



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 25, 2020 – 06:30 PM BST

PDB ID : 3GPJ
Title : Crystal structure of the yeast 20S proteasome in complex with syringolin B
Authors : Groll, M.; Huber, R.; Kaiser, M.
Deposited on : 2009-03-23
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13

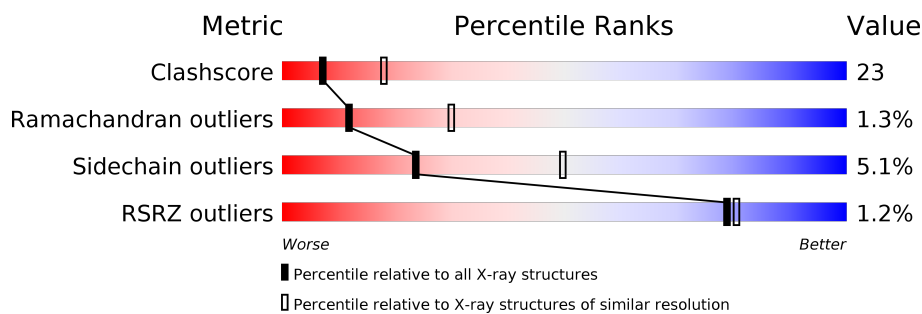
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	250	<div> <div>2%</div> <div>64%</div> <div>33%</div> <div>.</div> </div>
1	O	250	<div> <div>%</div> <div>62%</div> <div>35%</div> <div>.</div> </div>
2	B	244	<div> <div>%</div> <div>52%</div> <div>43%</div> <div>6%</div> </div>
2	P	244	<div> <div>2%</div> <div>52%</div> <div>42%</div> <div>6%</div> </div>
3	C	241	<div> <div>2%</div> <div>55%</div> <div>41%</div> <div>.</div> </div>
3	Q	241	<div> <div>4%</div> <div>56%</div> <div>40%</div> <div>.</div> </div>
4	D	242	<div> <div>3%</div> <div>63%</div> <div>34%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
4	R	242	 3% 64% 32% .
5	E	233	 61% 34% .
5	S	233	 2% 60% 36% .
6	F	244	 58% 38% .
6	T	244	 56% 39% .
7	G	243	 2% 62% 35% .
7	U	243	 60% 37% .
8	H	222	 64% 34% .
8	V	222	 64% 34% .
9	I	204	 61% 37% .
9	W	204	 58% 40% .
10	J	198	 2% 52% 45% .
10	X	198	 2% 54% 43% .
11	K	212	 2% 62% 35% .
11	Y	212	 59% 37% .
12	L	222	 60% 35% .
12	Z	222	 61% 34% 5% .
13	1	233	 63% 35% .
13	M	233	 63% 34% .
14	2	196	 66% 31% .
14	N	196	 62% 35% .

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 51023 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Proteasome component Y7.

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

- Molecule 2 is a protein called Proteasome component Y13.

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

- Molecule 3 is a protein called Proteasome component PRE6.

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

- Molecule 4 is a protein called Proteasome component PUP2.

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

- Molecule 5 is a protein called Proteasome component PRE5.

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

- Molecule 6 is a protein called Proteasome component C1.

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

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

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

- Molecule 8 is a protein called Proteasome component PUP1.

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

- Molecule 9 is a protein called Proteasome component PUP3.

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

- Molecule 10 is a protein called Proteasome component C11.

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

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

- Molecule 11 is a protein called Proteasome component PRE2.

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

- Molecule 12 is a protein called Proteasome component C5.

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

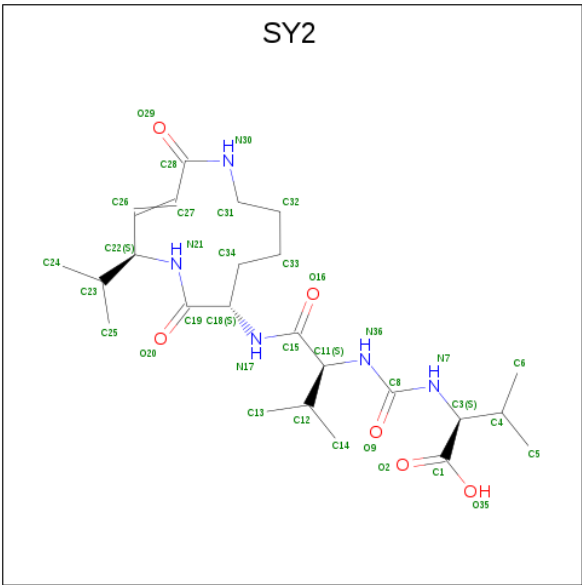
- Molecule 13 is a protein called Proteasome component PRE4.

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

- Molecule 14 is a protein called Proteasome component PRE3.

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

- Molecule 15 is N-([(1S)-2-methyl-1-([(5S,8S)-5-(1-methylethyl)-2,7-dioxo-1,6-diazacyclo dodec-3-en-8-yl]carbamoyl)propyl]carbamoyl)-L-valine (three-letter code: SY2) (formula: C₂₄H₄₁N₅O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
15	H	1	Total	C	N	O	0	0
			35	24	5	6		
15	K	1	Total	C	N	O	0	0
			35	24	5	6		
15	V	1	Total	C	N	O	0	0
			35	24	5	6		
15	Y	1	Total	C	N	O	0	0
			35	24	5	6		

- Molecule 16 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	58	Total	O	0	0
			58	58		
16	B	39	Total	O	0	0
			39	39		
16	C	44	Total	O	0	0
			44	44		
16	D	42	Total	O	0	0
			42	42		
16	E	24	Total	O	0	0
			24	24		
16	F	49	Total	O	0	0
			49	49		
16	G	61	Total	O	0	0
			61	61		
16	H	48	Total	O	0	0
			48	48		

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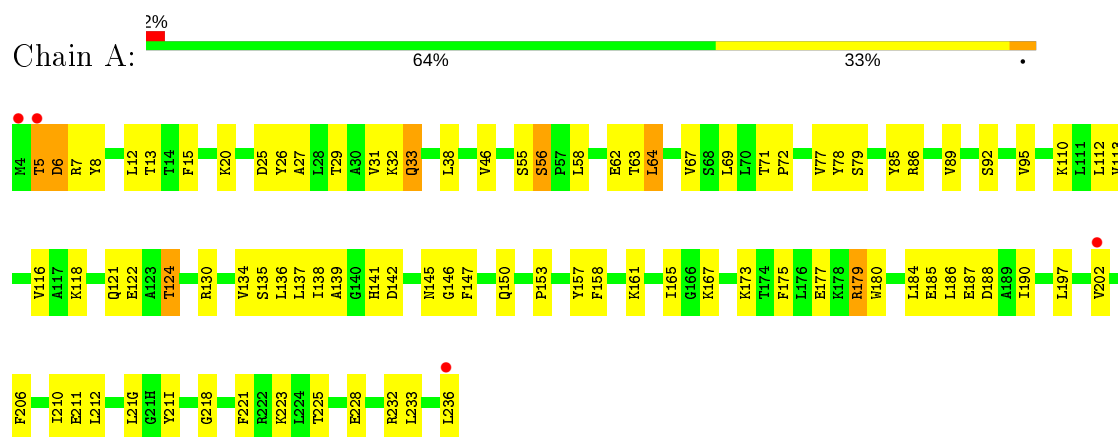
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	I	65	Total 65	O 65	0	0
16	J	49	Total 49	O 49	0	0
16	K	43	Total 43	O 43	0	0
16	L	58	Total 58	O 58	0	0
16	M	70	Total 70	O 70	0	0
16	N	55	Total 55	O 55	0	0
16	O	33	Total 33	O 33	0	0
16	P	30	Total 30	O 30	0	0
16	Q	27	Total 27	O 27	0	0
16	R	30	Total 30	O 30	0	0
16	S	23	Total 23	O 23	0	0
16	T	42	Total 42	O 42	0	0
16	U	60	Total 60	O 60	0	0
16	V	43	Total 43	O 43	0	0
16	W	62	Total 62	O 62	0	0
16	X	45	Total 45	O 45	0	0
16	Y	50	Total 50	O 50	0	0
16	Z	52	Total 52	O 52	0	0
16	1	71	Total 71	O 71	0	0
16	2	62	Total 62	O 62	0	0

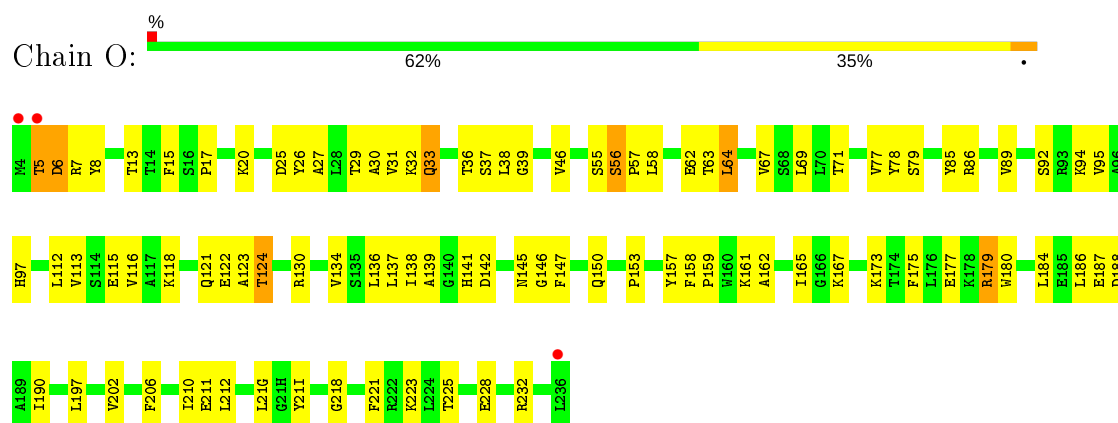
3 Residue-property plots

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

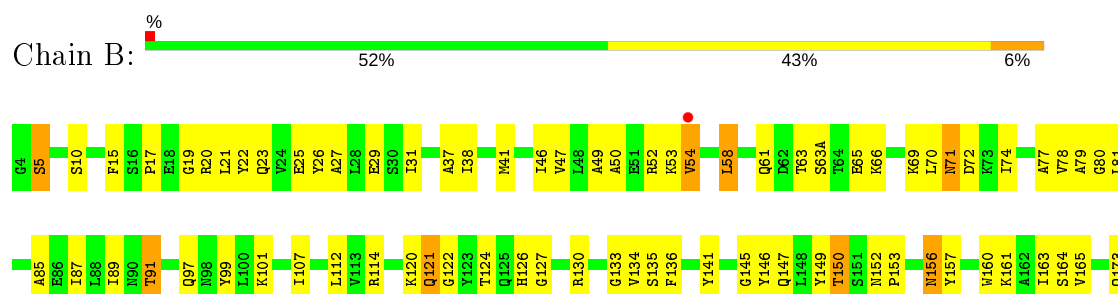
• Molecule 1: Proteasome component Y7



• Molecule 1: Proteasome component Y7

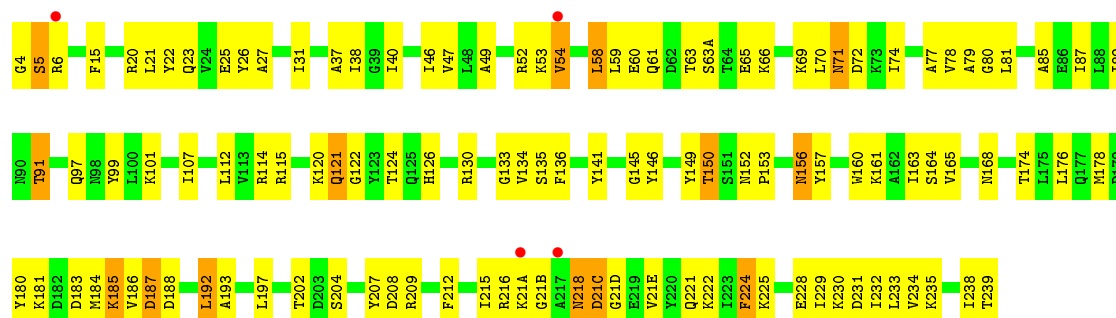


• Molecule 2: Proteasome component Y13

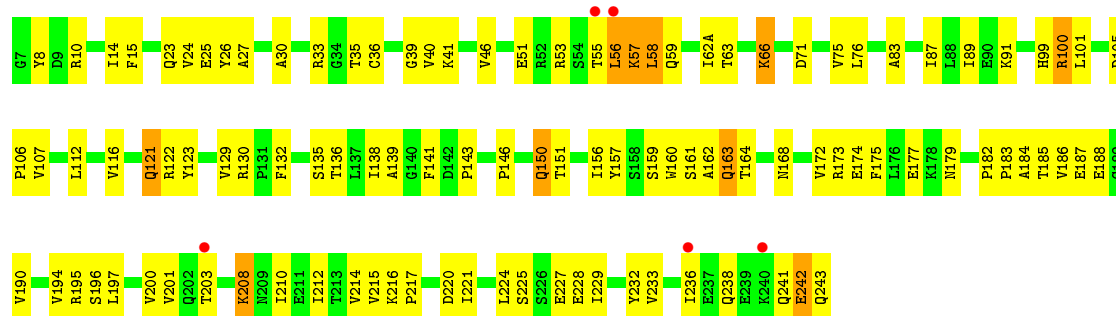




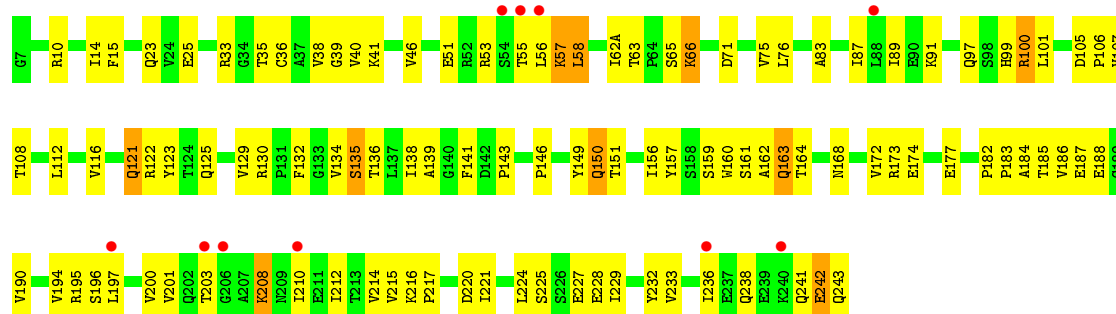
• Molecule 2: Proteasome component Y13



• Molecule 3: Proteasome component PRE6

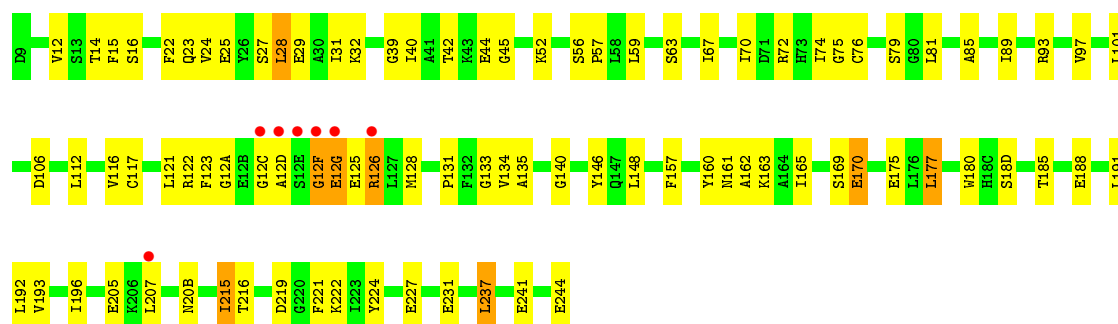


• Molecule 3: Proteasome component PRE6

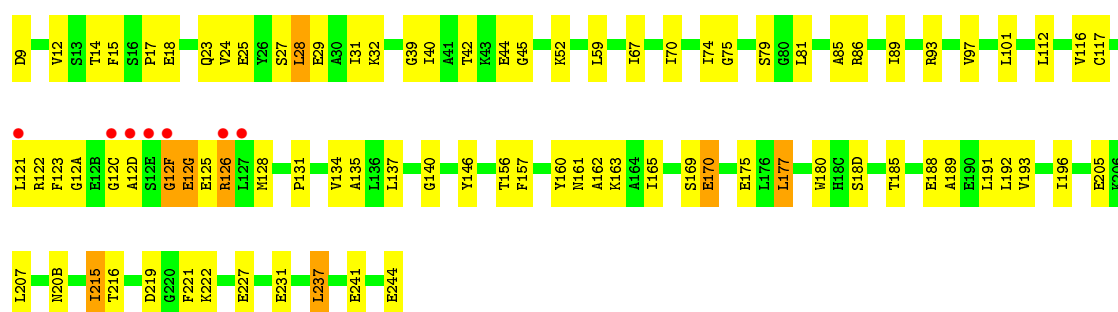


• Molecule 4: Proteasome component PUP2

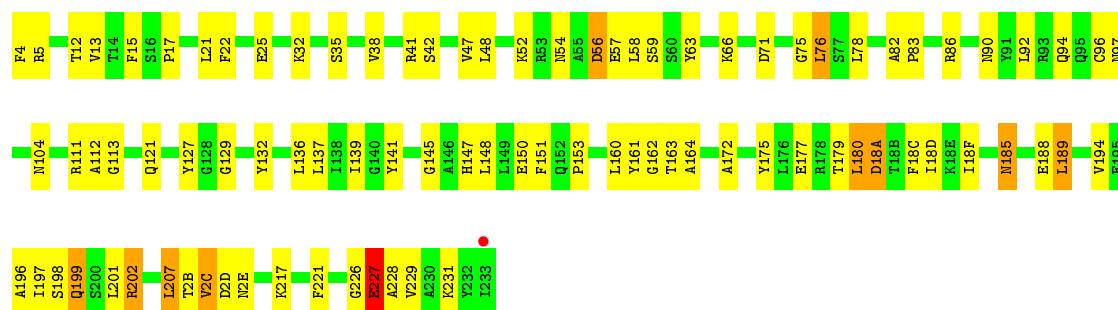




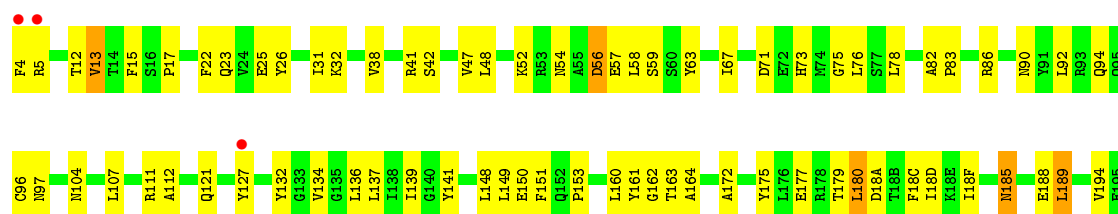
• Molecule 4: Proteasome component PUP2



• Molecule 5: Proteasome component PRE5



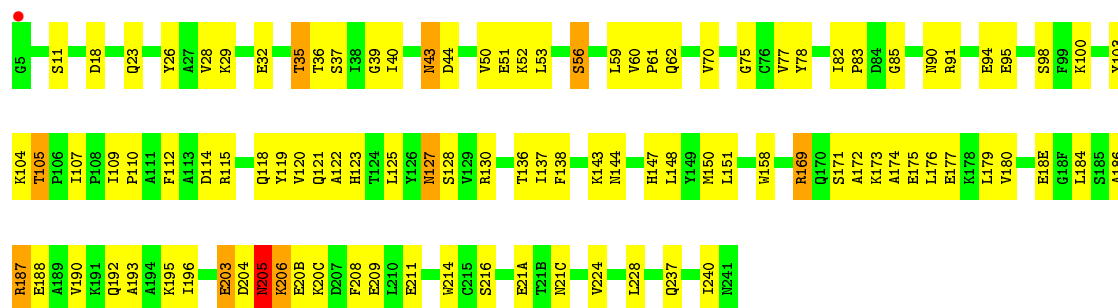
• Molecule 5: Proteasome component PRE5





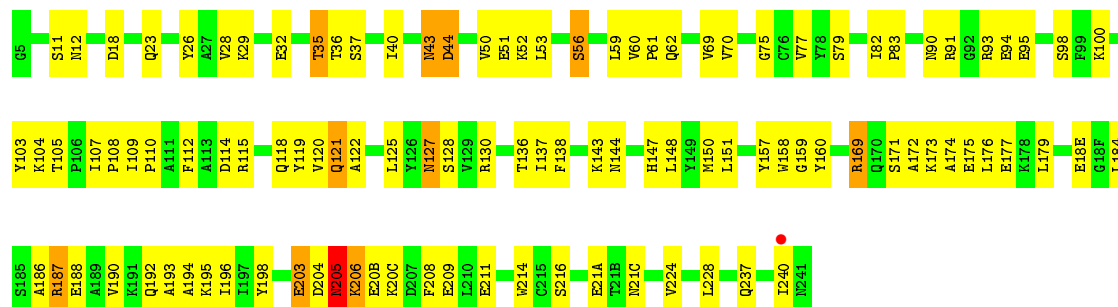
- Molecule 6: Proteasome component C1

Chain F: 58% 38%



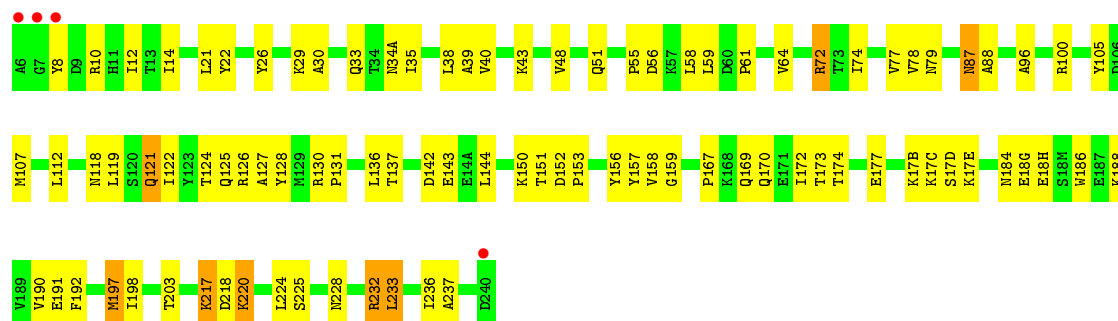
- Molecule 6: Proteasome component C1

Chain T: 56% 39%



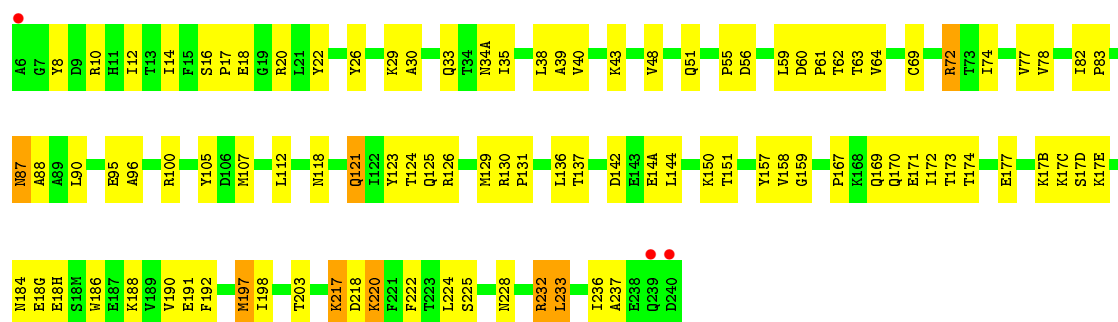
- Molecule 7: Proteasome component C7-alpha

