240	ILE	4.1
7	G	240	ASP	4.1
4	D	127	LEU	3.9
3	Q	239	GLU	3.9
4	R	121	LEU	3.9
3	Q	243	GLN	3.8
11	Y	208	ASN	3.8
2	P	21(B)	GLY	3.8
10	X	191	GLN	3.7
3	Q	202	GLN	3.5
6	F	204	ASP	3.5
2	B	54	VAL	3.5
3	Q	233	VAL	3.4
3	Q	241	GLN	3.4
11	Y	181	ASP	3.4
11	K	211	GLY	3.4
9	I	-8	SER	3.3
3	Q	207	ALA	3.3
11	K	208	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
6	T	241	ASN	3.2
5	E	5	ARG	3.2
11	K	40	PHE	3.2
1	O	53	LYS	3.2
5	S	204	GLU	3.1
10	J	189	ASP	3.1
10	X	188	ASP	3.1
4	R	12(G)	GLU	3.0
7	G	7	GLY	3.0
3	Q	208	LYS	3.0
8	V	222	CYS	3.0
2	P	239	THR	3.0
3	Q	175	PHE	2.9
4	R	12(A)	GLY	2.9
3	Q	235	GLN	2.9
11	Y	211	GLY	2.9
11	K	181	ASP	2.8
10	J	191	GLN	2.8
3	C	203	THR	2.8
6	F	5	GLY	2.8
10	J	-1	MET	2.8
2	P	21(C)	ASP	2.7
3	Q	53	ARG	2.7
8	V	223	ASP	2.7
3	C	208	LYS	2.7
5	S	2(C)	VAL	2.7
1	A	236	LEU	2.7
2	B	21(B)	GLY	2.7
3	C	54	SER	2.6
10	X	133	TYR	2.6
11	Y	180	GLU	2.6
6	T	238	LYS	2.6
3	C	202	GLN	2.6
11	K	180	GLU	2.6
5	S	178	ARG	2.6
3	Q	18(C)	LYS	2.6
2	P	219	GLU	2.6
2	P	21(A)	LYS	2.5
1	O	56	SER	2.5
3	C	237	GLU	2.5
9	W	182	ASP	2.5
3	Q	206	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
8	H	222	CYS	2.5
3	Q	18(D)	GLU	2.5
3	Q	201	VAL	2.4
11	K	104	TYR	2.4
1	A	203	GLU	2.4
11	K	210	ILE	2.4
3	C	241	GLN	2.4
3	Q	238	GLN	2.4
5	S	6	ASN	2.4
3	Q	54	SER	2.4
3	Q	178	LYS	2.4
9	W	181	LYS	2.4
10	X	-1	MET	2.4
3	C	209	ASN	2.3
8	H	199	GLU	2.3
11	Y	104	TYR	2.3
5	E	204	GLU	2.3
14	2	18(I)	GLN	2.3
3	Q	187	GLU	2.3
3	Q	237	GLU	2.3
6	F	18(A)	ASP	2.3
6	T	5	GLY	2.3
10	X	168	MET	2.2
2	P	220	TYR	2.2
11	K	207	ASN	2.2
4	R	127	LEU	2.2
5	S	33	GLN	2.2
11	Y	209	VAL	2.2
3	Q	58	LEU	2.2
3	Q	194	VAL	2.2
6	F	20(B)	GLU	2.2
5	E	195	GLU	2.1
5	E	202	ARG	2.1
6	T	6	THR	2.1
7	G	239	GLN	2.1
7	U	8	TYR	2.1
3	C	243	GLN	2.1
1	A	5	THR	2.1
4	D	125	GLU	2.1
7	G	18(H)	GLU	2.1
2	B	235	LYS	2.1
2	P	232	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
5	S	232	TYR	2.1
3	Q	63	THR	2.1
3	Q	40	VAL	2.1
5	E	178	ARG	2.1
3	Q	229	ILE	2.1
2	B	227	GLN	2.0
2	P	236	THR	2.0
9	I	121	GLU	2.0
9	I	12(A)	LYS	2.0
8	H	223	ASP	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
15	TRO	3	4	15/16	0.93	0.16	-	53,62,64,65	0
15	TY5	3	2	19/20	0.94	0.22	-	57,61,70,70	0
15	TY5	4	2	19/20	0.93	0.17	-	58,60,70,70	0
15	TRO	4	4	15/16	0.89	0.19	-	56,63,64,65	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
16	MES	K	212	12/12	0.95	0.18	3.11	71,75,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
16	MES	Y	212	12/12	0.93	0.15	0.90	74,77,79,79	0

6.5 Other polymers [i](#)

There are no such residues in this entry.