Chain G: 2% 62% 35%

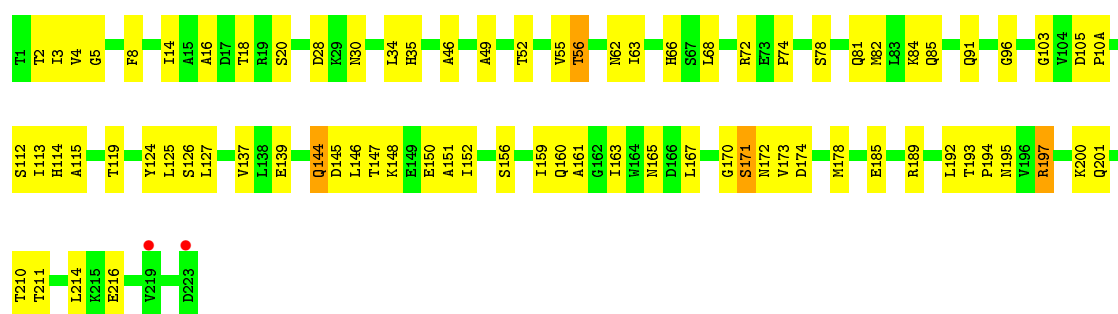


- Molecule 7: Proteasome component C7-alpha

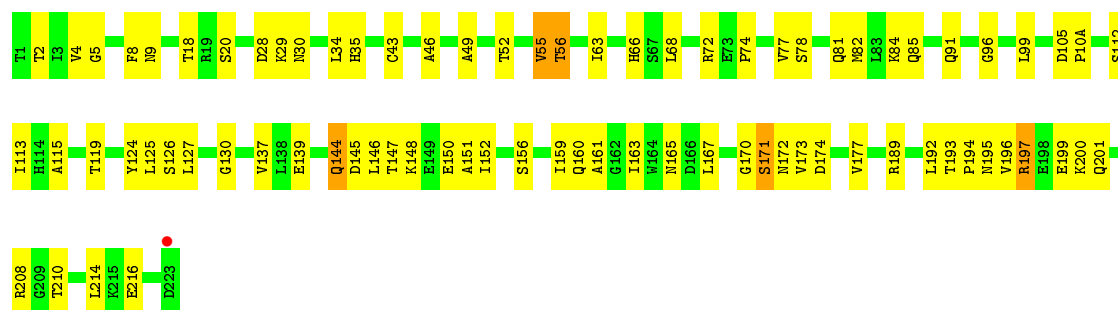
Chain U: 60% 37%



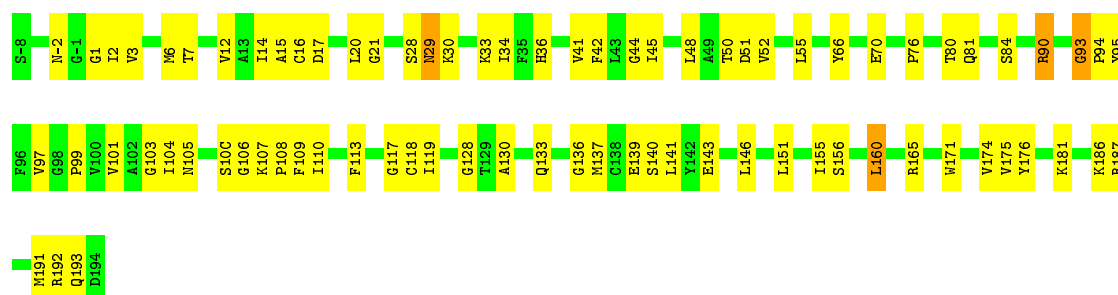
● Molecule 8: Proteasome component PUP1



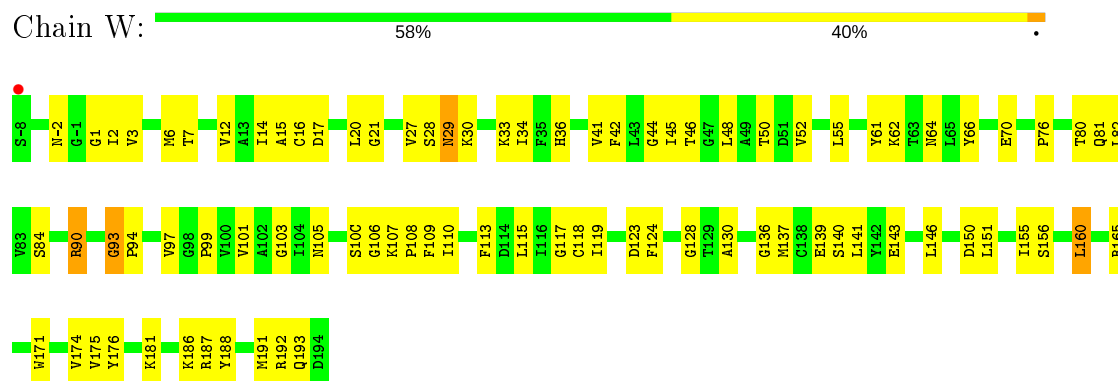
● Molecule 8: Proteasome component PUP1



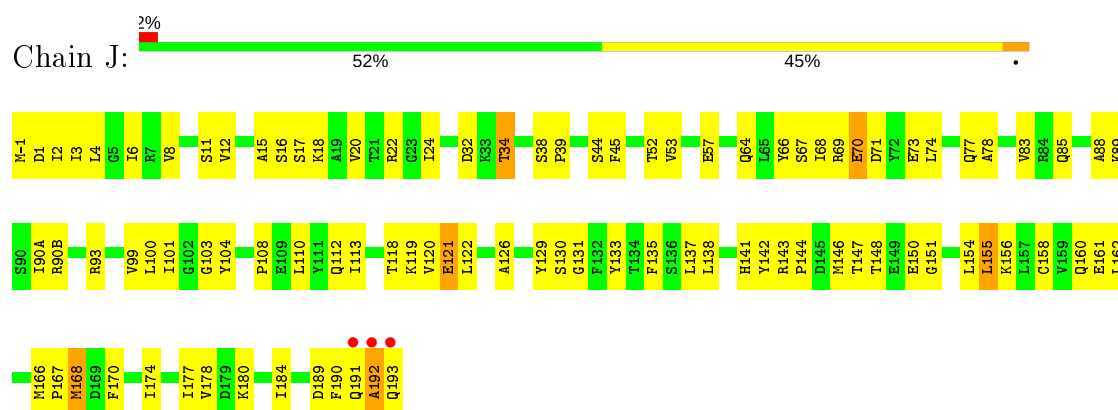
● Molecule 9: Proteasome component PUP3



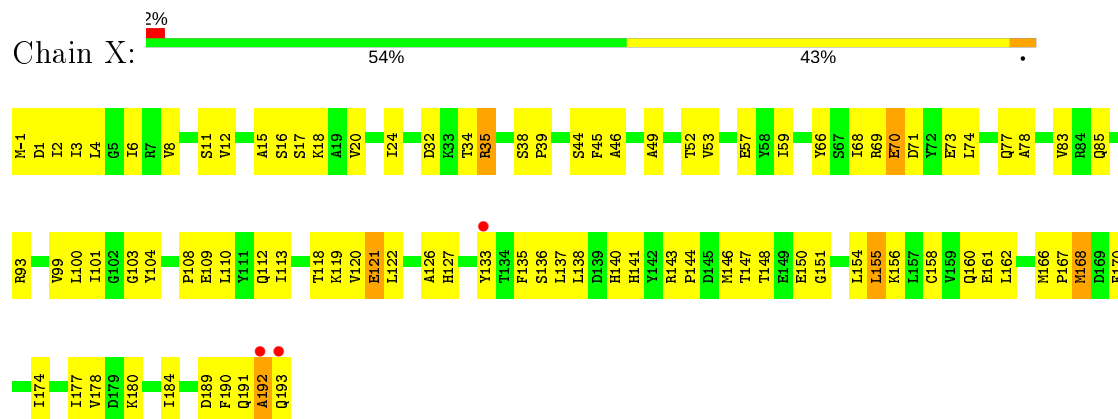
- Molecule 9: Proteasome component PUP3



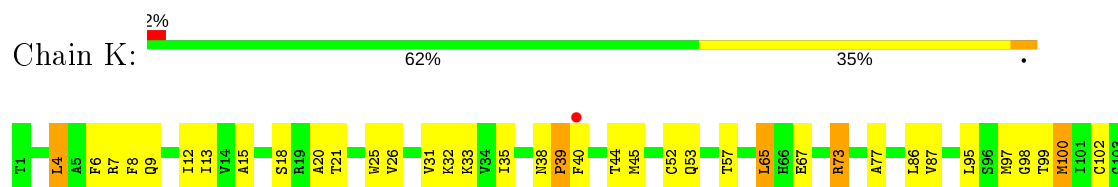
- Molecule 10: Proteasome component C11

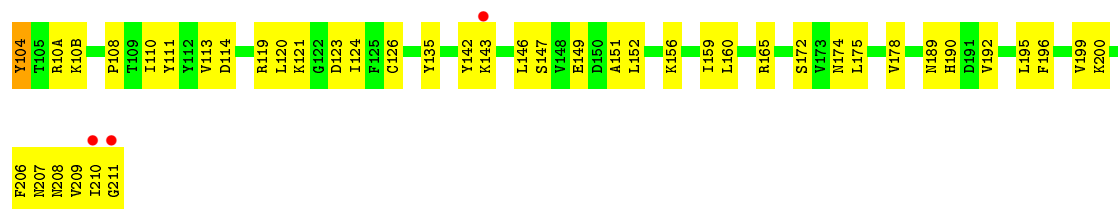


- Molecule 10: Proteasome component C11

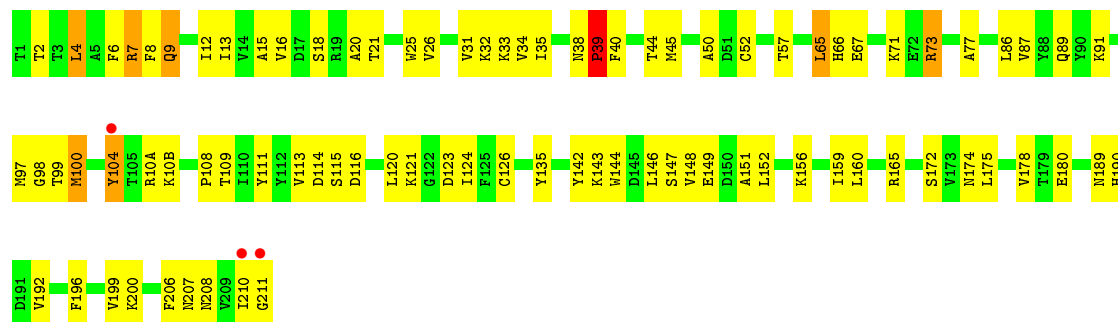


- Molecule 11: Proteasome component PRE2

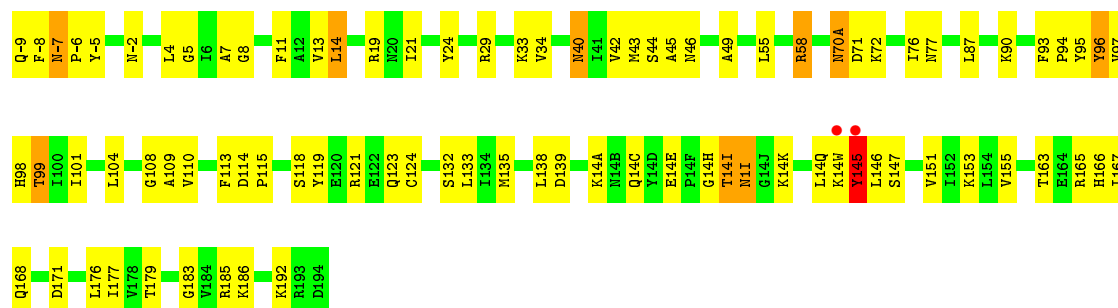




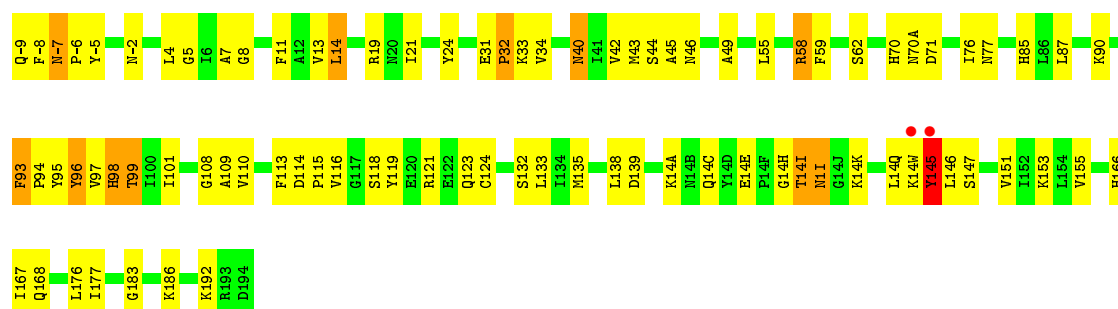
• Molecule 11: Proteasome component PRE2



• Molecule 12: Proteasome component C5

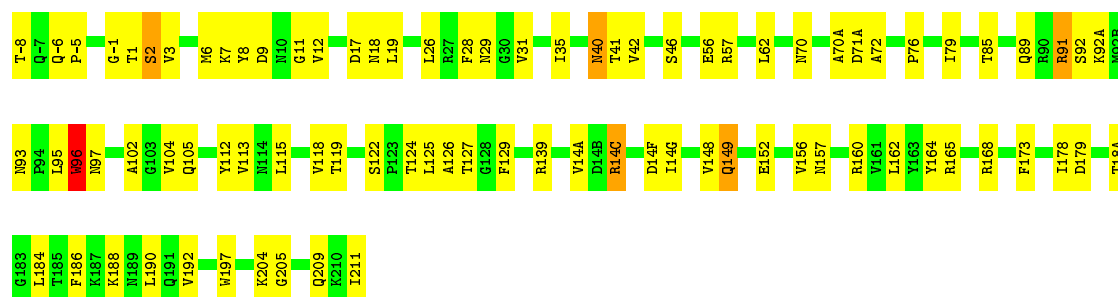


• Molecule 12: Proteasome component C5



• Molecule 13: Proteasome component PRE4

Chain M:  63% 34% .



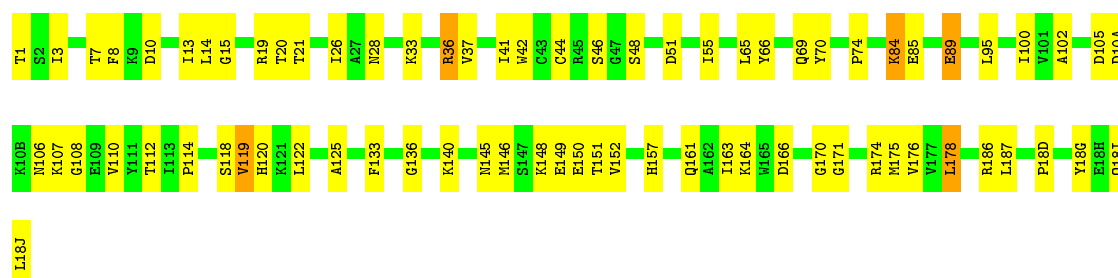
• Molecule 13: Proteasome component PRE4

Chain 1:  63% 35% .



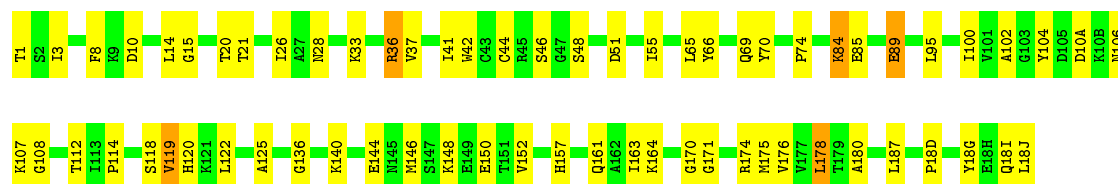
• Molecule 14: Proteasome component PRE3

Chain N:  62% 35% .



• Molecule 14: Proteasome component PRE3

Chain 2:  66% 31% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	133.51Å 301.59Å 143.37Å 90.00° 112.59° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 50.05 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.0 (15.00-2.70) 98.4 (50.05-2.69)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 2.69Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.250 , 0.264 0.234 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	31.1	Xtriage
Anisotropy	0.911	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 19.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	51023	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SY2

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	0.41	0/1952	0.65	0/2642
1	O	0.41	0/1952	0.66	0/2642
2	B	0.39	0/1935	0.64	0/2618
2	P	0.39	0/1935	0.65	0/2618
3	C	0.38	0/1920	0.62	1/2598 (0.0%)
3	Q	0.38	0/1920	0.62	0/2598
4	D	0.39	0/1887	0.64	0/2541
4	R	0.38	0/1887	0.63	0/2541
5	E	0.40	0/1823	0.64	0/2463
5	S	0.40	0/1823	0.64	0/2463
6	F	0.41	0/1937	0.63	0/2614
6	T	0.41	0/1937	0.64	0/2614
7	G	0.43	0/1959	0.66	0/2652
7	U	0.44	0/1959	0.66	0/2652
8	H	0.42	0/1716	0.69	0/2326
8	V	0.40	0/1716	0.67	0/2326
9	I	0.41	0/1611	0.67	0/2174
9	W	0.44	0/1611	0.68	0/2174
10	J	0.41	0/1613	0.66	0/2173
10	X	0.43	0/1613	0.67	0/2173
11	K	0.41	0/1681	0.65	1/2274 (0.0%)
11	Y	0.42	0/1681	0.65	1/2274 (0.0%)
12	L	0.44	0/1795	0.68	0/2420
12	Z	0.44	0/1795	0.67	0/2420
13	1	0.43	0/1855	0.68	0/2514
13	M	0.41	0/1855	0.68	0/2514
14	2	0.42	0/1541	0.66	0/2087
14	N	0.44	0/1541	0.67	0/2087
All	All	0.41	0/50450	0.65	3/68192 (0.0%)

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

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

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

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	K	98	GLY	N-CA-C	-5.60	99.09	113.10
11	Y	98	GLY	N-CA-C	-5.58	99.16	113.10
3	C	56	LEU	CA-CB-CG	5.09	127.00	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

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

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1926	82	0
1	O	1915	0	1926	92	0
2	B	1905	0	1901	123	0
2	P	1905	0	1901	128	0
3	C	1891	0	1900	116	0
3	Q	1891	0	1900	114	0
4	D	1862	0	1836	75	0
4	R	1862	0	1836	82	0
5	E	1795	0	1797	86	0
5	S	1795	0	1797	99	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	1897	0	1886	94	0
6	T	1897	0	1886	102	0
7	G	1921	0	1910	83	0
7	U	1921	0	1910	91	0
8	H	1685	0	1687	65	0
8	V	1685	0	1687	66	0
9	I	1581	0	1574	75	0
9	W	1581	0	1574	85	0
10	J	1585	0	1590	101	0
10	X	1585	0	1590	93	0
11	K	1644	0	1594	87	0
11	Y	1644	0	1594	95	0
12	L	1757	0	1711	87	0
12	Z	1757	0	1711	87	0
13	1	1824	0	1832	88	0
13	M	1824	0	1832	83	0
14	2	1512	0	1481	54	0
14	N	1512	0	1481	61	0
15	H	35	0	39	2	0
15	K	35	0	40	0	0
15	V	35	0	39	2	0
15	Y	35	0	39	0	0
16	1	71	0	0	15	0
16	2	62	0	0	4	0
16	A	58	0	0	2	0
16	B	39	0	0	6	0
16	C	44	0	0	5	0
16	D	42	0	0	6	0
16	E	24	0	0	3	0
16	F	49	0	0	5	0
16	G	61	0	0	6	0
16	H	48	0	0	6	0
16	I	65	0	0	2	0
16	J	49	0	0	6	0
16	K	43	0	0	3	0
16	L	58	0	0	4	0
16	M	70	0	0	11	0
16	N	55	0	0	6	0
16	O	33	0	0	2	0
16	P	30	0	0	5	0
16	Q	27	0	0	3	0
16	R	30	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	S	23	0	0	1	0
16	T	42	0	0	7	0
16	U	60	0	0	9	0
16	V	43	0	0	6	0
16	W	62	0	0	6	0
16	X	45	0	0	8	0
16	Y	50	0	0	13	0
16	Z	52	0	0	7	0
All	All	51023	0	49407	2243	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 23.

All (2243) 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)
11:K:4:LEU:HD12	11:K:159:ILE:HD11	1.38	1.05
7:G:96:ALA:HA	7:G:107:MET:HE2	1.40	1.03
1:O:130:ARG:HH21	7:U:124:THR:HG22	1.23	1.01
11:Y:10(B):LYS:HD2	11:Y:10(B):LYS:H	1.26	1.00
11:Y:4:LEU:HD12	11:Y:159:ILE:HD11	1.43	1.00
14:N:136:GLY:HA2	14:2:161:GLN:HE21	1.20	1.00
14:N:161:GLN:HE21	14:2:136:GLY:HA2	1.21	1.00
2:B:15:PHE:H	3:C:23:GLN:HE22	1.05	0.99
2:B:202:THR:HG22	2:B:204:SER:H	1.27	0.99
9:W:6:MET:HE1	9:W:155:ILE:HA	1.42	0.99
2:P:202:THR:HG22	2:P:204:SER:H	1.23	0.98
13:1:157:ASN:HD22	13:1:160:ARG:HH11	1.05	0.97
7:U:96:ALA:HA	7:U:107:MET:HE2	1.43	0.97
9:I:6:MET:HE1	9:I:155:ILE:HA	1.46	0.96
11:K:10(B):LYS:H	11:K:10(B):LYS:HD2	1.27	0.96
2:P:71:ASN:ND2	2:P:72:ASP:H	1.64	0.95
3:Q:100:ARG:NH1	3:Q:106:PRO:HB3	1.81	0.95
8:V:35:HIS:HB3	8:V:56:THR:HG21	1.48	0.94
2:B:71:ASN:ND2	2:B:72:ASP:H	1.64	0.94
8:V:163:ILE:HG23	8:V:170:GLY:HA2	1.49	0.94
3:C:100:ARG:NH1	3:C:106:PRO:HB3	1.83	0.93
1:A:130:ARG:HH21	7:G:124:THR:HG22	1.31	0.93
13:M:157:ASN:HD22	13:M:160:ARG:HH11	1.05	0.92
8:H:35:HIS:HB3	8:H:56:THR:HG21	1.49	0.92
10:J:2:ILE:HD13	10:J:162:LEU:HD13	1.51	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:X:2:ILE:HD13	10:X:162:LEU:HD13	1.53	0.90
10:J:-1:MET:HG2	10:J:1:ASP:H	1.36	0.89
10:X:-1:MET:HG2	10:X:1:ASP:H	1.38	0.89
3:C:15:PHE:H	4:D:23:GLN:HE22	1.21	0.88
3:Q:15:PHE:H	4:R:23:GLN:HE22	1.21	0.87
2:P:15:PHE:H	3:Q:23:GLN:HE22	1.17	0.87
5:S:15:PHE:HB2	6:T:23:GLN:HE22	1.39	0.87
10:J:133:TYR:HD1	16:Y:593:HOH:O	1.56	0.86
8:H:163:ILE:HG23	8:H:170:GLY:HA2	1.55	0.86
3:Q:185:THR:HG22	3:Q:187:GLU:H	1.39	0.86
5:E:201:LEU:HD11	5:E:207:LEU:HD22	1.56	0.86
4:D:97:VAL:HG21	11:K:65:LEU:HD13	1.59	0.85
3:C:185:THR:HG22	3:C:187:GLU:H	1.41	0.85
3:Q:185:THR:HB	3:Q:188:GLU:HG2	1.58	0.85
1:O:124:THR:HG22	2:P:130:ARG:HH21	1.41	0.85
5:S:201:LEU:HD11	5:S:207:LEU:HD22	1.56	0.84
14:N:161:GLN:NE2	14:2:136:GLY:HA2	1.92	0.84
6:T:36:THR:HG22	6:T:51:GLU:OE2	1.77	0.84
3:C:100:ARG:HH11	3:C:106:PRO:HB3	1.43	0.84
11:Y:143:LYS:O	11:Y:146:LEU:HD13	1.74	0.84
11:K:143:LYS:O	11:K:146:LEU:HD13	1.77	0.84
2:B:124:THR:HG22	3:C:130:ARG:HH21	1.42	0.84
14:N:136:GLY:HA2	14:2:161:GLN:NE2	1.92	0.83
5:E:15:PHE:HB2	6:F:23:GLN:HE22	1.43	0.83
3:C:185:THR:HB	3:C:188:GLU:HG2	1.60	0.83
11:Y:174:ASN:HD21	11:Y:189:ASN:HD22	1.26	0.81
3:C:163:GLN:HE21	3:C:164:THR:H	1.27	0.81
2:P:124:THR:HG22	3:Q:130:ARG:HH21	1.43	0.81
2:P:202:THR:HG22	2:P:204:SER:N	1.96	0.81
10:J:133:TYR:HE1	16:X:876:HOH:O	1.63	0.81
1:O:130:ARG:HH21	7:U:124:THR:CG2	1.92	0.80
6:F:36:THR:HG22	6:F:51:GLU:OE2	1.79	0.80
9:I:137:MET:HE3	9:I:141:LEU:HD11	1.61	0.80
2:P:224:PHE:H	2:P:224:PHE:HD2	1.30	0.80
13:M:157:ASN:ND2	13:M:160:ARG:HH11	1.79	0.80
5:S:207:LEU:HA	5:S:2(E):ASN:ND2	1.97	0.79
12:Z:33:LYS:HD2	12:Z:46:ASN:HD22	1.48	0.79
8:H:165:ASN:HD22	13:1:139:ARG:HH11	1.29	0.79
3:Q:100:ARG:HH11	3:Q:106:PRO:HB3	1.42	0.79
11:Y:142:TYR:O	11:Y:143:LYS:HD2	1.83	0.79
2:B:224:PHE:HD2	2:B:224:PHE:H	1.29	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:207:LEU:HA	5:E:2(E):ASN:ND2	1.97	0.79
12:Z:4:LEU:HD11	12:Z:138:LEU:HD21	1.65	0.79
1:A:130:ARG:HH21	7:G:124:THR:CG2	1.94	0.79
1:O:15:PHE:H	2:P:23:GLN:HE22	1.31	0.79
11:K:174:ASN:HD21	11:K:189:ASN:HD22	1.31	0.79
5:S:75:GLY:HA3	5:S:221:PHE:CE2	2.17	0.78
9:W:137:MET:HE3	9:W:141:LEU:HD11	1.65	0.78
13:1:157:ASN:ND2	13:1:160:ARG:HH11	1.80	0.78
13:1:40:ASN:HD22	13:1:40:ASN:H	1.32	0.78
12:L:4:LEU:HD11	12:L:138:LEU:HD21	1.64	0.78
6:T:95:GLU:HG2	6:T:115:ARG:HB3	1.65	0.78
11:K:142:TYR:O	11:K:143:LYS:HD2	1.84	0.77
1:O:124:THR:CG2	2:P:130:ARG:HH21	1.97	0.77
11:Y:35:ILE:HD11	11:Y:45:MET:CE	2.14	0.77
1:O:86:ARG:HE	7:U:118:ASN:ND2	1.83	0.77
3:Q:185:THR:HG22	3:Q:187:GLU:N	1.98	0.77
13:M:139:ARG:HH11	8:V:165:ASN:HD22	1.32	0.77
7:G:87:ASN:HD22	7:G:87:ASN:C	1.87	0.77
6:T:79:SER:HA	16:T:1238:HOH:O	1.84	0.77
7:G:96:ALA:HA	7:G:107:MET:CE	2.14	0.77
2:B:202:THR:HG22	2:B:204:SER:N	1.99	0.77
8:V:81:GLN:O	8:V:85:GLN:HG3	1.84	0.77
1:O:33:GLN:HA	1:O:33:GLN:HE21	1.49	0.76
6:F:216:SER:HB3	6:F:21(A):GLU:HB2	1.66	0.76
3:C:185:THR:HG22	3:C:187:GLU:N	1.98	0.76
13:M:40:ASN:H	13:M:40:ASN:HD22	1.32	0.76
10:J:20:VAL:HG11	11:K:120:LEU:HD11	1.66	0.76
2:P:65:GLU:HG3	2:P:66:LYS:HG3	1.67	0.76
7:U:96:ALA:HA	7:U:107:MET:CE	2.14	0.76
1:A:33:GLN:HE21	1:A:33:GLN:HA	1.51	0.76
14:2:36:ARG:HG3	14:2:42:TRP:CE2	2.21	0.76
1:A:21(G):LEU:HD13	1:A:218:GLY:HA2	1.67	0.75
10:X:20:VAL:HG11	11:Y:120:LEU:HD11	1.68	0.75
9:W:29:ASN:H	9:W:29:ASN:ND2	1.83	0.75
12:L:33:LYS:HD2	12:L:46:ASN:HD22	1.51	0.75
13:M:149:GLN:NE2	13:M:149:GLN:H	1.84	0.75
7:U:87:ASN:HD22	7:U:87:ASN:C	1.88	0.75
2:B:126:HIS:HB3	3:C:129:VAL:HG12	1.68	0.75
11:K:35:ILE:HD11	11:K:45:MET:CE	2.16	0.75
13:1:104:VAL:HG23	13:1:178:ILE:HG22	1.68	0.75
6:F:95:GLU:HG2	6:F:115:ARG:HB3	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:217:LYS:HE3	7:U:217:LYS:HA	1.69	0.75
2:P:126:HIS:HB3	3:Q:129:VAL:HG12	1.69	0.74
6:T:216:SER:HB3	6:T:21(A):GLU:HB2	1.68	0.74
13:1:157:ASN:HD22	13:1:160:ARG:NH1	1.84	0.74
5:E:75:GLY:HA3	5:E:221:PHE:CE2	2.22	0.74
7:U:236:ILE:HD12	7:U:237:ALA:N	2.02	0.74
1:A:124:THR:HG22	2:B:130:ARG:HH21	1.51	0.74
13:M:41:THR:HG21	13:M:79:ILE:HD12	1.70	0.74
9:I:29:ASN:H	9:I:29:ASN:ND2	1.83	0.74
14:N:36:ARG:HG3	14:N:42:TRP:CE2	2.22	0.74
3:C:71:ASP:HA	10:J:68:ILE:CD1	2.18	0.74
12:L:123:GLN:HG3	12:L:145:TYR:OH	1.87	0.74
6:T:35:THR:HG23	6:T:51:GLU:HB3	1.70	0.74
10:J:133:TYR:OH	10:X:24:ILE:HG12	1.87	0.74
2:B:186:VAL:HG21	2:B:216:ARG:HD3	1.70	0.74
2:B:15:PHE:N	3:C:23:GLN:HE22	1.85	0.74
5:E:207:LEU:HD23	5:E:207:LEU:H	1.53	0.74
8:H:81:GLN:O	8:H:85:GLN:HG3	1.88	0.74
10:J:12:VAL:HG23	10:J:108:PRO:HB2	1.69	0.74
3:Q:33:ARG:HB2	3:Q:33:ARG:NH1	2.03	0.74
12:L:-7:ASN:HD22	12:L:-6:PRO:HD2	1.50	0.73
7:U:121:GLN:O	7:U:124:THR:HB	1.88	0.73
13:1:76:PRO:HD2	13:1:105:GLN:OE1	1.88	0.73
3:Q:163:GLN:HE21	3:Q:164:THR:H	1.34	0.73
7:G:198:ILE:HG23	7:G:203:THR:O	1.88	0.73
6:F:35:THR:HG23	6:F:51:GLU:HB3	1.70	0.73
2:P:186:VAL:HG21	2:P:216:ARG:HD3	1.69	0.73
5:S:207:LEU:HD23	5:S:207:LEU:H	1.54	0.73
13:M:8:TYR:CE2	13:M:148:VAL:HG22	2.23	0.73
10:X:46:ALA:HA	16:X:891:HOH:O	1.89	0.73
2:B:65:GLU:HG3	2:B:66:LYS:HG3	1.69	0.73
5:S:141:TYR:CE2	5:S:217:LYS:HA	2.24	0.73
5:E:207:LEU:HA	5:E:2(E):ASN:HD22	1.54	0.72
5:S:207:LEU:HA	5:S:2(E):ASN:HD22	1.54	0.72
13:1:149:GLN:H	13:1:149:GLN:NE2	1.88	0.72
1:A:124:THR:CG2	2:B:130:ARG:HH21	2.02	0.72
2:B:124:THR:CG2	3:C:130:ARG:HH21	2.01	0.72
12:Z:123:GLN:HG3	12:Z:145:TYR:OH	1.89	0.72
7:G:217:LYS:HA	7:G:217:LYS:HE3	1.71	0.72
2:P:71:ASN:ND2	2:P:72:ASP:N	2.37	0.72
11:K:4:LEU:HD12	11:K:159:ILE:CD1	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:33:ARG:HH11	3:Q:33:ARG:CB	2.02	0.72
4:R:97:VAL:HG21	11:Y:65:LEU:HD13	1.72	0.72
2:B:71:ASN:ND2	2:B:72:ASP:N	2.37	0.72
13:M:76:PRO:HD2	13:M:105:GLN:OE1	1.90	0.72
5:E:132:TYR:O	5:E:153:PRO:HB3	1.90	0.72
9:I:29:ASN:HD22	9:I:29:ASN:H	1.38	0.72
11:Y:10(B):LYS:N	11:Y:10(B):LYS:HD2	2.03	0.72
13:M:157:ASN:HD22	13:M:160:ARG:NH1	1.84	0.71
5:S:198:SER:HA	5:S:201:LEU:HG	1.72	0.71
10:X:12:VAL:HG23	10:X:108:PRO:HB2	1.72	0.71
6:F:179:LEU:HD21	6:F:192:GLN:HG2	1.71	0.71
1:O:86:ARG:HE	7:U:118:ASN:HD21	1.38	0.71
11:K:207:ASN:HD21	10:X:144:PRO:CG	2.04	0.71
3:C:164:THR:HG21	3:C:172:VAL:HG13	1.73	0.71
3:C:33:ARG:HB2	3:C:33:ARG:NH1	2.05	0.71
8:V:18:THR:HB	8:V:30:ASN:HD22	1.56	0.71
6:T:179:LEU:HD21	6:T:192:GLN:HG2	1.72	0.71
11:Y:45:MET:HG3	11:Y:52:CYS:CB	2.21	0.71
2:B:152:ASN:HB2	2:B:153:PRO:HD2	1.71	0.71
5:E:141:TYR:CE2	5:E:217:LYS:HA	2.26	0.71
12:Z:-7:ASN:HD22	12:Z:-6:PRO:HD2	1.54	0.71
10:X:44:SER:OG	10:X:100:LEU:HB2	1.90	0.71
2:P:124:THR:CG2	3:Q:130:ARG:HH21	2.04	0.70
3:C:106:PRO:HG2	3:C:143:PRO:CG	2.21	0.70
3:Q:106:PRO:HG2	3:Q:143:PRO:CG	2.21	0.70
8:V:84:LYS:HG3	8:V:85:GLN:N	2.07	0.70
10:J:69:ARG:HD2	16:J:514:HOH:O	1.91	0.70
2:P:152:ASN:HB2	2:P:153:PRO:HD2	1.72	0.70
1:O:179:ARG:HH11	1:O:179:ARG:HB3	1.56	0.70
1:O:21(G):LEU:HD13	1:O:218:GLY:HA2	1.72	0.70
13:1:8:TYR:CE2	13:1:148:VAL:HG22	2.26	0.70
3:C:33:ARG:CB	3:C:33:ARG:HH11	2.04	0.70
10:J:38:SER:HB2	10:J:39:PRO:HD2	1.74	0.70
3:Q:164:THR:HG21	3:Q:172:VAL:HG13	1.73	0.70
7:U:197:MET:HA	7:U:197:MET:HE3	1.73	0.70
5:E:198:SER:HA	5:E:201:LEU:HG	1.72	0.70
10:X:38:SER:HB2	10:X:39:PRO:HD2	1.73	0.70
10:J:52:THR:HG23	10:J:53:VAL:N	2.06	0.70
11:K:10(B):LYS:N	11:K:10(B):LYS:HD2	2.03	0.70
10:X:103:GLY:HA2	10:X:178:VAL:HG11	1.73	0.70
2:B:15:PHE:H	3:C:23:GLN:NE2	1.86	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:81:LEU:HD23	2:P:133:GLY:HA3	1.74	0.69
1:O:67:VAL:HB	1:O:223:LYS:NZ	2.07	0.69
12:L:135:MET:CE	9:W:165:ARG:NH2	2.55	0.69
2:B:185:LYS:HD3	2:B:186:VAL:N	2.07	0.69
7:G:236:ILE:HD12	7:G:237:ALA:N	2.07	0.69
4:D:175:GLU:HG2	4:D:196:ILE:HG12	1.74	0.69
13:M:35:ILE:HG12	13:M:56:GLU:HG3	1.73	0.69
3:Q:168:ASN:HB2	3:Q:200:VAL:HG11	1.75	0.69
5:S:17:PRO:HA	6:T:26:TYR:CD1	2.27	0.69
10:X:52:THR:HG23	10:X:53:VAL:N	2.07	0.69
7:G:121:GLN:O	7:G:124:THR:HB	1.92	0.69
2:B:121:GLN:O	2:B:124:THR:HB	1.92	0.69
13:1:40:ASN:HD22	13:1:40:ASN:N	1.89	0.69
8:H:18:THR:HB	8:H:30:ASN:HD22	1.58	0.69
11:K:45:MET:HG3	11:K:52:CYS:CB	2.22	0.68
3:C:168:ASN:HB2	3:C:200:VAL:HG11	1.74	0.68
13:M:40:ASN:HD22	13:M:40:ASN:N	1.89	0.68
3:Q:173:ARG:O	3:Q:177:GLU:HG3	1.93	0.68
12:Z:109:ALA:HA	16:Z:375:HOH:O	1.91	0.68
6:T:82:ILE:HB	6:T:83:PRO:HD3	1.75	0.68
12:Z:90:LYS:HD3	12:Z:95:TYR:CZ	2.29	0.68
7:U:198:ILE:HG23	7:U:203:THR:O	1.94	0.68
2:B:156:ASN:HD22	2:B:157:TYR:H	1.42	0.68
1:A:15:PHE:H	2:B:23:GLN:HE22	1.40	0.68
2:B:81:LEU:HD23	2:B:133:GLY:HA3	1.76	0.68
4:D:40:ILE:HD12	4:D:193:VAL:HG23	1.75	0.68
10:J:44:SER:OG	10:J:100:LEU:HB2	1.93	0.68
10:J:52:THR:HG23	10:J:53:VAL:H	1.58	0.68
9:W:29:ASN:H	9:W:29:ASN:HD22	1.40	0.68
10:X:52:THR:HG23	10:X:53:VAL:H	1.58	0.68
2:P:185:LYS:HD3	2:P:186:VAL:N	2.09	0.68
1:A:179:ARG:HB3	1:A:179:ARG:HH11	1.58	0.68
2:P:156:ASN:HD22	2:P:157:TYR:H	1.42	0.68
3:C:41:LYS:HG2	3:C:161:SER:O	1.94	0.67
11:K:38:ASN:O	11:K:40:PHE:N	2.27	0.67
5:E:207:LEU:CD2	5:E:207:LEU:H	2.07	0.67
9:I:1:GLY:HA3	9:I:33:LYS:HE2	1.75	0.67
13:1:152:GLU:O	13:1:156:VAL:HG23	1.94	0.67
13:1:35:ILE:HG12	13:1:56:GLU:HG3	1.76	0.67
9:I:6:MET:CE	9:I:155:ILE:HA	2.22	0.67
13:M:104:VAL:HG23	13:M:178:ILE:HG22	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:165:ARG:NH2	12:Z:135:MET:CE	2.57	0.67
1:A:232:ARG:HG3	1:A:232:ARG:HH11	1.58	0.67
9:I:48:LEU:HG	9:I:50:THR:HG22	1.77	0.67
4:R:70:ILE:HB	4:R:74:ILE:HG22	1.77	0.67
12:Z:166:HIS:HD2	12:Z:168:GLN:H	1.42	0.67
12:L:166:HIS:HD2	12:L:168:GLN:H	1.40	0.67
12:L:90:LYS:HD3	12:L:95:TYR:CZ	2.29	0.67
9:W:-2:ASN:HA	9:W:21:GLY:O	1.94	0.67
11:K:207:ASN:ND2	10:X:144:PRO:CG	2.58	0.67
8:V:172:ASN:HD22	8:V:193:THR:HA	1.60	0.67
3:C:173:ARG:O	3:C:177:GLU:HG3	1.94	0.67
5:E:175:TYR:CD2	5:E:196:ALA:HA	2.30	0.67
8:H:173:VAL:HB	8:H:192:LEU:HB2	1.77	0.67
4:R:185:THR:HG23	4:R:188:GLU:OE1	1.95	0.67
5:S:132:TYR:O	5:S:153:PRO:HB3	1.94	0.67
14:2:144:GLU:HG2	16:2:1115:HOH:O	1.93	0.67
1:A:67:VAL:HB	1:A:223:LYS:NZ	2.09	0.67
11:K:40:PHE:HB3	11:K:73:ARG:NH2	2.10	0.67
7:U:18(G):GLU:HG2	7:U:188:LYS:HB2	1.77	0.67
9:W:20:LEU:HA	16:W:240:HOH:O	1.93	0.67
7:G:197:MET:HE3	7:G:197:MET:HA	1.76	0.67
4:R:175:GLU:HG2	4:R:196:ILE:HG12	1.77	0.67
7:U:12:ILE:HG13	7:U:14:ILE:HG23	1.74	0.67
2:B:152:ASN:HB2	2:B:153:PRO:CD	2.25	0.67
13:M:149:GLN:HE21	13:M:149:GLN:H	1.43	0.67
11:Y:12:ILE:HB	11:Y:178:VAL:HB	1.77	0.67
4:D:185:THR:HG23	4:D:188:GLU:OE1	1.94	0.66
6:F:20(B):GLU:HG3	6:F:20(C):LYS:N	2.11	0.66
12:L:109:ALA:HA	16:L:975:HOH:O	1.94	0.66
11:K:12:ILE:HB	11:K:178:VAL:HB	1.76	0.66
8:V:173:VAL:HB	8:V:192:LEU:HB2	1.76	0.66
9:W:6:MET:CE	9:W:155:ILE:HA	2.21	0.66
6:F:20(B):GLU:HG3	6:F:20(C):LYS:HG3	1.76	0.66
2:P:101:LYS:NZ	10:X:85:GLN:HE22	1.93	0.66
2:P:121:GLN:O	2:P:124:THR:HB	1.96	0.66
2:P:61:GLN:OE1	2:P:208:ASP:HA	1.95	0.66
6:F:82:ILE:HB	6:F:83:PRO:HD3	1.77	0.66
12:L:8:GLY:HA3	12:L:11:PHE:CE2	2.31	0.66
9:W:48:LEU:HG	9:W:50:THR:HG22	1.77	0.66
7:G:12:ILE:HG13	7:G:14:ILE:HG23	1.77	0.66
9:I:6:MET:HE3	9:I:155:ILE:HG13	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:232:ARG:HG3	1:O:232:ARG:HH11	1.59	0.66
5:S:175:TYR:CD2	5:S:196:ALA:HA	2.30	0.66
5:S:207:LEU:H	5:S:207:LEU:CD2	2.08	0.66
7:U:35:ILE:HG23	7:U:51:GLN:HB2	1.78	0.66
12:Z:33:LYS:HD2	12:Z:46:ASN:ND2	2.10	0.66
2:B:49:ALA:HB2	2:B:212:PHE:CE1	2.30	0.66
2:B:61:GLN:OE1	2:B:208:ASP:HA	1.96	0.66
1:O:179:ARG:NH1	1:O:179:ARG:HB3	2.10	0.65
9:I:-2:ASN:HA	9:I:21:GLY:O	1.97	0.65
12:L:33:LYS:HD2	12:L:46:ASN:ND2	2.11	0.65
14:N:21:THR:HG22	14:N:26:ILE:HA	1.78	0.65
3:Q:163:GLN:HE22	3:Q:173:ARG:HE	1.44	0.65
7:G:18(G):GLU:HG2	7:G:188:LYS:HB2	1.79	0.65
14:2:21:THR:HG22	14:2:26:ILE:HA	1.77	0.65
8:H:4:VAL:HG22	8:H:159:ILE:HD11	1.79	0.65
4:D:70:ILE:HB	4:D:74:ILE:HG22	1.79	0.65
9:W:1:GLY:HA3	9:W:33:LYS:HE2	1.78	0.65
8:H:84:LYS:HG3	8:H:85:GLN:N	2.10	0.65
4:R:40:ILE:HD12	4:R:193:VAL:HG23	1.78	0.65
6:T:20(B):GLU:HG3	6:T:20(C):LYS:HG3	1.78	0.65
8:V:34:LEU:HB2	16:V:578:HOH:O	1.96	0.65
14:2:55:ILE:HD11	14:2:95:LEU:HD13	1.79	0.65
7:U:87:ASN:ND2	7:U:87:ASN:C	2.50	0.65
11:Y:38:ASN:O	11:Y:40:PHE:N	2.29	0.65
7:G:218:ASP:O	7:G:220:LYS:HB2	1.96	0.65
7:G:77:VAL:HG12	7:G:137:THR:HB	1.78	0.65
11:K:209:VAL:HG13	16:W:348:HOH:O	1.97	0.65
11:Y:71:LYS:HA	16:Y:912:HOH:O	1.97	0.65
11:Y:4:LEU:HD12	11:Y:159:ILE:CD1	2.23	0.64
12:Z:21:ILE:HD12	12:Z:21:ILE:C	2.18	0.64
2:B:149:TYR:OH	3:C:62(A):ILE:HB	1.97	0.64
6:F:119:TYR:O	6:F:122:ALA:HB3	1.97	0.64
6:F:35:THR:HG21	6:F:51:GLU:O	1.97	0.64
11:K:35:ILE:HD11	11:K:45:MET:HE2	1.80	0.64
7:U:218:ASP:O	7:U:220:LYS:HB2	1.96	0.64
1:A:179:ARG:HB3	1:A:179:ARG:NH1	2.12	0.64
7:G:87:ASN:ND2	7:G:87:ASN:C	2.50	0.64
4:D:122:ARG:HG2	4:D:122:ARG:HH11	1.62	0.64
10:J:103:GLY:HA2	10:J:178:VAL:HG11	1.78	0.64
16:P:462:HOH:O	3:Q:87:ILE:HD11	1.95	0.64
5:E:47:VAL:HG23	5:E:189:LEU:HD13	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:49:ALA:HB2	2:P:212:PHE:CE1	2.33	0.64
11:Y:40:PHE:HB3	11:Y:73:ARG:NH2	2.11	0.64
4:D:177:LEU:HD13	5:E:58:LEU:HD11	1.79	0.64
6:F:28:VAL:O	6:F:32:GLU:HG3	1.98	0.64
6:T:184:LEU:HD11	6:T:188:GLU:HB3	1.80	0.64
4:D:12(F):GLY:HA3	16:D:965:HOH:O	1.97	0.64
2:P:152:ASN:HB2	2:P:153:PRO:CD	2.28	0.64
8:V:78:SER:O	8:V:82:MET:HG3	1.98	0.64
9:W:160:LEU:HD11	9:W:191:MET:HB3	1.79	0.64
12:Z:7:ALA:HB2	12:Z:110:VAL:HG23	1.78	0.64
12:Z:-2:ASN:HD21	13:1:118:VAL:HG11	1.63	0.64
3:C:201:VAL:HG21	3:C:210:ILE:HD11	1.79	0.64
10:J:18:LYS:HG2	10:J:174:ILE:HG13	1.80	0.64
7:G:35:ILE:HG23	7:G:51:GLN:HB2	1.80	0.64
9:I:105:ASN:HB3	9:I:10(C):SER:OG	1.98	0.64
10:J:147:THR:HG23	10:J:150:GLU:OE2	1.98	0.64
10:X:147:THR:HG23	10:X:150:GLU:OE2	1.98	0.64
13:1:41:THR:HG21	13:1:79:ILE:HD12	1.79	0.64
3:C:35:THR:HB	3:C:51:GLU:HG3	1.80	0.64
12:L:93:PHE:N	12:L:94:PRO:HD3	2.12	0.64
13:M:152:GLU:O	13:M:156:VAL:HG23	1.97	0.64
2:P:239:THR:OXT	2:P:239:THR:HG22	1.98	0.64
13:1:-6:GLN:O	13:1:-6:GLN:HG3	1.98	0.63
5:E:82:ALA:HB3	5:E:83:PRO:HD3	1.80	0.63
8:H:172:ASN:HD22	8:H:193:THR:HA	1.63	0.63
11:Y:210:ILE:HB	16:Y:1150:HOH:O	1.97	0.63
9:I:1:GLY:HA2	9:I:17:ASP:OD1	1.98	0.63
12:L:13:VAL:HG12	12:L:177:ILE:HG13	1.80	0.63
1:O:67:VAL:HB	1:O:223:LYS:HZ1	1.62	0.63
9:W:156:SER:O	9:W:160:LEU:HB2	1.97	0.63
12:Z:8:GLY:HA3	12:Z:11:PHE:CE2	2.34	0.63
5:E:2(B):THR:H	5:E:2(E):ASN:HD22	1.45	0.63
12:L:21:ILE:HD12	12:L:21:ILE:C	2.18	0.63
3:Q:106:PRO:HG2	3:Q:143:PRO:HG3	1.81	0.63
10:J:144:PRO:CG	11:Y:207:ASN:HD21	2.12	0.63
12:Z:40:ASN:HD21	12:Z:183:GLY:HA2	1.62	0.63
13:M:3:VAL:HG23	13:M:46:SER:HB3	1.81	0.63
3:Q:33:ARG:HH11	3:Q:33:ARG:HB2	1.62	0.63
10:J:15:ALA:HB2	10:J:155:LEU:HD11	1.80	0.63
12:L:40:ASN:HD21	12:L:183:GLY:HA2	1.62	0.63
6:T:119:TYR:O	6:T:122:ALA:HB3	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:226:GLY:O	5:E:229:VAL:HG22	1.98	0.63
9:I:55:LEU:CD1	9:I:97:VAL:HG21	2.29	0.63
3:Q:201:VAL:HG21	3:Q:210:ILE:HD11	1.79	0.63
11:K:207:ASN:ND2	10:X:144:PRO:HG3	2.13	0.63
11:Y:10(B):LYS:CD	11:Y:10(B):LYS:H	2.07	0.63
6:F:120:VAL:HG21	6:F:151:LEU:HD21	1.80	0.63
6:T:20(B):GLU:HG3	6:T:20(C):LYS:N	2.12	0.63
8:V:4:VAL:HG22	8:V:159:ILE:HD11	1.81	0.63
12:Z:93:PHE:N	12:Z:94:PRO:HD3	2.14	0.63
3:Q:41:LYS:HG2	3:Q:161:SER:O	1.99	0.62
5:S:15:PHE:HB2	6:T:23:GLN:NE2	2.10	0.62
3:C:160:TRP:CE2	4:D:59:LEU:HD23	2.34	0.62
9:W:6:MET:HE3	9:W:155:ILE:HG13	1.79	0.62
3:C:71:ASP:HA	10:J:68:ILE:HD11	1.81	0.62
2:P:141:TYR:CD1	2:P:21(E):VAL:HG21	2.34	0.62
11:Y:35:ILE:HD11	11:Y:45:MET:HE2	1.80	0.62
1:A:86:ARG:HE	7:G:118:ASN:ND2	1.98	0.62
13:M:122:SER:HA	16:M:1128:HOH:O	1.98	0.62
14:N:55:ILE:HD11	14:N:95:LEU:HD13	1.80	0.62
5:S:2(B):THR:H	5:S:2(E):ASN:HD22	1.46	0.62
6:F:127:ASN:HD22	6:F:128:SER:N	1.97	0.62
4:R:29:GLU:OE2	4:R:32:LYS:HD2	1.99	0.62
8:V:172:ASN:ND2	8:V:193:THR:HA	2.15	0.62
10:X:18:LYS:HG2	10:X:174:ILE:HG13	1.80	0.62
5:S:47:VAL:HG23	5:S:189:LEU:HD13	1.80	0.62
10:X:156:LYS:O	10:X:160:GLN:HG3	2.00	0.62
2:B:121:GLN:CG	3:C:83:ALA:HB1	2.30	0.62
3:C:216:LYS:HB2	3:C:220:ASP:HB3	1.81	0.62
10:X:178:VAL:HG22	10:X:184:ILE:HG12	1.81	0.62
13:1:148:VAL:HG23	16:1:182:HOH:O	2.00	0.62
13:1:149:GLN:H	13:1:149:GLN:HE21	1.47	0.62
1:O:33:GLN:CA	1:O:33:GLN:HE21	2.11	0.62
2:P:121:GLN:CG	3:Q:83:ALA:HB1	2.30	0.62
5:S:148:LEU:CD2	5:S:162:GLY:HA2	2.30	0.62
5:S:207:LEU:N	5:S:207:LEU:HD23	2.15	0.62
2:B:156:ASN:HB2	16:C:1179:HOH:O	2.00	0.62
3:C:106:PRO:HG2	3:C:143:PRO:HG3	1.80	0.62
6:F:184:LEU:HD11	6:F:188:GLU:HB3	1.82	0.62
5:E:17:PRO:HA	6:F:26:TYR:CD1	2.35	0.62
10:X:113:ILE:HA	10:X:118:THR:O	2.00	0.62
13:1:41:THR:OG1	13:1:76:PRO:HG3	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:161:LYS:HD3	1:O:180:TRP:CZ3	2.34	0.62
2:P:234:VAL:HA	2:P:239:THR:HA	1.82	0.62
9:W:105:ASN:HB3	9:W:10(C):SER:OG	2.00	0.62
3:Q:216:LYS:HB2	3:Q:220:ASP:HB3	1.82	0.61
3:Q:71:ASP:HA	10:X:68:ILE:CD1	2.31	0.61
5:E:207:LEU:HD23	5:E:207:LEU:N	2.15	0.61
10:J:162:LEU:O	10:J:166:MET:HB2	1.99	0.61
10:J:-1:MET:HG2	10:J:1:ASP:N	2.12	0.61
9:W:14:ILE:HG23	9:W:34:ILE:HD13	1.80	0.61
2:B:160:TRP:HA	3:C:59:GLN:HA	1.82	0.61
9:I:160:LEU:HD11	9:I:191:MET:HB3	1.81	0.61
14:N:14:LEU:HD11	14:N:102:ALA:HB3	1.83	0.61
6:T:32:GLU:HB3	6:T:169:ARG:NH2	2.14	0.61
10:X:162:LEU:O	10:X:166:MET:HB2	2.00	0.61
2:B:141:TYR:CD1	2:B:21(E):VAL:HG21	2.34	0.61
12:L:-2:ASN:HA	12:L:21:ILE:O	2.00	0.61
5:S:82:ALA:HB3	5:S:83:PRO:HD3	1.82	0.61
9:W:101:VAL:O	9:W:110:ILE:HA	2.00	0.61
16:L:200:HOH:O	9:W:192:ARG:HG3	1.99	0.61
12:Z:58:ARG:NH2	16:Z:1275:HOH:O	2.33	0.61
7:G:136:LEU:O	7:G:150:LYS:HA	2.00	0.61
6:T:127:ASN:HD22	6:T:128:SER:N	1.99	0.61
11:Y:180:GLU:N	16:Y:812:HOH:O	2.32	0.61
3:C:215:VAL:HG23	3:C:221:ILE:HG12	1.82	0.61
10:X:133:TYR:CE2	10:X:166:MET:HG3	2.35	0.61
7:U:77:VAL:HG12	7:U:137:THR:HB	1.82	0.61
7:U:95:GLU:HB3	16:U:925:HOH:O	1.99	0.61
8:V:35:HIS:CB	8:V:56:THR:HG21	2.27	0.61
4:R:122:ARG:HH11	4:R:122:ARG:HG2	1.66	0.61
8:V:18:THR:CB	8:V:30:ASN:HD22	2.13	0.61
10:X:15:ALA:HB2	10:X:155:LEU:HD11	1.82	0.61
10:J:156:LYS:O	10:J:160:GLN:HG3	1.99	0.61
10:J:178:VAL:HG22	10:J:184:ILE:HG12	1.83	0.61
11:K:200:LYS:HE3	11:K:206:PHE:O	2.00	0.61
13:M:-6:GLN:O	13:M:-6:GLN:HG3	1.99	0.61
3:Q:186:VAL:O	3:Q:190:VAL:HG23	2.01	0.61
3:Q:215:VAL:HG23	3:Q:221:ILE:HG12	1.83	0.61
3:Q:35:THR:HB	3:Q:51:GLU:HG3	1.82	0.61
10:J:24:ILE:HG12	10:X:133:TYR:OH	2.01	0.61
1:A:33:GLN:HE21	1:A:33:GLN:CA	2.14	0.61
5:E:86:ARG:HH11	5:E:86:ARG:HG3	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:34:LEU:HB2	16:H:540:HOH:O	2.01	0.61
9:I:90:ARG:HH11	9:I:90:ARG:HA	1.66	0.61
12:L:7:ALA:HB2	12:L:110:VAL:HG23	1.81	0.61
9:W:174:VAL:HG21	9:W:186:LYS:HE3	1.83	0.61
2:B:239:THR:OXT	2:B:239:THR:HG22	2.01	0.60
7:G:18(G):GLU:HG2	7:G:188:LYS:CB	2.31	0.60
11:K:208:ASN:HB3	16:X:776:HOH:O	2.01	0.60
12:L:14:LEU:HD13	12:L:34:VAL:HG13	1.83	0.60
9:W:27:VAL:HG13	16:X:622:HOH:O	2.01	0.60
10:X:-1:MET:CG	10:X:1:ASP:H	2.13	0.60
12:Z:13:VAL:HG12	12:Z:177:ILE:HG13	1.83	0.60
1:A:20:LYS:HE3	1:A:25:ASP:OD1	2.02	0.60
4:D:25:GLU:HA	4:D:28:LEU:HD22	1.83	0.60
9:W:113:PHE:HA	9:W:118:CYS:O	2.00	0.60
1:A:161:LYS:HD3	1:A:180:TRP:CZ3	2.36	0.60
3:C:163:GLN:HE22	3:C:173:ARG:HE	1.46	0.60
9:I:137:MET:HE3	9:I:141:LEU:CD1	2.31	0.60
5:S:86:ARG:HH11	5:S:86:ARG:HG3	1.65	0.60
7:U:100:ARG:HG3	7:U:100:ARG:HH11	1.67	0.60
9:W:46:THR:HA	16:W:608:HOH:O	2.01	0.60
10:X:49:ALA:HB2	16:X:1094:HOH:O	2.01	0.60
6:F:192:GLN:O	6:F:196:ILE:HG13	2.02	0.60
2:P:146:TYR:HE1	2:P:215:ILE:HG22	1.67	0.60
2:P:21(A):LYS:HE2	2:P:21(D):GLY:O	2.01	0.60
12:L:135:MET:HE2	9:W:165:ARG:NH2	2.15	0.60
11:Y:45:MET:HG3	11:Y:52:CYS:HB2	1.81	0.60
14:2:65:LEU:HG	14:2:69:GLN:HE21	1.66	0.60
2:B:21(A):LYS:HE2	2:B:21(D):GLY:O	2.01	0.60
12:L:-2:ASN:HD21	13:M:118:VAL:HG11	1.66	0.60
4:R:25:GLU:HA	4:R:28:LEU:HD22	1.84	0.60
9:W:7:THR:HG23	9:W:110:ILE:HD13	1.84	0.60
9:I:165:ARG:NH2	12:Z:135:MET:HE3	2.17	0.60
3:C:186:VAL:O	3:C:190:VAL:HG23	2.01	0.60
1:A:86:ARG:HE	7:G:118:ASN:HD21	1.49	0.60
1:O:118:LYS:HE2	1:O:122:GLU:OE1	2.02	0.60
4:R:177:LEU:HD13	5:S:58:LEU:HD11	1.83	0.60
6:T:173:LYS:O	6:T:177:GLU:HG3	2.01	0.60
7:U:186:TRP:O	7:U:190:VAL:HG23	2.01	0.60
9:W:55:LEU:CD1	9:W:97:VAL:HG21	2.32	0.60
9:W:90:ARG:HH11	9:W:90:ARG:HA	1.66	0.60
12:Z:4:LEU:CD1	12:Z:138:LEU:HD21	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:121:GLN:C	3:C:121:GLN:NE2	2.55	0.60
8:H:18:THR:CB	8:H:30:ASN:HD22	2.15	0.60
11:K:142:TYR:C	11:K:143:LYS:HD2	2.22	0.60
2:P:71:ASN:HD22	2:P:72:ASP:N	1.98	0.60
12:Z:14:LEU:HD13	12:Z:34:VAL:HG13	1.84	0.60
2:B:71:ASN:HD22	2:B:72:ASP:N	1.99	0.60
3:C:156:ILE:HA	16:C:1013:HOH:O	2.01	0.60
4:R:205:GLU:OE2	4:R:205:GLU:HA	2.01	0.60
12:Z:-2:ASN:HA	12:Z:21:ILE:O	2.01	0.60
12:Z:-6:PRO:O	13:1:91:ARG:NH1	2.34	0.59
8:H:172:ASN:ND2	8:H:193:THR:HA	2.17	0.59
12:L:135:MET:HE3	9:W:165:ARG:NH2	2.16	0.59
3:Q:121:GLN:C	3:Q:121:GLN:NE2	2.55	0.59
13:1:3:VAL:HG23	13:1:46:SER:HB3	1.84	0.59
9:I:156:SER:O	9:I:160:LEU:HB2	2.01	0.59
13:M:29:ASN:N	16:M:802:HOH:O	2.33	0.59
3:Q:160:TRP:CE2	4:R:59:LEU:HD23	2.37	0.59
7:U:18(G):GLU:HG2	7:U:188:LYS:CB	2.31	0.59
11:K:207:ASN:HD21	10:X:144:PRO:HG3	1.67	0.59
10:J:143:ARG:HB2	10:J:146:MET:HG3	1.83	0.59
5:S:175:TYR:HB2	5:S:199:GLN:HG2	1.83	0.59
1:A:118:LYS:HE2	1:A:122:GLU:OE1	2.02	0.59
2:B:234:VAL:HA	2:B:239:THR:HA	1.82	0.59
6:T:120:VAL:HG21	6:T:151:LEU:HD21	1.82	0.59
7:U:136:LEU:O	7:U:150:LYS:HA	2.02	0.59
9:W:1:GLY:HA2	9:W:17:ASP:OD1	2.01	0.59
10:X:143:ARG:HB2	10:X:146:MET:HG3	1.84	0.59
10:J:144:PRO:CG	11:Y:207:ASN:ND2	2.65	0.59
5:E:148:LEU:CD2	5:E:162:GLY:HA2	2.32	0.59
9:I:2:ILE:HG21	9:I:130:ALA:HB3	1.85	0.59
10:J:24:ILE:O	10:X:133:TYR:OH	2.21	0.59
11:K:10(B):LYS:H	11:K:10(B):LYS:CD	2.08	0.59
5:S:226:GLY:O	5:S:229:VAL:HG22	2.02	0.59
6:T:28:VAL:O	6:T:32:GLU:HG3	2.01	0.59
6:T:35:THR:HG21	6:T:51:GLU:O	2.01	0.59
14:2:14:LEU:HD11	14:2:102:ALA:HB3	1.84	0.59
2:B:10:SER:HB2	16:B:248:HOH:O	2.02	0.59
6:F:32:GLU:HB3	6:F:169:ARG:NH2	2.17	0.59
10:J:113:ILE:HA	10:J:118:THR:O	2.01	0.59
11:K:67:GLU:CD	11:K:73:ARG:HA	2.22	0.59
1:O:161:LYS:HD3	1:O:180:TRP:CH2	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:181:LYS:HG3	2:P:184:MET:HG3	1.85	0.59
3:C:163:GLN:NE2	3:C:164:THR:H	1.99	0.59
9:I:7:THR:HG23	9:I:110:ILE:HD13	1.85	0.59
11:K:156:LYS:HE2	11:K:190:HIS:CD2	2.38	0.59
11:Y:6:PHE:HA	11:Y:123:ASP:O	2.02	0.59
9:I:113:PHE:HA	9:I:118:CYS:O	2.03	0.59
9:I:137:MET:CE	9:I:141:LEU:HD11	2.32	0.59
4:D:112:LEU:C	4:D:112:LEU:HD13	2.23	0.59
1:O:134:VAL:O	1:O:153:PRO:HG3	2.02	0.59
10:X:-1:MET:HG2	10:X:1:ASP:N	2.14	0.59
1:A:150:GLN:O	1:A:157:TYR:HA	2.03	0.59
4:D:205:GLU:HA	4:D:205:GLU:OE2	2.01	0.59
6:F:90:ASN:O	6:F:94:GLU:HG3	2.02	0.59
9:I:174:VAL:HG21	9:I:186:LYS:HE3	1.84	0.59
12:L:-7:ASN:HD22	12:L:-6:PRO:CD	2.15	0.59
1:O:57:PRO:HG3	7:U:177:GLU:CD	2.22	0.59
11:Y:143:LYS:HB2	11:Y:146:LEU:CD1	2.33	0.59
11:Y:174:ASN:HD21	11:Y:189:ASN:ND2	1.98	0.59
2:B:163:ILE:HG13	2:B:164:SER:N	2.18	0.58
11:K:13:ILE:HD12	11:K:152:LEU:HD23	1.85	0.58
11:K:45:MET:HG3	11:K:52:CYS:HB2	1.83	0.58
9:I:165:ARG:NH2	12:Z:135:MET:HE2	2.18	0.58
5:S:78:LEU:HD12	5:S:78:LEU:C	2.23	0.58
9:W:29:ASN:N	9:W:29:ASN:HD22	2.00	0.58
2:B:156:ASN:ND2	2:B:157:TYR:H	2.01	0.58
6:F:109:ILE:HB	6:F:110:PRO:HD3	1.85	0.58
1:O:20:LYS:HE3	1:O:25:ASP:OD1	2.03	0.58
1:O:7:ARG:HD3	5:S:127:TYR:HD2	1.68	0.58
2:P:121:GLN:HG2	3:Q:83:ALA:HB1	1.85	0.58
11:Y:67:GLU:CD	11:Y:73:ARG:HA	2.24	0.58
1:A:161:LYS:HD3	1:A:180:TRP:CH2	2.39	0.58
5:E:15:PHE:HB2	6:F:23:GLN:NE2	2.14	0.58
9:I:101:VAL:O	9:I:110:ILE:HA	2.04	0.58
5:S:92:LEU:HD11	5:S:112:ALA:HB1	1.86	0.58
4:D:29:GLU:OE2	4:D:32:LYS:HD2	2.03	0.58
6:F:136:THR:HB	16:F:1005:HOH:O	2.04	0.58
13:1:91:ARG:HG3	13:1:92:SER:N	2.18	0.58
1:A:232:ARG:HG3	1:A:232:ARG:NH1	2.19	0.58
1:A:79:SER:HB2	1:A:165:ILE:HD12	1.86	0.58
2:B:181:LYS:HG3	2:B:184:MET:HG3	1.85	0.58
3:C:227:GLU:OE1	3:C:227:GLU:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:156:ASN:ND2	2:P:157:TYR:H	2.02	0.58
8:V:200:LYS:HE3	9:W:140:SER:O	2.03	0.58
4:D:161:ASN:HB3	4:D:180:TRP:CE2	2.39	0.58
12:L:4:LEU:CD1	12:L:138:LEU:HD21	2.34	0.58
6:T:237:GLN:O	6:T:240:ILE:HG22	2.03	0.58
10:X:6:ILE:HD11	10:X:154:LEU:HD23	1.86	0.58
12:Z:151:VAL:O	12:Z:155:VAL:HG23	2.04	0.58
13:M:57:ARG:NE	16:M:621:HOH:O	2.37	0.58
1:O:112:LEU:O	1:O:116:VAL:HG23	2.03	0.58
4:R:75:GLY:HA3	4:R:221:PHE:CD2	2.39	0.58
4:R:85:ALA:O	4:R:89:ILE:HG12	2.03	0.58
8:V:208:ARG:HG3	16:V:1135:HOH:O	2.03	0.58
11:K:211:GLY:HA2	8:V:214:LEU:HD22	1.83	0.58
10:X:6:ILE:CD1	10:X:154:LEU:HD23	2.34	0.58
6:F:173:LYS:O	6:F:177:GLU:HG3	2.04	0.58
9:I:14:ILE:HG23	9:I:34:ILE:HD13	1.84	0.58
3:C:101:LEU:HD11	10:J:57:GLU:HB3	1.86	0.58
10:J:6:ILE:CD1	10:J:154:LEU:HD23	2.34	0.58
5:S:41:ARG:NH1	5:S:42:SER:O	2.37	0.58
4:D:75:GLY:HA3	4:D:221:PHE:CD2	2.37	0.58
3:Q:190:VAL:HG13	3:Q:212:ILE:HG21	1.86	0.58
2:P:15:PHE:N	3:Q:23:GLN:HE22	1.97	0.58
4:R:40:ILE:HD13	4:R:192:LEU:HD23	1.86	0.58
9:W:137:MET:CE	9:W:141:LEU:HD11	2.34	0.58
3:Q:101:LEU:HD11	10:X:57:GLU:HB3	1.84	0.58
11:Y:200:LYS:HE3	11:Y:206:PHE:O	2.03	0.58
2:B:121:GLN:HG2	3:C:83:ALA:HB1	1.86	0.57
3:C:232:TYR:O	3:C:236:ILE:HG13	2.04	0.57
3:C:241:GLN:C	3:C:243:GLN:H	2.08	0.57
14:N:157:HIS:HD2	14:2:140:LYS:NZ	2.02	0.57
1:O:202:VAL:HG21	1:O:206:PHE:CD1	2.39	0.57
3:Q:232:TYR:O	3:Q:236:ILE:HG13	2.04	0.57
5:S:136:LEU:HB2	5:S:151:PHE:HB3	1.86	0.57
14:N:140:LYS:NZ	14:2:157:HIS:HD2	2.02	0.57
1:A:69:LEU:HD23	1:A:69:LEU:C	2.25	0.57
2:B:238:ILE:O	2:B:239:THR:O	2.21	0.57
10:J:133:TYR:OH	10:X:24:ILE:O	2.21	0.57
11:K:143:LYS:HB2	11:K:146:LEU:CD1	2.34	0.57
4:R:15:PHE:HB2	5:S:23:GLN:OE1	2.04	0.57
2:B:146:TYR:HE1	2:B:215:ILE:HG22	1.68	0.57
14:N:120:HIS:HA	16:N:1107:HOH:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:90:ASN:O	6:T:94:GLU:HG3	2.04	0.57
10:X:127:HIS:O	16:X:1164:HOH:O	2.17	0.57
1:A:142:ASP:OD1	1:A:145:ASN:HB2	2.04	0.57
2:B:185:LYS:HE2	2:B:187:ASP:OD1	2.04	0.57
12:L:139:ASP:O	12:L:14(A):LYS:HG2	2.04	0.57
7:U:100:ARG:HG3	7:U:100:ARG:NH1	2.19	0.57
1:A:202:VAL:HG21	1:A:206:PHE:CD1	2.39	0.57
3:C:151:THR:HG22	3:C:157:TYR:HB3	1.84	0.57
5:E:136:LEU:HB2	5:E:151:PHE:HB3	1.87	0.57
5:E:78:LEU:HD12	5:E:78:LEU:C	2.25	0.57
11:K:6:PHE:HA	11:K:123:ASP:O	2.04	0.57
2:P:38:ILE:HD12	2:P:197:LEU:HG	1.86	0.57
11:Y:111:TYR:OH	16:Y:471:HOH:O	2.16	0.57
11:Y:142:TYR:C	11:Y:143:LYS:HD2	2.23	0.57
11:Y:45:MET:HG3	11:Y:52:CYS:HB3	1.86	0.57
13:1:112:TYR:HE1	13:1:127:THR:HG22	1.70	0.57
3:C:33:ARG:HB2	3:C:33:ARG:HH11	1.64	0.57
7:G:170:GLN:HE21	7:G:174:THR:HG23	1.68	0.57
10:J:133:TYR:CE2	10:J:166:MET:HG3	2.39	0.57
1:O:79:SER:HB2	1:O:165:ILE:HD12	1.86	0.57
9:W:2:ILE:HG21	9:W:130:ALA:HB3	1.85	0.57
5:E:92:LEU:HD11	5:E:112:ALA:HB1	1.87	0.57
6:F:20(B):GLU:HG3	6:F:20(C):LYS:H	1.68	0.57
1:O:150:GLN:O	1:O:157:TYR:HA	2.03	0.57
2:P:163:ILE:HG13	2:P:164:SER:N	2.19	0.57
3:Q:227:GLU:N	3:Q:227:GLU:OE1	2.37	0.57
3:Q:241:GLN:C	3:Q:243:GLN:H	2.08	0.57
7:U:170:GLN:HE21	7:U:174:THR:HG23	1.68	0.57
11:Y:13:ILE:HD12	11:Y:152:LEU:HD23	1.86	0.57
2:P:87:ILE:O	2:P:91:THR:HG23	2.04	0.57
12:Z:-7:ASN:HD22	12:Z:-6:PRO:CD	2.17	0.57
13:1:12:VAL:HG21	13:1:102:ALA:HB1	1.86	0.57
2:B:173:GLN:HG2	3:C:56:LEU:HD12	1.87	0.57
4:D:93:ARG:HD2	16:D:248:HOH:O	2.04	0.57
14:N:106:ASN:O	14:N:107:LYS:HB3	2.03	0.57
2:P:101:LYS:HZ2	10:X:85:GLN:HE22	1.52	0.57
13:1:42:VAL:CG2	13:1:178:ILE:HD11	2.35	0.57
1:O:57:PRO:HG2	7:U:177:GLU:HG2	1.86	0.57
3:Q:57:LYS:HG2	3:Q:208:LYS:NZ	2.20	0.57
5:S:86:ARG:O	5:S:90:ASN:HB2	2.04	0.57
14:2:106:ASN:O	14:2:107:LYS:HB3	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:38:ILE:HD12	2:B:197:LEU:HG	1.87	0.56
2:B:225:LYS:HG3	2:B:228:GLU:OE1	2.04	0.56
5:E:86:ARG:O	5:E:90:ASN:HB2	2.05	0.56
9:W:137:MET:HE3	9:W:141:LEU:CD1	2.34	0.56
9:W:192:ARG:HD2	16:W:1258:HOH:O	2.03	0.56
1:A:112:LEU:O	1:A:116:VAL:HG23	2.04	0.56
5:E:145:GLY:HA3	16:E:1070:HOH:O	2.03	0.56
7:G:77:VAL:CG1	7:G:137:THR:HB	2.35	0.56
11:K:45:MET:HG3	11:K:52:CYS:HB3	1.87	0.56
3:Q:121:GLN:HE21	3:Q:122:ARG:N	2.03	0.56
10:J:144:PRO:HG3	11:Y:207:ASN:ND2	2.20	0.56
8:H:84:LYS:HD3	16:H:237:HOH:O	2.05	0.56
10:J:6:ILE:HD11	10:J:154:LEU:HD23	1.86	0.56
1:O:6:ASP:OD2	1:O:8:TYR:HB2	2.05	0.56
4:R:101:LEU:CD1	11:Y:57:THR:HG22	2.35	0.56
11:K:210:ILE:HD13	9:W:30:LYS:HE3	1.87	0.56
11:Y:86:LEU:C	11:Y:86:LEU:HD13	2.25	0.56
5:S:194:VAL:O	5:S:197:ILE:HG22	2.05	0.56
2:B:19:GLY:O	16:B:565:HOH:O	2.17	0.56
13:M:12:VAL:HG21	13:M:102:ALA:HB1	1.86	0.56
1:O:232:ARG:HG3	1:O:232:ARG:NH1	2.19	0.56
4:R:12(G):GLU:HG2	4:R:125:GLU:H	1.69	0.56
4:R:161:ASN:HB3	4:R:180:TRP:CE2	2.40	0.56
8:H:35:HIS:CB	8:H:56:THR:HG21	2.28	0.56
1:O:69:LEU:HD23	1:O:69:LEU:C	2.25	0.56
2:P:202:THR:CG2	2:P:204:SER:H	2.08	0.56
9:W:12:VAL:CG1	9:W:108:PRO:HB3	2.35	0.56
3:C:163:GLN:HG3	3:C:164:THR:N	2.21	0.56
4:D:24:VAL:O	4:D:27:SER:HB3	2.06	0.56
8:H:200:LYS:HE3	9:I:140:SER:O	2.06	0.56
2:B:228:GLU:O	2:B:232:ILE:HG22	2.05	0.56
4:D:12(G):GLU:HG2	4:D:125:GLU:H	1.70	0.56
5:E:175:TYR:HB2	5:E:199:GLN:HG2	1.85	0.56
6:F:179:LEU:HD11	6:F:192:GLN:CG	2.36	0.56
11:K:99:THR:HG22	11:K:113:VAL:O	2.05	0.56
12:L:14(C):GLN:HG2	8:V:210:THR:CG2	2.35	0.56
2:P:225:LYS:HG3	2:P:228:GLU:OE1	2.05	0.56
7:U:10:ARG:HG2	7:U:22:TYR:CD2	2.40	0.56
7:U:17(D):SER:O	7:U:17(E):LYS:HB2	2.05	0.56
10:X:136:SER:HA	16:X:559:HOH:O	2.06	0.56
1:A:186:LEU:O	1:A:190:ILE:HG13	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:PRO:HD3	16:H:1303:HOH:O	2.04	0.56
1:A:6:ASP:OD2	1:A:8:TYR:HB2	2.05	0.56
13:M:112:TYR:HE1	13:M:127:THR:HG22	1.71	0.56
2:P:228:GLU:O	2:P:232:ILE:HG22	2.06	0.56
14:2:28:ASN:HA	16:2:199:HOH:O	2.06	0.56
3:C:15:PHE:N	4:D:23:GLN:HE22	1.99	0.56
5:E:194:VAL:O	5:E:197:ILE:HG22	2.06	0.56
6:F:171:SER:O	6:F:174:ALA:HB3	2.05	0.56
8:H:210:THR:CG2	12:Z:14(C):GLN:HG2	2.36	0.56
14:N:14:LEU:O	14:N:175:MET:HA	2.04	0.56
2:P:185:LYS:HE2	2:P:187:ASP:OD1	2.06	0.56
3:Q:55:THR:HG22	3:Q:56:LEU:HD22	1.88	0.56
4:R:177:LEU:HD22	5:S:58:LEU:HD13	1.88	0.56
6:T:171:SER:O	6:T:174:ALA:HB3	2.05	0.56
11:K:86:LEU:HD13	11:K:86:LEU:C	2.26	0.56
3:Q:112:LEU:O	3:Q:116:VAL:HG23	2.06	0.56
3:Q:76:LEU:HD12	3:Q:138:ILE:HG12	1.88	0.56
8:V:8:PHE:HB2	8:V:146:LEU:O	2.05	0.56
9:I:12:VAL:CG1	9:I:108:PRO:HB3	2.35	0.55
6:T:179:LEU:HD21	6:T:192:GLN:CG	2.36	0.55
11:Y:66:HIS:HA	16:Y:1210:HOH:O	2.06	0.55
8:H:165:ASN:ND2	13:I:139:ARG:HH11	2.01	0.55
8:H:147:THR:HG23	8:H:150:GLU:OE1	2.05	0.55
13:M:40:ASN:ND2	13:M:40:ASN:N	2.55	0.55
2:P:112:LEU:HD23	2:P:112:LEU:C	2.26	0.55
14:2:14:LEU:O	14:2:175:MET:HA	2.05	0.55
1:A:29:THR:O	1:A:33:GLN:HG2	2.06	0.55
6:T:20(B):GLU:HG3	6:T:20(C):LYS:H	1.69	0.55
12:Z:11:PHE:O	12:Z:108:GLY:HA3	2.06	0.55
3:C:76:LEU:HD22	3:C:89:ILE:HG12	1.89	0.55
9:I:6:MET:HB3	9:I:151:LEU:HD11	1.87	0.55
13:M:211:ILE:HG12	16:M:544:HOH:O	2.06	0.55
3:Q:224:LEU:N	3:Q:224:LEU:HD12	2.22	0.55
6:T:147:HIS:HD2	16:T:242:HOH:O	1.88	0.55
10:X:4:LEU:HD23	10:X:126:ALA:HB2	1.88	0.55
11:Y:18:SER:HA	11:Y:33:LYS:HE3	1.88	0.55
12:L:185:ARG:HA	16:L:1212:HOH:O	2.04	0.55
14:N:8:PHE:CE1	14:N:10:ASP:HB2	2.42	0.55
7:U:8:TYR:C	7:U:10:ARG:H	2.10	0.55
13:I:205:GLY:HA3	13:I:209:GLN:HB3	1.89	0.55
10:J:-1:MET:CG	10:J:1:ASP:H	2.12	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:87:ASN:HD22	7:U:88:ALA:N	2.04	0.55
12:Z:139:ASP:O	12:Z:14(A):LYS:HG2	2.06	0.55
3:C:57:LYS:HG2	3:C:208:LYS:NZ	2.22	0.55
5:E:41:ARG:NH1	5:E:42:SER:O	2.39	0.55
14:N:84:LYS:HG3	14:N:119:VAL:CG2	2.37	0.55
14:2:112:THR:HG22	14:2:120:HIS:HB2	1.89	0.55
1:A:130:ARG:HG2	7:G:125:GLN:HG3	1.89	0.55
11:K:7:ARG:HG3	11:K:12:ILE:HG12	1.89	0.55
12:L:90:LYS:HD3	12:L:95:TYR:CE1	2.41	0.55
11:Y:156:LYS:HE2	11:Y:190:HIS:CD2	2.42	0.55
1:A:173:LYS:O	1:A:177:GLU:HG3	2.07	0.55
6:F:179:LEU:HD21	6:F:192:GLN:CG	2.35	0.55
4:D:85:ALA:O	4:D:89:ILE:HG12	2.07	0.55
13:M:17:ASP:HA	13:M:173:PHE:HA	1.89	0.55
1:O:142:ASP:OD1	1:O:145:ASN:HB2	2.07	0.55
3:Q:172:VAL:HG23	3:Q:196:SER:HB2	1.89	0.55
10:X:32:ASP:OD2	10:X:34:THR:HG22	2.07	0.55
11:Y:174:ASN:ND2	11:Y:189:ASN:HD22	2.01	0.55
14:2:36:ARG:HG3	14:2:42:TRP:CZ2	2.41	0.54
14:2:84:LYS:HG3	14:2:119:VAL:CG2	2.37	0.54
2:B:87:ILE:O	2:B:91:THR:HG23	2.06	0.54
3:C:190:VAL:HG13	3:C:212:ILE:HG21	1.89	0.54
4:D:219:ASP:O	4:D:222:LYS:HE2	2.06	0.54
5:E:21:LEU:HA	16:E:346:HOH:O	2.06	0.54
7:G:17(D):SER:O	7:G:17(E):LYS:HB2	2.07	0.54
10:J:66:TYR:CE2	10:J:74:LEU:HG	2.43	0.54
11:K:73:ARG:NH2	11:K:104:TYR:O	2.40	0.54
12:L:-6:PRO:O	13:M:91:ARG:NH1	2.40	0.54
9:W:28:SER:HB2	10:X:120:VAL:HG21	1.89	0.54
3:C:121:GLN:HE21	3:C:122:ARG:N	2.05	0.54
14:N:65:LEU:HG	14:N:69:GLN:HE21	1.70	0.54
7:U:228:ASN:HB3	16:U:242:HOH:O	2.07	0.54
12:L:192:LYS:HE3	8:V:195:ASN:HB3	1.89	0.54
11:Y:7:ARG:HG3	11:Y:12:ILE:HG12	1.88	0.54
1:O:173:LYS:O	1:O:177:GLU:HG3	2.07	0.54
1:O:186:LEU:O	1:O:190:ILE:HG13	2.07	0.54
11:Y:12:ILE:HG13	11:Y:108:PRO:HB3	1.89	0.54
14:2:48:SER:HB3	14:2:51:ASP:HB2	1.90	0.54
13:M:41:THR:OG1	13:M:76:PRO:HG3	2.08	0.54
9:W:143:GLU:HG3	9:W:146:LEU:HD21	1.90	0.54
9:I:29:ASN:HD22	9:I:29:ASN:N	1.99	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:151:VAL:O	12:L:155:VAL:HG23	2.07	0.54
1:O:225:THR:OG1	1:O:228:GLU:HG3	2.07	0.54
2:P:136:PHE:O	2:P:150:THR:HA	2.08	0.54
3:Q:14:ILE:HB	4:R:23:GLN:NE2	2.23	0.54
6:T:192:GLN:O	6:T:196:ILE:HG13	2.07	0.54
3:C:224:LEU:N	3:C:224:LEU:HD12	2.23	0.54
3:C:57:LYS:O	3:C:58:LEU:HB2	2.08	0.54
14:N:48:SER:HB3	14:N:51:ASP:HB2	1.89	0.54
1:O:29:THR:O	1:O:33:GLN:HG2	2.07	0.54
7:U:59:LEU:O	7:U:61:PRO:HD3	2.06	0.54
7:U:151:THR:HG22	7:U:157:TYR:HB2	1.89	0.54
8:H:167:LEU:HD22	12:Z:167:ILE:O	2.07	0.54
2:B:112:LEU:C	2:B:112:LEU:HD23	2.28	0.54
3:C:182:PRO:O	3:C:184:ALA:N	2.41	0.54
13:M:91:ARG:HG3	13:M:92:SER:N	2.22	0.54
5:S:18(C):PHE:HA	5:S:18(F):ILE:HG13	1.90	0.54
12:Z:-5:TYR:CD2	12:Z:96:TYR:HB2	2.43	0.54
13:1:40:ASN:ND2	13:1:40:ASN:N	2.55	0.54
3:C:14:ILE:HB	4:D:23:GLN:NE2	2.23	0.54
3:C:55:THR:HG22	3:C:56:LEU:HD22	1.90	0.54
4:D:112:LEU:O	4:D:116:VAL:HG23	2.08	0.54
7:G:151:THR:HG22	7:G:157:TYR:HB2	1.90	0.54
7:G:87:ASN:HD22	7:G:88:ALA:N	2.05	0.54
11:K:12:ILE:HG13	11:K:108:PRO:HB3	1.89	0.54
5:S:185:ASN:OD1	5:S:188:GLU:HG2	2.08	0.54
7:U:16:SER:HA	16:U:584:HOH:O	2.07	0.54
9:W:81:GLN:NE2	9:W:81:GLN:HA	2.22	0.54
14:N:136:GLY:CA	14:2:161:GLN:HE21	2.08	0.54
1:A:7:ARG:HB2	2:B:5:SER:OG	2.08	0.54
6:F:40:ILE:HD12	6:F:193:ALA:HB2	1.90	0.54
9:I:28:SER:HB2	10:J:120:VAL:HG21	1.88	0.54
13:M:42:VAL:CG2	13:M:178:ILE:HD11	2.38	0.54
2:P:238:ILE:O	2:P:239:THR:O	2.26	0.54
8:V:148:LYS:O	8:V:152:ILE:HG13	2.08	0.54
12:Z:34:VAL:HG12	12:Z:176:LEU:HD22	1.89	0.54
12:L:11:PHE:O	12:L:108:GLY:HA3	2.07	0.53
13:M:17:ASP:HA	13:M:173:PHE:CB	2.38	0.53
2:P:224:PHE:N	2:P:224:PHE:CD2	2.74	0.53
6:T:53:LEU:HD11	6:T:205:ASN:OD1	2.08	0.53
10:X:133:TYR:CE2	10:X:166:MET:CG	2.92	0.53
6:F:187:ARG:HB2	16:F:698:HOH:O	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:186:TRP:O	7:G:190:VAL:HG23	2.08	0.53
8:H:78:SER:O	8:H:82:MET:HG3	2.07	0.53
10:J:74:LEU:HD22	10:J:78:ALA:CB	2.39	0.53
11:K:208:ASN:ND2	9:W:29:ASN:HD21	2.06	0.53
2:P:229:ILE:O	2:P:233:LEU:HB2	2.07	0.53
3:Q:71:ASP:HA	10:X:68:ILE:HD11	1.90	0.53
6:T:179:LEU:HD11	6:T:192:GLN:CG	2.37	0.53
7:U:77:VAL:CG1	7:U:137:THR:HB	2.38	0.53
13:1:14(C):ARG:HG3	13:1:14(C):ARG:HH11	1.72	0.53
5:E:185:ASN:OD1	5:E:188:GLU:HG2	2.08	0.53
5:E:18(C):PHE:HA	5:E:18(F):ILE:HG13	1.90	0.53
3:Q:228:GLU:O	3:Q:232:TYR:HD1	1.91	0.53
3:Q:76:LEU:HD22	3:Q:89:ILE:HG12	1.91	0.53
5:S:47:VAL:HG12	5:S:48:LEU:N	2.23	0.53
1:A:67:VAL:HB	1:A:223:LYS:HZ1	1.72	0.53
1:A:85:TYR:O	1:A:89:VAL:HG23	2.09	0.53
3:C:76:LEU:HD12	3:C:138:ILE:HG12	1.91	0.53
4:D:79:SER:HB3	4:D:165:ILE:HD12	1.91	0.53
5:E:47:VAL:HG12	5:E:48:LEU:N	2.22	0.53
5:S:71:ASP:OD1	5:S:96:CYS:HB3	2.09	0.53
4:R:156:THR:HG22	5:S:83:PRO:HD3	1.90	0.53
6:T:172:ALA:C	6:T:176:LEU:HD23	2.29	0.53
6:T:35:THR:CG2	6:T:36:THR:N	2.70	0.53
13:1:112:TYR:CE1	13:1:127:THR:HG22	2.44	0.53
3:C:112:LEU:O	3:C:116:VAL:HG23	2.09	0.53
8:H:174:ASP:OD2	8:H:189:ARG:NH1	2.37	0.53
9:I:30:LYS:HE3	11:Y:210:ILE:HD13	1.90	0.53
11:K:208:ASN:HD21	9:W:29:ASN:HD21	1.55	0.53
12:L:1(I):ASN:O	12:L:14(K):LYS:HG2	2.09	0.53
3:Q:15:PHE:N	4:R:23:GLN:HE22	1.98	0.53
8:V:147:THR:HG23	8:V:150:GLU:OE1	2.08	0.53
9:W:6:MET:HB3	9:W:151:LEU:HD11	1.89	0.53
1:A:15:PHE:HB2	2:B:23:GLN:NE2	2.24	0.53
8:H:211:THR:HA	16:Z:781:HOH:O	2.07	0.53
16:T:515:HOH:O	7:U:130:ARG:HB2	2.06	0.53
10:J:52:THR:CG2	10:J:53:VAL:H	2.22	0.53
4:R:45:GLY:HA2	4:R:146:TYR:CE1	2.44	0.53
6:T:95:GLU:OE1	6:T:115:ARG:HD2	2.09	0.53
7:U:225:SER:H	7:U:228:ASN:HB2	1.74	0.53
8:H:195:ASN:HB3	12:Z:192:LYS:HE3	1.91	0.53
3:C:15:PHE:H	4:D:23:GLN:NE2	2.00	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:115:ARG:HG2	16:F:382:HOH:O	2.09	0.53
10:J:141:HIS:HB2	10:J:154:LEU:HD11	1.91	0.53
11:Y:210:ILE:N	16:Y:1226:HOH:O	2.34	0.53
12:Z:147:SER:O	12:Z:151:VAL:HG23	2.08	0.53
2:B:229:ILE:O	2:B:233:LEU:HB2	2.08	0.53
9:I:81:GLN:HA	9:I:81:GLN:NE2	2.23	0.53
13:M:205:GLY:HA3	13:M:209:GLN:HB3	1.91	0.53
2:P:63:THR:HG22	2:P:63:THR:O	2.09	0.53
3:Q:46:VAL:HG11	3:Q:139:ALA:HB1	1.91	0.53
12:Z:177:ILE:HD12	12:Z:177:ILE:N	2.23	0.53
12:Z:1(I):ASN:O	12:Z:14(K):LYS:HG2	2.08	0.53
2:B:63:THR:HG22	2:B:63:THR:O	2.09	0.53
3:C:46:VAL:HG11	3:C:139:ALA:HB1	1.91	0.53
7:G:100:ARG:HG3	7:G:100:ARG:HH11	1.74	0.53
7:G:8:TYR:C	7:G:10:ARG:H	2.10	0.53
10:J:17:SER:HB2	10:J:170:PHE:HB2	1.91	0.53
12:L:43:MET:HG2	12:L:44:SER:N	2.24	0.53
1:O:212:LEU:C	1:O:212:LEU:HD23	2.30	0.53
2:P:156:ASN:HD22	2:P:157:TYR:N	2.07	0.53
10:X:74:LEU:HD22	10:X:78:ALA:CB	2.38	0.53
12:Z:95:TYR:O	12:Z:97:VAL:N	2.41	0.53
1:A:212:LEU:HD23	1:A:212:LEU:C	2.29	0.52
2:B:156:ASN:HD22	2:B:157:TYR:N	2.07	0.52
8:H:5:GLY:O	8:H:124:TYR:HA	2.09	0.52
1:O:113:VAL:HG22	1:O:138:ILE:HD12	1.90	0.52
3:Q:105:ASP:OD2	3:Q:106:PRO:HD2	2.09	0.52
1:A:46:VAL:HG11	1:A:139:ALA:HB1	1.90	0.52
8:H:126:SER:O	8:H:127:LEU:HD23	2.09	0.52
4:R:112:LEU:C	4:R:112:LEU:HD13	2.30	0.52
8:V:196:VAL:HG23	16:V:652:HOH:O	2.09	0.52
1:A:110:LYS:HG2	16:A:285:HOH:O	2.08	0.52
2:B:97:GLN:NE2	2:B:97:GLN:HA	2.24	0.52
3:C:172:VAL:HG23	3:C:196:SER:HB2	1.89	0.52
9:I:176:TYR:CE1	9:I:186:LYS:HD2	2.44	0.52
4:R:24:VAL:O	4:R:27:SER:HB3	2.09	0.52
10:X:52:THR:CG2	10:X:53:VAL:H	2.20	0.52
6:F:237:GLN:O	6:F:240:ILE:HG22	2.09	0.52
9:I:143:GLU:HG3	9:I:146:LEU:HD21	1.90	0.52
14:N:112:THR:HG22	14:N:120:HIS:HB2	1.91	0.52
3:Q:125:GLN:NE2	16:Q:872:HOH:O	2.41	0.52
3:Q:182:PRO:O	3:Q:184:ALA:N	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:57:LYS:HG2	3:Q:208:LYS:HZ3	1.73	0.52
4:R:160:TYR:CG	4:R:163:LYS:HB2	2.44	0.52
8:V:112:SER:HB3	8:V:125:LEU:HD13	1.92	0.52
13:1:105:GLN:HG3	16:1:769:HOH:O	2.09	0.52
7:G:142:ASP:OD2	7:G:144:LEU:N	2.42	0.52
10:J:4:LEU:HD23	10:J:126:ALA:HB2	1.91	0.52
11:K:174:ASN:HD21	11:K:189:ASN:ND2	2.03	0.52
1:O:38:LEU:HD12	1:O:38:LEU:C	2.29	0.52
1:O:46:VAL:HG11	1:O:139:ALA:HB1	1.90	0.52
4:R:219:ASP:O	4:R:222:LYS:HE2	2.09	0.52
4:R:79:SER:HB3	4:R:165:ILE:HD12	1.92	0.52
6:F:53:LEU:HD11	6:F:205:ASN:OD1	2.10	0.52
7:G:228:ASN:HB3	16:G:255:HOH:O	2.08	0.52
3:Q:33:ARG:NH1	3:Q:33:ARG:CB	2.67	0.52
6:T:35:THR:HG23	6:T:36:THR:N	2.23	0.52
9:W:41:VAL:HG22	9:W:76:PRO:HG3	1.90	0.52
12:Z:43:MET:HG2	12:Z:44:SER:N	2.24	0.52
1:A:6:ASP:OD1	7:G:126:ARG:NH2	2.40	0.52
4:D:123:PHE:CZ	4:D:131:PRO:HG3	2.44	0.52
11:K:25:TRP:CH2	12:L:132:SER:HA	2.45	0.52
13:1:169:SER:HB2	16:1:295:HOH:O	2.10	0.52
1:A:225:THR:OG1	1:A:228:GLU:HG3	2.10	0.52
9:I:29:ASN:HD21	11:Y:208:ASN:HD21	1.56	0.52
10:J:146:MET:HE3	10:J:150:GLU:HB3	1.92	0.52
11:K:174:ASN:ND2	11:K:189:ASN:HD22	2.05	0.52
11:K:18:SER:HA	11:K:33:LYS:HE3	1.91	0.52
13:M:112:TYR:CE1	13:M:127:THR:HG22	2.45	0.52
14:N:176:VAL:HG12	14:N:178:LEU:HD13	1.92	0.52
14:N:36:ARG:HG3	14:N:42:TRP:CZ2	2.44	0.52
2:P:222:LYS:NZ	2:P:228:GLU:OE2	2.43	0.52
3:Q:151:THR:HG22	3:Q:157:TYR:HB3	1.90	0.52
13:1:113:VAL:HA	13:1:118:VAL:O	2.10	0.52
1:A:38:LEU:HD12	1:A:38:LEU:C	2.29	0.52
3:C:105:ASP:OD2	3:C:106:PRO:HD2	2.10	0.52
9:I:15:ALA:CB	9:I:175:VAL:HG22	2.39	0.52
2:B:163:ILE:HG13	2:B:164:SER:H	1.74	0.52
6:F:109:ILE:HG21	6:F:147:HIS:HB2	1.92	0.52
9:I:2:ILE:HG22	9:I:128:GLY:HA3	1.91	0.52
11:K:20:ALA:HB2	11:K:31:VAL:HG21	1.92	0.52
2:P:97:GLN:HA	2:P:97:GLN:NE2	2.24	0.52
5:S:111:ARG:HG2	5:S:111:ARG:HH11	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:12:VAL:HG13	9:W:108:PRO:HB3	1.92	0.52
10:X:141:HIS:HB2	10:X:154:LEU:HD11	1.92	0.52
12:Z:114:ASP:HB2	12:Z:118:SER:HB3	1.92	0.52
4:D:160:TYR:CG	4:D:163:LYS:HB2	2.45	0.51
1:O:121:GLN:O	1:O:124:THR:HB	2.10	0.51
4:R:52:LYS:HB2	4:R:20(B):ASN:HA	1.91	0.51
5:S:75:GLY:HA3	5:S:221:PHE:CZ	2.45	0.51
8:V:20:SER:HB3	8:V:28:ASP:HB3	1.92	0.51
7:G:151:THR:HG22	7:G:157:TYR:CB	2.40	0.51
10:J:52:THR:CG2	10:J:53:VAL:N	2.73	0.51
4:R:86:ARG:HB2	16:R:1021:HOH:O	2.09	0.51
6:T:40:ILE:HD12	6:T:193:ALA:HB2	1.92	0.51
7:U:158:VAL:HG22	7:U:159:GLY:N	2.25	0.51
10:X:52:THR:CG2	10:X:53:VAL:N	2.73	0.51
11:Y:10(A):ARG:HH11	11:Y:10(A):ARG:HG2	1.75	0.51
11:Y:38:ASN:OD1	11:Y:38:ASN:C	2.48	0.51
2:B:224:PHE:CD2	2:B:224:PHE:N	2.74	0.51
12:L:147:SER:O	12:L:151:VAL:HG23	2.10	0.51
3:Q:163:GLN:NE2	3:Q:164:THR:H	2.06	0.51
4:R:123:PHE:CZ	4:R:131:PRO:HG3	2.45	0.51
7:U:233:LEU:O	7:U:236:ILE:HG13	2.10	0.51
13:I:17:ASP:HA	13:I:173:PHE:HA	1.91	0.51
14:2:176:VAL:HG12	14:2:178:LEU:HD13	1.92	0.51
2:B:141:TYR:C	2:B:141:TYR:CD1	2.84	0.51
3:C:75:VAL:HG13	3:C:221:ILE:HD13	1.92	0.51
9:I:41:VAL:HG22	9:I:76:PRO:HG3	1.93	0.51
12:L:123:GLN:CG	12:L:145:TYR:OH	2.57	0.51
13:M:35:ILE:N	13:M:35:ILE:HD12	2.25	0.51
12:L:-8:PHE:CB	13:M:-8:THR:HG23	2.41	0.51
2:P:163:ILE:HG13	2:P:164:SER:H	1.76	0.51
9:I:29:ASN:HD21	11:Y:208:ASN:ND2	2.07	0.51
12:Z:49:ALA:HB3	13:I:118:VAL:HG13	1.93	0.51
4:D:40:ILE:HD13	4:D:192:LEU:HD23	1.91	0.51
9:I:104:ILE:HB	16:I:202:HOH:O	2.10	0.51
9:I:12:VAL:HG13	9:I:108:PRO:HB3	1.93	0.51
12:L:14(H):GLY:C	12:L:1(I):ASN:H	2.13	0.51
8:V:63:ILE:HG23	8:V:74:PRO:HB3	1.92	0.51
11:Y:99:THR:HG22	11:Y:113:VAL:O	2.10	0.51
7:G:172:ILE:HD13	7:G:197:MET:HE1	1.93	0.51
13:M:125:LEU:HA	16:M:224:HOH:O	2.09	0.51
4:R:207:LEU:C	4:R:207:LEU:HD23	2.30	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:136:LEU:HD12	5:S:151:PHE:CD2	2.46	0.51
11:Y:73:ARG:NH2	11:Y:104:TYR:O	2.43	0.51
12:Z:123:GLN:CG	12:Z:145:TYR:OH	2.58	0.51
11:K:7:ARG:HD2	11:K:108:PRO:O	2.11	0.51
12:L:14(H):GLY:O	12:L:1(I):ASN:N	2.43	0.51
3:Q:87:ILE:N	3:Q:87:ILE:HD12	2.26	0.51
10:J:168:MET:HE2	10:X:168:MET:HE2	1.93	0.51
1:A:32:LYS:HE2	1:A:32:LYS:HA	1.93	0.51
6:F:187:ARG:HH12	6:F:228:LEU:HD13	1.76	0.51
11:K:38:ASN:OD1	11:K:38:ASN:C	2.49	0.51
14:N:161:GLN:O	14:N:164:LYS:HB3	2.11	0.51
4:R:81:LEU:HB3	16:R:599:HOH:O	2.10	0.51
10:X:39:PRO:HG2	10:X:73:GLU:OE2	2.10	0.51
14:2:8:PHE:CE1	14:2:10:ASP:HB2	2.46	0.51
9:W:2:ILE:HG22	9:W:128:GLY:HA3	1.93	0.51
9:W:45:ILE:HB	9:W:52:VAL:HG13	1.93	0.51
10:X:2:ILE:O	10:X:16:SER:HA	2.11	0.51
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	1.92	0.51
14:2:37:VAL:CG2	14:2:41:ILE:HG22	2.41	0.51
11:K:44:THR:OG1	11:K:100:MET:HB2	2.11	0.51
2:P:78:VAL:HG11	2:P:85:ALA:HB2	1.91	0.51
3:Q:163:GLN:HG3	3:Q:164:THR:N	2.25	0.51
3:Q:201:VAL:HG21	3:Q:210:ILE:CD1	2.41	0.51
3:Q:57:LYS:O	3:Q:58:LEU:HB2	2.10	0.51
5:S:15:PHE:H	6:T:23:GLN:HE22	1.59	0.51
2:B:136:PHE:O	2:B:150:THR:HA	2.10	0.50
6:F:35:THR:CG2	6:F:36:THR:N	2.74	0.50
10:X:66:TYR:CE2	10:X:74:LEU:HG	2.46	0.50
8:H:214:LEU:HD22	11:Y:211:GLY:HA2	1.93	0.50
4:D:207:LEU:HD23	4:D:207:LEU:C	2.31	0.50
7:G:55:PRO:HG2	7:G:56:ASP:H	1.76	0.50
10:J:39:PRO:HG2	10:J:73:GLU:OE2	2.11	0.50
5:S:162:GLY:O	5:S:163:THR:HB	2.10	0.50
13:1:170:SER:HA	16:1:1294:HOH:O	2.10	0.50
5:E:75:GLY:HA3	5:E:221:PHE:CZ	2.46	0.50
7:G:233:LEU:O	7:G:236:ILE:HG13	2.12	0.50
8:H:148:LYS:O	8:H:152:ILE:HG13	2.11	0.50
10:J:168:MET:HA	10:J:168:MET:HE2	1.93	0.50
13:M:179:ASP:HB3	13:M:18(A):THR:OG1	2.10	0.50
14:N:145:ASN:N	16:N:601:HOH:O	2.43	0.50
14:N:37:VAL:CG2	14:N:41:ILE:HG22	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:32:LYS:HE2	1:O:32:LYS:HA	1.93	0.50
6:T:93:ARG:NH1	16:T:378:HOH:O	2.42	0.50
7:U:55:PRO:HG2	7:U:56:ASP:H	1.77	0.50
12:Z:-5:TYR:CE2	12:Z:96:TYR:HB2	2.47	0.50
14:2:1:THR:HG23	14:2:33:LYS:HD3	1.92	0.50
2:B:78:VAL:HG11	2:B:85:ALA:HB2	1.92	0.50
6:F:203:GLU:O	6:F:206:LYS:HD2	2.11	0.50
6:F:35:THR:HG23	6:F:36:THR:N	2.25	0.50
2:P:134:VAL:O	2:P:153:PRO:HD3	2.12	0.50
10:X:138:LEU:HD21	10:X:158:CYS:SG	2.51	0.50
12:Z:14(H):GLY:C	12:Z:1(I):ASN:H	2.15	0.50
16:T:1339:HOH:O	13:1:67:ALA:HB3	2.12	0.50
1:A:26:TYR:N	1:A:26:TYR:CD1	2.79	0.50
2:B:101:LYS:NZ	10:J:85:GLN:HE22	2.08	0.50
2:B:222:LYS:NZ	2:B:228:GLU:OE2	2.44	0.50
1:O:62:GLU:C	1:O:64:LEU:H	2.14	0.50
6:T:158:TRP:CZ3	7:U:64:VAL:HA	2.46	0.50
14:N:157:HIS:HD2	14:2:140:LYS:HZ1	1.56	0.50
14:2:1:THR:HG23	14:2:33:LYS:NZ	2.27	0.50
13:M:164:TYR:O	14:2:26:ILE:HD12	2.12	0.50
2:B:17:PRO:HA	3:C:26:TYR:CE1	2.45	0.50
5:E:162:GLY:O	5:E:163:THR:HB	2.12	0.50
12:L:-5:TYR:CD2	12:L:96:TYR:HB2	2.47	0.50
3:Q:241:GLN:O	3:Q:243:GLN:N	2.40	0.50
4:R:12:VAL:CG2	4:R:12(A):GLY:HA2	2.42	0.50
5:S:177:GLU:OE1	6:T:56:SER:HB2	2.12	0.50
6:T:130:ARG:HG2	6:T:130:ARG:HH11	1.76	0.50
1:O:58:LEU:HD12	7:U:173:THR:HG23	1.93	0.50
13:1:17:ASP:HA	13:1:173:PHE:CB	2.41	0.50
2:B:156:ASN:ND2	2:B:157:TYR:N	2.60	0.50
3:C:228:GLU:O	3:C:232:TYR:HD1	1.94	0.50
4:D:101:LEU:CD1	11:K:57:THR:HG22	2.42	0.50
6:F:122:ALA:HA	6:F:125:LEU:HD12	1.94	0.50
7:G:191:GLU:HG3	7:G:232:ARG:HG3	1.93	0.50
12:L:109:ALA:HB2	12:L:121:ARG:NH2	2.27	0.50
13:M:14(C):ARG:HH11	13:M:14(C):ARG:HG3	1.76	0.50
13:M:1:THR:OG1	13:M:2:SER:N	2.44	0.50
14:N:1:THR:HG23	14:N:33:LYS:HD3	1.94	0.50
1:O:187:GLU:HA	1:O:190:ILE:HD12	1.94	0.50
5:S:132:TYR:HD1	16:S:1059:HOH:O	1.94	0.50
6:T:122:ALA:HA	6:T:125:LEU:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2:122:LEU:HD12	14:2:125:ALA:HB2	1.94	0.50
3:C:136:THR:O	3:C:150:GLN:HA	2.11	0.50
5:E:177:GLU:OE1	6:F:56:SER:HB2	2.11	0.50
7:G:100:ARG:HG3	7:G:100:ARG:NH1	2.25	0.50
8:H:20:SER:HB3	8:H:28:ASP:HB3	1.93	0.50
12:L:-9:GLN:HE21	13:M:-8:THR:HG21	1.76	0.50
5:S:52:LYS:HB3	5:S:63:TYR:HB3	1.94	0.50
6:T:100:LYS:O	6:T:104:LYS:N	2.43	0.50
6:T:203:GLU:O	6:T:206:LYS:HD2	2.11	0.50
8:V:5:GLY:O	8:V:124:TYR:HA	2.12	0.50
8:V:126:SER:O	8:V:127:LEU:HD23	2.12	0.50
10:J:144:PRO:HG3	11:Y:207:ASN:HD21	1.74	0.50
3:C:141:PHE:CE1	3:C:217:PRO:HG3	2.47	0.50
4:D:45:GLY:HA2	4:D:146:TYR:CE1	2.46	0.50
7:G:177:GLU:O	7:G:17(B):LYS:HG3	2.11	0.50
11:K:4:LEU:HD11	11:K:15:ALA:HB3	1.94	0.50
11:K:38:ASN:C	11:K:40:PHE:H	2.15	0.50
1:O:159:PRO:HB2	2:P:60:GLU:HB3	1.94	0.50
2:P:15:PHE:H	3:Q:23:GLN:NE2	1.98	0.50
4:R:160:TYR:HB3	4:R:162:ALA:O	2.12	0.50
7:U:236:ILE:HD12	7:U:236:ILE:C	2.32	0.50
1:A:187:GLU:HA	1:A:190:ILE:HD12	1.94	0.49
5:E:227:GLU:CD	5:E:227:GLU:N	2.65	0.49
4:R:67:ILE:HG22	4:R:221:PHE:HZ	1.77	0.49
12:Z:-9:GLN:HE21	13:1:-8:THR:HG21	1.77	0.49
3:C:40:VAL:HG12	3:C:162:ALA:HB1	1.94	0.49
4:D:67:ILE:HG22	4:D:221:PHE:HZ	1.77	0.49
6:F:172:ALA:C	6:F:176:LEU:HD23	2.33	0.49
6:F:179:LEU:CD2	6:F:192:GLN:HG2	2.42	0.49
7:G:10:ARG:HG2	7:G:22:TYR:CD2	2.46	0.49
7:G:21:LEU:HA	16:G:246:HOH:O	2.12	0.49
12:L:34:VAL:HG12	12:L:176:LEU:HD22	1.94	0.49
14:N:84:LYS:HG3	14:N:119:VAL:HG22	1.94	0.49
2:P:27:ALA:O	2:P:31:ILE:HG13	2.12	0.49
6:T:192:GLN:NE2	6:T:195:LYS:CE	2.75	0.49
7:U:72:ARG:O	7:U:220:LYS:HA	2.11	0.49
10:X:17:SER:HB2	10:X:170:PHE:HB2	1.94	0.49
1:A:134:VAL:O	1:A:153:PRO:HG3	2.11	0.49
2:B:20:ARG:NH1	2:B:20:ARG:HG2	2.27	0.49
2:B:230:LYS:O	2:B:234:VAL:HG23	2.13	0.49
2:P:78:VAL:HG11	2:P:85:ALA:CB	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:R:12(D):ALA:HB3	4:R:126:ARG:HG3	1.94	0.49
4:R:29:GLU:HA	4:R:29:GLU:OE2	2.12	0.49
8:V:84:LYS:HE2	8:V:119:THR:HG23	1.94	0.49
9:W:20:LEU:C	9:W:20:LEU:HD13	2.32	0.49
4:D:52:LYS:HB2	4:D:20(B):ASN:HA	1.93	0.49
8:H:46:ALA:HA	15:H:7710:SY2:H24A	1.93	0.49
9:I:3:VAL:HG22	9:I:16:CYS:HB3	1.93	0.49
2:P:186:VAL:HG21	2:P:216:ARG:CD	2.39	0.49
6:T:103:TYR:O	6:T:104:LYS:HB3	2.12	0.49
2:B:186:VAL:HG21	2:B:216:ARG:CD	2.41	0.49
2:B:27:ALA:O	2:B:31:ILE:HG13	2.12	0.49
6:F:127:ASN:HD22	6:F:127:ASN:C	2.15	0.49
12:L:114:ASP:HB2	12:L:118:SER:HB3	1.93	0.49
3:Q:15:PHE:H	4:R:23:GLN:NE2	2.00	0.49
5:S:111:ARG:HG2	5:S:111:ARG:NH1	2.28	0.49
5:S:226:GLY:O	5:S:228:ALA:N	2.46	0.49
9:W:176:TYR:CE1	9:W:186:LYS:HD2	2.48	0.49
13:1:1:THR:OG1	13:1:2:SER:N	2.44	0.49
2:B:120:LYS:HZ1	2:B:136:PHE:HD1	1.60	0.49
2:B:202:THR:CG2	2:B:204:SER:H	2.11	0.49
2:B:74:ILE:C	2:B:221:GLN:HE22	2.16	0.49
11:K:207:ASN:HD21	10:X:144:PRO:HG2	1.76	0.49
13:M:184:LEU:C	13:M:184:LEU:HD23	2.33	0.49
2:P:141:TYR:C	2:P:141:TYR:CD1	2.84	0.49
2:P:20:ARG:NH1	2:P:20:ARG:HG2	2.28	0.49
4:R:59:LEU:HD13	4:R:59:LEU:C	2.33	0.49
5:S:148:LEU:HD23	5:S:162:GLY:HA2	1.94	0.49
4:R:160:TYR:CE2	5:S:59:SER:HB3	2.48	0.49
6:T:95:GLU:CD	6:T:115:ARG:HD2	2.33	0.49
7:U:173:THR:HG22	7:U:177:GLU:OE2	2.13	0.49
1:A:113:VAL:HG22	1:A:138:ILE:HD12	1.94	0.49
8:H:156:SER:O	8:H:160:GLN:HG3	2.13	0.49
10:J:133:TYR:CE2	10:J:166:MET:CG	2.96	0.49
12:L:177:ILE:N	12:L:177:ILE:HD12	2.27	0.49
12:L:176:LEU:CD1	12:L:186:LYS:HG2	2.43	0.49
1:O:7:ARG:HD3	5:S:127:TYR:CD2	2.47	0.49
2:P:122:GLY:C	2:P:124:THR:H	2.16	0.49
2:P:156:ASN:ND2	2:P:157:TYR:N	2.61	0.49
1:O:15:PHE:HB2	2:P:23:GLN:NE2	2.27	0.49
4:R:112:LEU:O	4:R:116:VAL:HG23	2.13	0.49
9:W:84:SER:HB2	9:W:119:ILE:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:196:PHE:CE1	9:W:193:GLN:HG3	2.48	0.49
11:Y:21:THR:HG22	11:Y:26:VAL:HA	1.94	0.49
11:Y:38:ASN:C	11:Y:40:PHE:H	2.16	0.49
13:1:104:VAL:CG2	13:1:178:ILE:HG22	2.40	0.49
14:2:107:LYS:HG2	14:2:108:GLY:N	2.27	0.49
3:C:151:THR:HG22	3:C:157:TYR:CB	2.43	0.49
3:C:214:VAL:HG23	3:C:224:LEU:HD11	1.95	0.49
4:D:12:VAL:CG2	4:D:12(A):GLY:HA2	2.43	0.49
7:G:72:ARG:O	7:G:220:LYS:HA	2.12	0.49
8:H:8:PHE:HB2	8:H:146:LEU:O	2.12	0.49
12:L:95:TYR:O	12:L:97:VAL:N	2.42	0.49
13:M:211:ILE:HD11	14:2:36:ARG:CD	2.42	0.49
14:N:107:LYS:HG2	14:N:108:GLY:N	2.27	0.49
14:N:148:LYS:O	14:N:152:VAL:HG23	2.13	0.49
3:Q:136:THR:O	3:Q:150:GLN:HA	2.11	0.49
3:Q:197:LEU:O	3:Q:201:VAL:HG23	2.13	0.49
11:Y:25:TRP:CH2	12:Z:132:SER:HA	2.47	0.49
14:2:161:GLN:O	14:2:164:LYS:HB3	2.13	0.49
4:D:12(D):ALA:HB3	4:D:126:ARG:HG3	1.95	0.49
6:F:205:ASN:C	6:F:20(B):GLU:H	2.15	0.49
11:K:172:SER:HA	11:K:192:VAL:HG23	1.95	0.49
2:P:101:LYS:HA	16:W:530:HOH:O	2.11	0.49
2:P:150:THR:CG2	2:P:160:TRP:HE1	2.25	0.49
1:O:161:LYS:HG3	2:P:58:LEU:O	2.12	0.49
3:Q:75:VAL:HG13	3:Q:221:ILE:HD13	1.95	0.49
4:R:79:SER:O	4:R:134:VAL:HG23	2.12	0.49
5:S:48:LEU:HG	5:S:139:ILE:HD13	1.95	0.49
5:S:227:GLU:N	5:S:227:GLU:CD	2.66	0.49
14:2:114:PRO:HD2	14:2:118:SER:O	2.13	0.49
2:B:41:MET:HE3	16:B:240:HOH:O	2.13	0.49
3:C:121:GLN:C	3:C:121:GLN:HE21	2.16	0.49
4:D:39:GLY:O	4:D:162:ALA:HA	2.13	0.49
5:E:22:PHE:O	5:E:25:GLU:N	2.46	0.49
7:G:225:SER:H	7:G:228:ASN:HB2	1.77	0.49
9:I:193:GLN:HG3	11:Y:196:PHE:CE1	2.47	0.49
11:K:10(A):ARG:HG2	11:K:10(A):ARG:HH11	1.78	0.49
12:L:167:ILE:O	8:V:167:LEU:HD22	2.13	0.49
13:M:57:ARG:HH11	13:M:57:ARG:HG2	1.77	0.49
3:Q:33:ARG:HH11	3:Q:33:ARG:HB3	1.78	0.49
6:T:136:THR:O	6:T:150:MET:HA	2.12	0.49
12:Z:-8:PHE:CB	13:1:-8:THR:HG23	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:140:LYS:HZ1	14:2:157:HIS:HD2	1.61	0.48
9:I:20:LEU:C	9:I:20:LEU:HD13	2.33	0.48
11:K:195:LEU:O	11:K:199:VAL:HG23	2.13	0.48
4:R:162:ALA:HB3	5:S:58:LEU:HD23	1.94	0.48
6:T:109:ILE:HB	6:T:110:PRO:HD3	1.94	0.48
6:T:186:ALA:O	6:T:190:VAL:HG23	2.13	0.48
6:T:205:ASN:C	6:T:20(B):GLU:H	2.15	0.48
9:W:15:ALA:CB	9:W:175:VAL:HG22	2.43	0.48
13:1:157:ASN:HB3	16:1:558:HOH:O	2.13	0.48
1:A:62:GLU:C	1:A:64:LEU:H	2.16	0.48
8:H:8:PHE:HB3	8:H:151:ALA:HB2	1.95	0.48
4:R:121:LEU:HA	4:R:123:PHE:CE1	2.48	0.48
12:Z:90:LYS:HD3	12:Z:95:TYR:CE1	2.47	0.48
14:2:44:CYS:HB2	14:2:100:ILE:HB	1.94	0.48
3:C:201:VAL:HG21	3:C:210:ILE:CD1	2.42	0.48
8:H:63:ILE:HG23	8:H:74:PRO:HB3	1.95	0.48
10:J:135:PHE:HB3	11:Y:165:ARG:NE	2.28	0.48
11:K:200:LYS:HG3	11:K:206:PHE:HB2	1.95	0.48
12:L:163:THR:HG21	16:L:1193:HOH:O	2.13	0.48
2:P:66:LYS:O	2:P:77:ALA:HA	2.13	0.48
8:V:174:ASP:OD2	8:V:189:ARG:NH1	2.40	0.48
11:Y:172:SER:HA	11:Y:192:VAL:HG23	1.95	0.48
2:B:127:GLY:N	16:B:710:HOH:O	2.45	0.48
4:D:79:SER:O	4:D:134:VAL:HG23	2.14	0.48
5:E:185:ASN:C	5:E:185:ASN:HD22	2.16	0.48
6:F:20(B):GLU:CD	6:F:20(C):LYS:HE3	2.34	0.48
8:H:72:ARG:HH11	8:H:72:ARG:HG3	1.78	0.48
1:O:85:TYR:O	1:O:89:VAL:HG23	2.12	0.48
2:P:101:LYS:NZ	10:X:85:GLN:NE2	2.60	0.48
6:T:187:ARG:HH12	6:T:228:LEU:HD13	1.77	0.48
7:U:17:PRO:HD3	16:U:584:HOH:O	2.14	0.48
11:Y:44:THR:OG1	11:Y:100:MET:HB2	2.13	0.48
13:1:179:ASP:HB3	13:1:18(A):THR:OG1	2.13	0.48
13:1:160:ARG:HG3	13:1:192:VAL:CG1	2.44	0.48
1:A:7:ARG:HD3	5:E:127:TYR:HD2	1.76	0.48
5:E:111:ARG:HG2	5:E:111:ARG:HH11	1.79	0.48
7:G:122:ILE:HG12	16:G:642:HOH:O	2.12	0.48
8:H:114:HIS:HB2	16:H:324:HOH:O	2.14	0.48
12:L:113:PHE:CD2	12:L:119:TYR:HB3	2.49	0.48
3:Q:141:PHE:CE1	3:Q:217:PRO:HG3	2.49	0.48
6:T:127:ASN:HD22	6:T:127:ASN:C	2.16	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:18:ASP:N	6:T:18:ASP:OD2	2.37	0.48
8:V:105:ASP:HB2	8:V:10(A):PRO:CD	2.43	0.48
9:W:99:PRO:HB2	9:W:113:PHE:CD2	2.48	0.48
10:X:168:MET:HA	10:X:168:MET:HE2	1.94	0.48
11:Y:149:GLU:N	16:Y:973:HOH:O	2.46	0.48
12:Z:43:MET:HB2	12:Z:101:ILE:HG22	1.95	0.48
1:A:175:PHE:O	1:A:179:ARG:HG2	2.12	0.48
5:E:48:LEU:HG	5:E:139:ILE:HD13	1.95	0.48
6:F:187:ARG:NH1	6:F:228:LEU:HD13	2.29	0.48
7:G:173:THR:HG22	7:G:177:GLU:OE2	2.12	0.48
12:L:145:TYR:CD1	12:L:146:LEU:N	2.82	0.48
13:M:85:THR:O	13:M:89:GLN:HG3	2.14	0.48
6:T:77:VAL:CG1	6:T:137:ILE:HB	2.43	0.48
2:B:150:THR:CG2	2:B:160:TRP:HE1	2.27	0.48
2:B:71:ASN:CG	2:B:72:ASP:H	2.16	0.48
2:B:97:GLN:NE2	16:B:246:HOH:O	2.43	0.48
6:F:43:ASN:HD22	6:F:43:ASN:N	2.11	0.48
2:P:149:TYR:OH	3:Q:62(A):ILE:HB	2.14	0.48
3:Q:65:SER:HB2	16:Q:303:HOH:O	2.14	0.48
14:2:15:GLY:HA2	14:2:174:ARG:O	2.13	0.48
1:A:13:THR:O	2:B:130:ARG:HD3	2.14	0.48
3:C:33:ARG:CB	3:C:33:ARG:NH1	2.69	0.48
3:Q:55:THR:O	3:Q:56:LEU:HD22	2.13	0.48
6:T:50:VAL:HG22	6:T:51:GLU:N	2.28	0.48
7:U:48:VAL:O	7:U:48:VAL:HG23	2.14	0.48
11:K:165:ARG:NE	10:X:135:PHE:HB3	2.28	0.48
12:Z:45:ALA:HA	12:Z:99:THR:HB	1.96	0.48
2:B:147:GLN:HG2	3:C:62(A):ILE:HG21	1.95	0.48
2:B:78:VAL:HG11	2:B:85:ALA:CB	2.43	0.48
5:E:52:LYS:HB3	5:E:63:TYR:HB3	1.94	0.48
8:H:112:SER:HB3	8:H:125:LEU:HD13	1.95	0.48
8:H:201:GLN:HG3	12:Z:153:LYS:HG2	1.96	0.48
11:K:38:ASN:OD1	11:K:40:PHE:N	2.46	0.48
14:N:15:GLY:HA2	14:N:174:ARG:O	2.13	0.48
14:N:163:ILE:HG23	14:N:170:GLY:HA2	1.95	0.48
1:O:130:ARG:HG2	7:U:125:GLN:HG3	1.95	0.48
1:O:175:PHE:O	1:O:179:ARG:HG2	2.14	0.48
1:O:26:TYR:N	1:O:26:TYR:CD1	2.80	0.48
8:V:8:PHE:HB3	8:V:151:ALA:HB2	1.96	0.48
10:X:53:VAL:HB	16:Y:726:HOH:O	2.12	0.48
13:1:150:VAL:HG21	16:1:323:HOH:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:168:ASN:CB	3:C:200:VAL:HG11	2.43	0.48
6:F:91:ARG:O	6:F:95:GLU:HB2	2.14	0.48
13:M:164:TYR:HA	16:M:639:HOH:O	2.14	0.48
16:R:886:HOH:O	12:Z:70:HIS:HE1	1.96	0.48
13:1:85:THR:O	13:1:89:GLN:HG3	2.14	0.47
14:2:175:MET:HB2	14:2:187:LEU:HB2	1.96	0.47
2:B:70:LEU:CD2	2:B:89:ILE:HG23	2.43	0.47
3:C:87:ILE:HD12	3:C:87:ILE:N	2.28	0.47
1:O:17:PRO:HA	2:P:26:TYR:CD1	2.49	0.47
3:Q:40:VAL:HG12	3:Q:162:ALA:HB1	1.96	0.47
6:T:20(B):GLU:CD	6:T:20(C):LYS:HE3	2.34	0.47
8:V:46:ALA:HA	15:V:7710:SY2:H24A	1.96	0.47
10:X:161:GLU:OE2	10:X:161:GLU:HA	2.14	0.47
13:1:19:LEU:HD21	13:1:26:LEU:HD22	1.95	0.47
13:1:35:ILE:HD12	13:1:35:ILE:N	2.30	0.47
13:M:197:TRP:CH2	14:2:171:GLY:HA2	2.49	0.47
6:F:114:ASP:O	6:F:118:GLN:HG2	2.14	0.47
6:F:136:THR:O	6:F:150:MET:HA	2.14	0.47
6:F:192:GLN:NE2	6:F:195:LYS:CE	2.76	0.47
6:F:52:LYS:HB2	6:F:209:GLU:O	2.13	0.47
2:P:184:MET:CE	2:P:188:ASP:HB3	2.44	0.47
14:2:146:MET:CE	14:2:150:GLU:HB3	2.44	0.47
6:F:95:GLU:OE1	6:F:115:ARG:HD2	2.14	0.47
11:K:95:LEU:HB2	16:K:511:HOH:O	2.15	0.47
12:L:5:GLY:O	12:L:124:CYS:HA	2.14	0.47
14:N:105:ASP:HB2	16:N:775:HOH:O	2.13	0.47
3:Q:35:THR:OG1	3:Q:66:LYS:NZ	2.47	0.47
10:X:190:PHE:C	10:X:192:ALA:H	2.18	0.47
12:Z:145:TYR:CD1	12:Z:146:LEU:N	2.83	0.47
2:B:160:TRP:CE3	2:B:163:ILE:HD13	2.49	0.47
2:B:20:ARG:HH11	2:B:20:ARG:HG2	1.79	0.47
12:L:-5:TYR:CE2	12:L:96:TYR:HB2	2.49	0.47
5:S:17:PRO:HA	6:T:26:TYR:CG	2.49	0.47
11:Y:200:LYS:HG3	11:Y:206:PHE:HB2	1.96	0.47
12:Z:14(H):GLY:O	12:Z:1(I):ASN:N	2.47	0.47
1:A:15:PHE:HB2	2:B:23:GLN:HE22	1.79	0.47
5:E:71:ASP:OD1	5:E:96:CYS:HB3	2.13	0.47
6:F:50:VAL:HG22	6:F:51:GLU:N	2.29	0.47
13:M:115:LEU:HD23	13:M:115:LEU:N	2.29	0.47
6:T:43:ASN:HD22	6:T:43:ASN:N	2.13	0.47
10:X:4:LEU:HD23	10:X:126:ALA:CB	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Z:-7:ASN:ND2	12:Z:-5:TYR:H	2.13	0.47
13:1:164:TYR:HA	16:1:284:HOH:O	2.14	0.47
14:2:18(D):PRO:HA	14:2:18(G):TYR:CE2	2.50	0.47
3:C:100:ARG:HD2	16:C:244:HOH:O	2.14	0.47
4:D:140:GLY:HA2	4:D:215:ILE:HG12	1.96	0.47
7:G:130:ARG:HG3	7:G:131:PRO:O	2.14	0.47
8:H:105:ASP:HB2	8:H:10(A):PRO:CD	2.44	0.47
10:J:189:ASP:O	10:J:193:GLN:HB2	2.15	0.47
2:B:114:ARG:NH1	10:J:70:GLU:OE2	2.38	0.47
12:L:153:LYS:HG2	8:V:201:GLN:HG3	1.96	0.47
12:L:19:ARG:HG2	12:L:21:ILE:HG23	1.97	0.47
13:M:139:ARG:HH11	8:V:165:ASN:ND2	2.05	0.47
7:U:151:THR:HG22	7:U:157:TYR:CB	2.44	0.47
6:T:159:GLY:HA3	7:U:63:THR:HG21	1.97	0.47
11:Y:4:LEU:HD11	11:Y:15:ALA:HB3	1.96	0.47
13:1:190:LEU:CD1	13:1:190:LEU:N	2.77	0.47
13:1:3:VAL:O	13:1:126:ALA:HA	2.15	0.47
12:L:21:ILE:HD11	12:L:168:GLN:NE2	2.30	0.47
2:P:107:ILE:HG22	16:P:410:HOH:O	2.14	0.47
5:S:185:ASN:HD22	5:S:185:ASN:C	2.17	0.47
9:W:93:GLY:C	16:W:266:HOH:O	2.53	0.47
13:1:-5:PRO:HD3	13:1:96:TRP:CE2	2.50	0.47
7:G:43:LYS:HB2	7:G:18(G):GLU:O	2.14	0.47
14:N:19:ARG:HB2	16:N:194:HOH:O	2.15	0.47
2:P:150:THR:HG22	2:P:160:TRP:HE1	1.79	0.47
5:S:38:VAL:HG22	5:S:164:ALA:HB2	1.96	0.47
13:1:91:ARG:NH2	16:1:213:HOH:O	2.48	0.47
14:2:20:THR:OG1	14:2:28:ASN:HB3	2.15	0.47
4:D:59:LEU:C	4:D:59:LEU:HD13	2.34	0.47
6:F:123:HIS:HB2	16:F:243:HOH:O	2.14	0.47
11:K:200:LYS:HE2	16:K:1088:HOH:O	2.14	0.47
12:L:45:ALA:HA	12:L:99:THR:HB	1.96	0.47
7:U:72:ARG:HG2	16:U:696:HOH:O	2.14	0.47
9:W:84:SER:CB	9:W:119:ILE:HD11	2.45	0.47
12:Z:-9:GLN:NE2	12:Z:-8:PHE:H	2.13	0.47
10:J:166:MET:HA	10:J:167:PRO:HD3	1.75	0.47
14:N:37:VAL:HG22	14:N:41:ILE:O	2.15	0.47
6:T:187:ARG:NH1	6:T:228:LEU:HD13	2.30	0.47
7:U:18(G):GLU:CG	7:U:188:LYS:HB2	2.45	0.47
7:U:172:ILE:HD13	7:U:197:MET:HE1	1.96	0.47
10:X:104:TYR:CD1	10:X:180:LYS:HA	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:X:11:SER:HB2	10:X:178:VAL:O	2.14	0.47
14:2:65:LEU:HG	14:2:69:GLN:NE2	2.30	0.47
2:B:122:GLY:C	2:B:124:THR:H	2.17	0.47
2:B:184:MET:CE	2:B:188:ASP:HB3	2.45	0.47
5:E:113:GLY:HA3	16:E:1004:HOH:O	2.14	0.47
7:G:59:LEU:O	7:G:61:PRO:HD3	2.14	0.47
16:B:242:HOH:O	10:J:85:GLN:HB2	2.15	0.47
1:O:184:LEU:HD22	1:O:188:ASP:HB3	1.96	0.47
2:P:168:ASN:HA	16:P:943:HOH:O	2.13	0.47
3:Q:190:VAL:O	3:Q:194:VAL:HG23	2.15	0.47
5:E:38:VAL:HG22	5:E:164:ALA:HB2	1.96	0.46
6:F:95:GLU:CD	6:F:115:ARG:HD2	2.36	0.46
8:H:84:LYS:HE2	8:H:119:THR:HG23	1.97	0.46
7:G:105:TYR:OH	8:H:66:HIS:HE1	1.98	0.46
2:P:160:TRP:CE3	2:P:163:ILE:HD13	2.50	0.46
2:P:74:ILE:C	2:P:221:GLN:HE22	2.18	0.46
2:P:230:LYS:O	2:P:234:VAL:HG23	2.15	0.46
8:V:216:GLU:HG3	9:W:187:ARG:HG2	1.97	0.46
5:E:76:LEU:O	5:E:76:LEU:HD23	2.15	0.46
6:F:130:ARG:HH11	6:F:130:ARG:HG2	1.79	0.46
7:G:34(A):ASN:HD22	7:G:167:PRO:HG2	1.79	0.46
11:K:40:PHE:CG	11:K:73:ARG:CZ	2.98	0.46
14:N:114:PRO:HD2	14:N:118:SER:O	2.14	0.46
14:2:163:ILE:HG23	14:2:170:GLY:HA2	1.96	0.46
1:A:177:GLU:HG2	2:B:58:LEU:HD22	1.96	0.46
2:B:66:LYS:O	2:B:77:ALA:HA	2.15	0.46
4:D:160:TYR:CE2	5:E:59:SER:HB3	2.51	0.46
5:E:15:PHE:H	6:F:23:GLN:HE22	1.61	0.46
7:G:158:VAL:HG22	7:G:159:GLY:N	2.31	0.46
9:I:55:LEU:HD12	9:I:97:VAL:HG21	1.96	0.46
13:M:3:VAL:O	13:M:126:ALA:HA	2.15	0.46
14:N:13:ILE:HD12	14:N:151:THR:HG22	1.96	0.46
4:R:237:LEU:O	4:R:241:GLU:HG3	2.15	0.46
11:Y:7:ARG:HD2	11:Y:108:PRO:O	2.16	0.46
13:1:186:PHE:CE1	13:1:188:LYS:HG3	2.51	0.46
13:1:57:ARG:HG2	13:1:57:ARG:HH11	1.80	0.46
6:F:77:VAL:CG1	6:F:137:ILE:HB	2.46	0.46
7:G:48:VAL:O	7:G:48:VAL:HG23	2.15	0.46
12:L:135:MET:HE2	9:W:165:ARG:HH22	1.80	0.46
12:L:33:LYS:HE2	12:L:33:LYS:HB3	1.75	0.46
12:L:49:ALA:HB3	13:M:118:VAL:HG13	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:127:THR:HB	16:M:918:HOH:O	2.16	0.46
14:N:20:THR:OG1	14:N:28:ASN:HB3	2.15	0.46
2:P:120:LYS:HZ1	2:P:136:PHE:HD1	1.61	0.46
4:R:237:LEU:HD22	4:R:241:GLU:HG3	1.97	0.46
6:T:172:ALA:O	6:T:176:LEU:HD23	2.16	0.46
6:T:192:GLN:NE2	6:T:195:LYS:HE3	2.30	0.46
9:W:62:LYS:HD3	9:W:82:LEU:HD11	1.97	0.46
11:Y:65:LEU:HD12	11:Y:65:LEU:HA	1.82	0.46
1:A:136:LEU:O	1:A:150:GLN:HA	2.16	0.46
5:E:226:GLY:O	5:E:228:ALA:N	2.48	0.46
14:N:8:PHE:HE1	14:N:10:ASP:HB2	1.80	0.46
1:O:141:HIS:HA	1:O:146:GLY:O	2.16	0.46
1:O:62:GLU:CD	1:O:62:GLU:H	2.19	0.46
9:W:99:PRO:HB2	9:W:113:PHE:HD2	1.81	0.46
6:F:192:GLN:NE2	6:F:195:LYS:HE3	2.31	0.46
8:H:216:GLU:HG3	9:I:187:ARG:HG2	1.97	0.46
3:Q:214:VAL:HG23	3:Q:224:LEU:HD11	1.97	0.46
4:R:227:GLU:O	4:R:231:GLU:HG3	2.16	0.46
2:P:4:GLY:HA3	5:S:127:TYR:CE1	2.50	0.46
6:T:130:ARG:NH1	6:T:130:ARG:HG2	2.31	0.46
6:T:91:ARG:O	6:T:95:GLU:HB2	2.15	0.46
7:U:18(H):GLU:N	7:U:18(H):GLU:CD	2.69	0.46
9:W:186:LYS:HE2	9:W:188:TYR:CE1	2.50	0.46
9:W:29:ASN:ND2	9:W:29:ASN:N	2.51	0.46
13:1:104:VAL:HG23	13:1:178:ILE:CG2	2.43	0.46
1:A:38:LEU:HD12	1:A:38:LEU:O	2.16	0.46
2:B:160:TRP:CD2	2:B:163:ILE:HD13	2.51	0.46
2:B:37:ALA:HB3	2:B:165:VAL:CG2	2.46	0.46
2:B:49:ALA:HB2	2:B:212:PHE:HE1	1.78	0.46
2:B:99:TYR:CD2	2:B:107:ILE:HA	2.51	0.46
6:F:186:ALA:O	6:F:190:VAL:HG23	2.15	0.46
8:H:113:ILE:HG12	8:H:119:THR:HG22	1.98	0.46
10:J:2:ILE:O	10:J:16:SER:HA	2.16	0.46
13:M:8:TYR:HD2	13:M:9:ASP:OD1	1.97	0.46
1:O:13:THR:O	2:P:130:ARG:HD3	2.15	0.46
2:P:186:VAL:CG2	2:P:216:ARG:HD3	2.43	0.46
3:Q:121:GLN:C	3:Q:121:GLN:HE21	2.18	0.46
7:U:29:LYS:HA	7:U:29:LYS:HD2	1.74	0.46
11:Y:143:LYS:HB2	11:Y:146:LEU:HD11	1.98	0.46
13:1:11:GLY:HA3	13:1:178:ILE:O	2.16	0.46
3:C:197:LEU:O	3:C:201:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:121:LEU:HA	4:D:123:PHE:CE1	2.51	0.46
4:D:237:LEU:HD22	4:D:241:GLU:HG3	1.97	0.46
4:D:177:LEU:HD22	5:E:58:LEU:HD13	1.98	0.46
7:G:30:ALA:O	7:G:33:GLN:HB2	2.15	0.46
10:J:131:GLY:HA3	16:J:594:HOH:O	2.16	0.46
10:J:15:ALA:HB2	10:J:155:LEU:CD1	2.44	0.46
13:M:113:VAL:HA	13:M:118:VAL:O	2.15	0.46
2:P:107:ILE:O	2:P:107:ILE:HG23	2.15	0.46
2:P:46:ILE:HG22	2:P:47:VAL:N	2.31	0.46
3:Q:87:ILE:N	3:Q:87:ILE:CD1	2.79	0.46
10:X:110:LEU:O	10:X:121:GLU:HG2	2.16	0.46
1:A:121:GLN:O	1:A:124:THR:HB	2.15	0.46
3:C:190:VAL:O	3:C:194:VAL:HG23	2.16	0.46
4:D:237:LEU:O	4:D:241:GLU:HG3	2.16	0.46
5:E:136:LEU:HD12	5:E:151:PHE:CD2	2.51	0.46
6:F:107:ILE:O	6:F:107:ILE:HG23	2.15	0.46
7:G:236:ILE:HD12	7:G:236:ILE:C	2.36	0.46
14:N:8:PHE:HB2	14:N:146:MET:O	2.16	0.46
1:O:57:PRO:CG	7:U:177:GLU:HG2	2.46	0.46
5:S:172:ALA:CB	5:S:196:ALA:O	2.64	0.46
10:X:15:ALA:HB2	10:X:155:LEU:CD1	2.46	0.46
10:X:70:GLU:O	10:X:71:ASP:C	2.54	0.46
4:D:42:THR:C	4:D:44:GLU:H	2.18	0.46
5:E:148:LEU:HD23	5:E:162:GLY:HA2	1.98	0.46
12:L:165:ARG:NH2	8:V:29:LYS:HE2	2.31	0.46
7:U:30:ALA:O	7:U:33:GLN:HB2	2.16	0.46
10:X:189:ASP:O	10:X:193:GLN:HB2	2.16	0.46
12:Z:58:ARG:NH1	12:Z:58:ARG:HG2	2.30	0.46
14:2:84:LYS:HG3	14:2:119:VAL:HG22	1.97	0.45
1:A:58:LEU:HD12	7:G:173:THR:HG23	1.99	0.45
1:A:5:THR:O	1:A:7:ARG:HG2	2.16	0.45
4:D:106:ASP:HA	16:D:1036:HOH:O	2.15	0.45
8:H:14:ILE:O	8:H:14:ILE:HG13	2.15	0.45
8:H:197:ARG:NH2	9:I:139:GLU:HG3	2.31	0.45
1:O:136:LEU:O	1:O:150:GLN:HA	2.17	0.45
2:P:161:LYS:HB3	2:P:180:TYR:CE2	2.51	0.45
6:T:109:ILE:HG21	6:T:147:HIS:HB2	1.97	0.45
1:A:141:HIS:HA	1:A:146:GLY:O	2.16	0.45
4:D:170:GLU:N	4:D:170:GLU:OE1	2.49	0.45
10:J:148:THR:HG21	10:J:177:ILE:HD13	1.99	0.45
11:K:21:THR:HG22	11:K:26:VAL:HA	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:11:GLY:HA3	13:M:178:ILE:O	2.16	0.45
6:T:127:ASN:ND2	6:T:127:ASN:C	2.69	0.45
10:X:12:VAL:HG21	10:X:109:GLU:O	2.16	0.45
13:1:8:TYR:HD2	13:1:9:ASP:OD1	1.98	0.45
7:G:18(G):GLU:CG	7:G:188:LYS:HB2	2.46	0.45
9:I:33:LYS:O	9:I:44:GLY:HA2	2.15	0.45
12:L:58:ARG:HG2	12:L:58:ARG:NH1	2.29	0.45
12:L:-8:PHE:HB2	13:M:-8:THR:HG23	1.98	0.45
1:O:122:GLU:C	1:O:124:THR:H	2.20	0.45
1:O:7:ARG:HB2	2:P:5:S:SER:OG	2.16	0.45
5:S:13:VAL:O	5:S:13:VAL:HG13	2.16	0.45
6:T:114:ASP:O	6:T:118:GLN:HG2	2.15	0.45
5:S:161:TYR:CE2	6:T:60:VAL:HA	2.52	0.45
12:Z:14(E):GLU:HB2	12:Z:14(I):THR:HG21	1.99	0.45
12:Z:59:PHE:O	12:Z:62:SER:HB3	2.17	0.45
2:B:149:TYR:CZ	3:C:62(A):ILE:HB	2.51	0.45
3:C:35:THR:OG1	3:C:66:LYS:NZ	2.49	0.45
3:C:87:ILE:O	3:C:91:LYS:HG3	2.16	0.45
5:E:111:ARG:NH1	5:E:111:ARG:HG2	2.31	0.45
6:F:127:ASN:ND2	6:F:127:ASN:C	2.69	0.45
6:F:179:LEU:HD11	6:F:192:GLN:HG2	1.98	0.45
8:H:52:THR:O	8:H:56:THR:HB	2.17	0.45
12:L:55:LEU:CD2	12:L:87:LEU:HD21	2.47	0.45
13:M:14(C):ARG:O	13:M:14(F):ASP:HB2	2.17	0.45
14:N:146:MET:HE3	14:N:150:GLU:HB3	1.98	0.45
4:R:17:PRO:HA	5:S:26:TYR:CG	2.51	0.45
5:S:17:PRO:HA	6:T:26:TYR:CE1	2.51	0.45
5:S:180:LEU:O	5:S:18(D):ILE:HG22	2.16	0.45
6:T:169:ARG:O	6:T:173:LYS:HG3	2.17	0.45
8:V:197:ARG:NH2	9:W:139:GLU:HG3	2.32	0.45
11:Y:15:ALA:HB2	11:Y:175:LEU:HD23	1.97	0.45
11:Y:40:PHE:CG	11:Y:73:ARG:CZ	2.99	0.45
2:B:21:LEU:HD13	2:B:124:THR:HG23	1.98	0.45
2:B:161:LYS:HB3	2:B:180:TYR:CE2	2.52	0.45
3:C:8:TYR:HB3	16:C:1062:HOH:O	2.17	0.45
6:F:100:LYS:O	6:F:104:LYS:N	2.46	0.45
6:F:180:VAL:HG21	7:G:58:LEU:HD23	1.97	0.45
7:G:74:ILE:HG21	7:G:112:LEU:HD23	1.99	0.45
10:J:85:GLN:HG2	16:J:202:HOH:O	2.16	0.45
13:M:19:LEU:HD21	13:M:26:LEU:HD22	1.99	0.45
14:N:175:MET:HB2	14:N:187:LEU:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:18(D):PRO:HA	14:N:18(G):TYR:CE2	2.51	0.45
7:U:69:CYS:HB3	16:U:1186:HOH:O	2.16	0.45
8:V:77:VAL:HG13	16:V:351:HOH:O	2.15	0.45
9:W:3:VAL:HG22	9:W:16:CYS:HB3	1.98	0.45
9:W:36:HIS:HB3	9:W:42:PHE:CD2	2.52	0.45
9:W:7:THR:HG23	9:W:110:ILE:CD1	2.46	0.45
2:B:134:VAL:HG12	2:B:135:SER:N	2.31	0.45
6:F:43:ASN:H	6:F:43:ASN:ND2	2.14	0.45
8:H:55:VAL:CG1	8:H:56:THR:N	2.79	0.45
9:I:93:GLY:N	9:I:94:PRO:CD	2.80	0.45
10:J:148:THR:CG2	10:J:177:ILE:HD13	2.47	0.45
13:M:41:THR:HG21	13:M:79:ILE:CD1	2.45	0.45
3:Q:149:TYR:CE1	3:Q:159:SER:HB3	2.52	0.45
3:Q:151:THR:HG22	3:Q:157:TYR:CB	2.46	0.45
3:Q:99:HIS:CG	3:Q:107:VAL:HG12	2.52	0.45
6:T:52:LYS:HB2	6:T:209:GLU:O	2.17	0.45
6:T:91:ARG:HG2	6:T:119:TYR:CD2	2.52	0.45
7:U:191:GLU:HG3	7:U:232:ARG:HG3	1.98	0.45
8:V:18:THR:HB	8:V:30:ASN:HA	1.99	0.45
12:Z:5:GLY:O	12:Z:124:CYS:HA	2.16	0.45
13:1:70:ASN:ND2	13:1:70(A):ALA:HA	2.31	0.45
4:D:227:GLU:O	4:D:231:GLU:HG3	2.16	0.45
4:D:29:GLU:HA	4:D:29:GLU:OE2	2.17	0.45
5:E:160:LEU:CD2	6:F:59:LEU:HD12	2.47	0.45
11:K:67:GLU:OE1	11:K:73:ARG:HA	2.16	0.45
3:Q:46:VAL:HB	3:Q:215:VAL:CG1	2.47	0.45
5:S:201:LEU:O	5:S:202:ARG:HB2	2.16	0.45
12:Z:113:PHE:CD2	12:Z:119:TYR:HB3	2.51	0.45
14:2:37:VAL:HG22	14:2:41:ILE:O	2.16	0.45
2:B:150:THR:HG22	2:B:160:TRP:HE1	1.81	0.45
3:C:33:ARG:HH11	3:C:33:ARG:HB3	1.79	0.45
7:G:79:ASN:HA	16:G:926:HOH:O	2.16	0.45
10:J:190:PHE:C	10:J:192:ALA:H	2.18	0.45
6:T:107:ILE:HG23	6:T:107:ILE:O	2.17	0.45
11:Y:6:PHE:HB2	11:Y:124:ILE:HG12	1.98	0.45
6:F:43:ASN:N	6:F:43:ASN:ND2	2.64	0.45
8:H:137:VAL:HG21	8:H:161:ALA:HB2	1.98	0.45
9:I:45:ILE:HB	9:I:52:VAL:HG13	1.99	0.45
11:K:143:LYS:HB2	11:K:146:LEU:HD11	1.99	0.45
12:L:33:LYS:CD	12:L:46:ASN:HD22	2.26	0.45
13:M:160:ARG:HG3	13:M:192:VAL:CG1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:171:GLY:HA2	13:1:197:TRP:CH2	2.52	0.45
2:P:99:TYR:CD2	2:P:107:ILE:HA	2.52	0.45
6:T:121:GLN:NE2	16:T:385:HOH:O	2.50	0.45
8:V:113:ILE:HG12	8:V:119:THR:HG22	1.99	0.45
8:V:72:ARG:HH11	8:V:72:ARG:HG3	1.80	0.45
10:X:113:ILE:HG12	10:X:119:LYS:HG3	1.99	0.45
11:Y:148:VAL:HB	16:Y:973:HOH:O	2.16	0.45
14:2:148:LYS:O	14:2:152:VAL:HG23	2.17	0.45
1:A:67:VAL:HB	1:A:223:LYS:HZ2	1.79	0.45
3:C:24:VAL:O	3:C:27:ALA:HB3	2.17	0.45
4:D:160:TYR:HB3	4:D:162:ALA:O	2.17	0.45
4:D:160:TYR:CZ	4:D:163:LYS:HD3	2.52	0.45
5:E:201:LEU:O	5:E:202:ARG:HB2	2.17	0.45
13:M:19:LEU:HD12	13:M:28:PHE:O	2.17	0.45
2:P:186:VAL:HG21	2:P:216:ARG:HG2	1.99	0.45
2:P:21:LEU:HD13	2:P:124:THR:HG23	1.99	0.45
2:P:52:ARG:HH22	2:P:63(A):SER:HB3	1.82	0.45
7:U:142:ASP:OD2	7:U:144:LEU:N	2.44	0.45
7:U:74:ILE:HG21	7:U:112:LEU:HD23	1.98	0.45
12:Z:166:HIS:CD2	12:Z:168:GLN:H	2.29	0.45
14:2:85:GLU:O	14:2:89:GLU:HB2	2.17	0.44
2:B:17:PRO:HA	3:C:26:TYR:CD1	2.52	0.44
5:E:18(A):ASP:OD2	5:E:18(A):ASP:N	2.49	0.44
5:E:86:ARG:NH1	5:E:86:ARG:HG3	2.32	0.44
9:I:84:SER:CB	9:I:119:ILE:HD11	2.47	0.44
14:N:146:MET:CE	14:N:150:GLU:HB3	2.46	0.44
7:U:130:ARG:HG3	7:U:131:PRO:O	2.17	0.44
13:M:165:ARG:NH1	8:V:139:GLU:OE1	2.46	0.44
9:W:115:LEU:HD23	9:W:115:LEU:H	1.83	0.44
12:Z:19:ARG:HG2	12:Z:21:ILE:HG23	1.99	0.44
3:C:99:HIS:CG	3:C:107:VAL:HG12	2.52	0.44
5:E:2(B):THR:OG1	5:E:2(E):ASN:HB3	2.17	0.44
7:G:18(H):GLU:N	7:G:18(H):GLU:CD	2.71	0.44
12:L:43:MET:HB2	12:L:101:ILE:HG22	1.99	0.44
1:O:184:LEU:HB2	16:O:486:HOH:O	2.17	0.44
1:O:69:LEU:HG	1:O:71:THR:O	2.17	0.44
3:Q:241:GLN:C	3:Q:243:GLN:N	2.71	0.44
4:R:42:THR:C	4:R:44:GLU:H	2.21	0.44
6:T:95:GLU:CG	6:T:115:ARG:HD2	2.48	0.44
7:U:34(A):ASN:HD22	7:U:167:PRO:HG2	1.82	0.44
7:U:18(H):GLU:H	7:U:18(H):GLU:CD	2.20	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:V:139:GLU:OE2	8:V:139:GLU:HA	2.18	0.44
9:W:106:GLY:HA2	9:W:181:LYS:HD3	1.99	0.44
14:2:112:THR:CG2	14:2:120:HIS:HB2	2.47	0.44
2:B:46:ILE:HG22	2:B:47:VAL:N	2.32	0.44
6:F:158:TRP:CZ3	7:G:64:VAL:HA	2.52	0.44
11:K:4:LEU:CD1	11:K:159:ILE:HD11	2.27	0.44
12:L:166:HIS:CD2	12:L:168:GLN:HB2	2.53	0.44
12:L:166:HIS:CD2	12:L:168:GLN:H	2.27	0.44
1:O:123:ALA:HB3	16:O:237:HOH:O	2.17	0.44
2:P:20:ARG:HH11	2:P:20:ARG:HG2	1.81	0.44
3:Q:46:VAL:HG22	3:Q:146:PRO:HB2	1.99	0.44
4:R:122:ARG:HG2	4:R:122:ARG:NH1	2.31	0.44
4:R:93:ARG:HD2	16:R:733:HOH:O	2.17	0.44
6:T:37:SER:HB3	6:T:50:VAL:HG23	2.00	0.44
13:1:115:LEU:N	13:1:115:LEU:HD23	2.33	0.44
6:F:136:THR:CB	16:F:1005:HOH:O	2.63	0.44
7:G:96:ALA:HB3	16:G:623:HOH:O	2.17	0.44
9:I:117:GLY:O	9:I:118:CYS:C	2.54	0.44
9:I:7:THR:HG23	9:I:110:ILE:CD1	2.47	0.44
10:J:74:LEU:HD22	10:J:78:ALA:HB1	2.00	0.44
14:N:161:GLN:HE21	14:2:136:GLY:CA	2.09	0.44
1:O:27:ALA:O	1:O:31:VAL:HG23	2.18	0.44
3:Q:168:ASN:CB	3:Q:200:VAL:HG11	2.44	0.44
4:R:18:GLU:OE2	4:R:18:GLU:N	2.50	0.44
5:S:134:VAL:O	5:S:153:PRO:HG3	2.17	0.44
6:T:12:ASN:OD1	6:T:12:ASN:O	2.35	0.44
3:C:241:GLN:C	3:C:243:GLN:N	2.70	0.44
4:D:123:PHE:CE2	4:D:131:PRO:HG3	2.52	0.44
6:F:50:VAL:HG12	6:F:211:GLU:HB3	2.00	0.44
13:M:186:PHE:CE1	13:M:188:LYS:HG3	2.51	0.44
2:P:160:TRP:CD2	2:P:163:ILE:HD13	2.52	0.44
3:Q:58:LEU:HA	3:Q:58:LEU:HD12	1.81	0.44
4:R:177:LEU:HD13	5:S:58:LEU:CD1	2.47	0.44
9:W:33:LYS:O	9:W:44:GLY:HA2	2.17	0.44
10:X:35:ARG:HD3	10:X:35:ARG:HA	1.85	0.44
13:1:209:GLN:N	16:1:367:HOH:O	2.51	0.44
1:A:62:GLU:H	1:A:62:GLU:CD	2.20	0.44
2:B:26:TYR:O	2:B:29:GLU:HB3	2.17	0.44
5:E:2(B):THR:N	5:E:2(E):ASN:HD22	2.15	0.44
5:E:54:ASN:ND2	5:E:56:ASP:O	2.51	0.44
7:G:151:THR:HA	7:G:156:TYR:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:84:SER:HB2	9:I:119:ILE:HD11	1.98	0.44
10:J:168:MET:CE	10:X:168:MET:CE	2.96	0.44
2:P:209:ARG:CZ	2:P:209:ARG:HB3	2.48	0.44
7:U:105:TYR:OH	8:V:66:HIS:HE1	2.00	0.44
8:V:156:SER:O	8:V:160:GLN:HG3	2.18	0.44
8:V:170:GLY:O	8:V:171:SER:HB2	2.18	0.44
10:X:148:THR:CG2	10:X:177:ILE:HD13	2.48	0.44
12:Z:176:LEU:CD1	12:Z:186:LYS:HG2	2.47	0.44
1:A:184:LEU:HD22	1:A:188:ASP:HB3	1.98	0.44
2:B:17:PRO:HA	3:C:26:TYR:CZ	2.52	0.44
3:C:55:THR:O	3:C:56:LEU:HD22	2.18	0.44
11:K:77:ALA:HA	11:K:111:TYR:CE2	2.53	0.44
3:Q:76:LEU:HD12	3:Q:138:ILE:CG1	2.48	0.44
11:Y:38:ASN:OD1	11:Y:40:PHE:N	2.47	0.44
11:Y:67:GLU:OE1	11:Y:73:ARG:HA	2.17	0.44
13:1:160:ARG:HG3	13:1:192:VAL:HG11	1.99	0.44
1:A:69:LEU:HG	1:A:71:THR:O	2.17	0.44
2:B:52:ARG:HH22	2:B:63(A):SER:HB3	1.82	0.44
4:D:56:SER:OG	4:D:57:PRO:HD2	2.18	0.44
5:E:227:GLU:CD	5:E:227:GLU:H	2.22	0.44
8:H:144:GLN:O	8:H:145:ASP:HB2	2.18	0.44
8:H:170:GLY:O	8:H:171:SER:HB2	2.18	0.44
16:A:658:HOH:O	8:H:185:GLU:HB2	2.17	0.44
14:N:112:THR:CG2	14:N:120:HIS:HB2	2.47	0.44
14:N:186:ARG:HD3	16:N:933:HOH:O	2.18	0.44
14:N:1:THR:HG23	14:N:33:LYS:NZ	2.32	0.44
14:N:85:GLU:O	14:N:89:GLU:HB2	2.17	0.44
1:O:27:ALA:O	1:O:30:ALA:HB3	2.17	0.44
2:P:176:LEU:HD23	2:P:192:LEU:HD22	2.00	0.44
5:S:220:PRO:O	5:S:222:THR:HG23	2.18	0.44
6:T:205:ASN:O	6:T:20(B):GLU:N	2.51	0.44
2:P:97:GLN:OE1	9:W:64:ASN:HB3	2.18	0.44
13:1:146:THR:HA	16:1:323:HOH:O	2.18	0.44
1:A:21(G):LEU:HG	1:A:21(I):TYR:CE1	2.53	0.44
5:E:226:GLY:HA3	5:E:227:GLU:OE2	2.18	0.44
6:F:91:ARG:HG2	6:F:119:TYR:CD2	2.52	0.44
9:I:90:ARG:HG3	9:I:95:TYR:CE1	2.53	0.44
11:K:65:LEU:HA	11:K:65:LEU:HD12	1.85	0.44
3:Q:224:LEU:H	3:Q:224:LEU:HD12	1.82	0.44
3:Q:87:ILE:O	3:Q:91:LYS:HG3	2.18	0.44
8:V:55:VAL:CG1	8:V:56:THR:N	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:55:LEU:HD12	9:W:97:VAL:HG21	1.99	0.44
10:X:93:ARG:HG2	10:X:93:ARG:HH11	1.83	0.44
8:H:3:ILE:HG22	8:H:16:ALA:CB	2.48	0.43
9:I:99:PRO:HB2	9:I:113:PHE:CD2	2.53	0.43
11:K:160:LEU:HD22	11:K:199:VAL:HG21	1.99	0.43
14:N:122:LEU:HD12	14:N:125:ALA:HB2	2.00	0.43
3:Q:108:THR:HG23	16:Q:1056:HOH:O	2.18	0.43
3:Q:123:TYR:CD1	3:Q:132:PHE:HE1	2.35	0.43
4:R:123:PHE:CE2	4:R:131:PRO:HG3	2.53	0.43
4:R:160:TYR:CZ	4:R:163:LYS:HD3	2.53	0.43
5:S:54:ASN:ND2	5:S:56:ASP:O	2.51	0.43
7:U:177:GLU:O	7:U:17(B):LYS:HG3	2.17	0.43
11:Y:144:TRP:HB2	16:Y:1321:HOH:O	2.17	0.43
11:Y:147:SER:C	11:Y:149:GLU:N	2.71	0.43
12:Z:85:HIS:HE1	16:Z:196:HOH:O	2.00	0.43
14:2:114:PRO:HG2	16:2:191:HOH:O	2.16	0.43
3:C:229:ILE:O	3:C:233:VAL:HG23	2.18	0.43
6:F:172:ALA:O	6:F:175:GLU:N	2.51	0.43
1:A:12:LEU:HD11	7:G:127:ALA:HB2	2.00	0.43
8:H:147:THR:HG23	8:H:150:GLU:CD	2.38	0.43
9:I:187:ARG:HG3	9:I:187:ARG:HH11	1.83	0.43
11:K:147:SER:C	11:K:149:GLU:N	2.71	0.43
13:M:17:ASP:HA	13:M:173:PHE:CA	2.48	0.43
1:O:92:SER:HA	1:O:95:VAL:HG12	1.99	0.43
2:P:141:TYR:CE2	2:P:145:GLY:HA2	2.53	0.43
2:P:186:VAL:HG11	2:P:216:ARG:HD3	2.00	0.43
2:P:25:GLU:OE2	2:P:25:GLU:HA	2.18	0.43
2:P:71:ASN:CG	2:P:72:ASP:H	2.15	0.43
5:S:18(A):ASP:OD2	5:S:18(A):ASP:N	2.50	0.43
6:T:43:ASN:ND2	6:T:43:ASN:N	2.66	0.43
9:W:93:GLY:N	9:W:94:PRO:CD	2.81	0.43
13:1:19:LEU:HB3	16:1:212:HOH:O	2.17	0.43
2:B:218:ASN:O	2:B:21(C):ASP:HB2	2.18	0.43
2:B:53:LYS:HG2	2:B:54:VAL:HG23	2.00	0.43
5:E:199:GLN:CA	5:E:199:GLN:HE21	2.31	0.43
8:H:62:ASN:ND2	16:H:227:HOH:O	2.30	0.43
9:I:106:GLY:HA2	9:I:181:LYS:HD3	1.98	0.43
9:I:55:LEU:HD23	9:I:55:LEU:HA	1.84	0.43
10:J:70:GLU:O	10:J:71:ASP:C	2.56	0.43
11:K:156:LYS:HB2	11:K:175:LEU:HD11	2.01	0.43
1:O:6:ASP:OD1	7:U:126:ARG:NH2	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:121:GLN:C	2:P:121:GLN:NE2	2.72	0.43
3:Q:159:SER:O	4:R:59:LEU:HD22	2.18	0.43
4:R:39:GLY:O	4:R:162:ALA:HA	2.18	0.43
6:T:179:LEU:CD2	6:T:192:GLN:HG2	2.43	0.43
6:T:224:VAL:HG13	6:T:228:LEU:HD23	2.01	0.43
6:T:43:ASN:ND2	6:T:43:ASN:H	2.16	0.43
7:U:158:VAL:HG22	7:U:159:GLY:H	1.82	0.43
9:W:66:TYR:CZ	9:W:70:GLU:HG3	2.54	0.43
12:Z:21:ILE:HD11	12:Z:168:GLN:NE2	2.32	0.43
13:1:112:TYR:O	13:1:119:THR:HA	2.17	0.43
1:A:92:SER:HA	1:A:95:VAL:HG12	2.00	0.43
3:C:241:GLN:O	3:C:243:GLN:N	2.39	0.43
4:D:121:LEU:HA	4:D:123:PHE:HE1	1.84	0.43
4:D:79:SER:HA	16:D:250:HOH:O	2.18	0.43
5:E:180:LEU:O	5:E:18(D):ILE:HG22	2.19	0.43
5:E:2(C):VAL:CG1	5:E:2(D):ASP:N	2.81	0.43
6:F:172:ALA:O	6:F:173:LYS:C	2.56	0.43
6:F:78:TYR:CE1	6:F:85:GLY:HA3	2.54	0.43
8:H:160:GLN:O	8:H:161:ALA:C	2.56	0.43
10:J:4:LEU:HD23	10:J:126:ALA:CB	2.47	0.43
11:K:126:CYS:HB2	11:K:135:TYR:CZ	2.52	0.43
13:M:14(A):VAL:O	13:M:14(A):VAL:HG23	2.18	0.43
2:P:207:TYR:CG	2:P:208:ASP:N	2.86	0.43
4:R:14:THR:HG22	4:R:15:PHE:N	2.34	0.43
6:T:118:GLN:HE21	7:U:90:LEU:HD22	1.84	0.43
6:T:44:ASP:OD2	6:T:44:ASP:C	2.57	0.43
7:U:17(C):LYS:HE3	7:U:17(C):LYS:HB2	1.78	0.43
9:W:107:LYS:HA	9:W:108:PRO:HD3	1.80	0.43
1:A:27:ALA:O	1:A:31:VAL:HG23	2.18	0.43
4:D:122:ARG:NH1	4:D:122:ARG:HG2	2.28	0.43
3:C:159:SER:OG	4:D:63:SER:HB3	2.18	0.43
5:E:199:GLN:HE21	5:E:199:GLN:N	2.17	0.43
5:E:201:LEU:HD11	5:E:207:LEU:CD2	2.40	0.43
8:H:105:ASP:HB2	8:H:10(A):PRO:HD2	2.01	0.43
10:J:142:TYR:O	10:J:143:ARG:HD3	2.18	0.43
11:K:97:MET:O	11:K:114:ASP:HA	2.18	0.43
11:K:13:ILE:HG13	11:K:151:ALA:HB1	2.01	0.43
14:N:44:CYS:HB2	14:N:100:ILE:HB	2.00	0.43
4:R:31:ILE:HD13	4:R:135:ALA:HB2	2.01	0.43
5:S:2(C):VAL:CG1	5:S:2(D):ASP:N	2.81	0.43
5:S:2(B):THR:OG1	5:S:2(E):ASN:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:118:GLN:NE2	7:U:90:LEU:HD22	2.33	0.43
5:S:160:LEU:CD2	6:T:59:LEU:HD12	2.48	0.43
7:U:100:ARG:HG3	16:U:937:HOH:O	2.18	0.43
7:U:192:PHE:C	7:U:192:PHE:CD1	2.92	0.43
9:W:117:GLY:O	9:W:118:CYS:C	2.57	0.43
10:X:45:PHE:HB3	10:X:99:VAL:HG12	2.01	0.43
13:1:184:LEU:C	13:1:184:LEU:HD23	2.39	0.43
6:F:203:GLU:HA	6:F:203:GLU:OE1	2.18	0.43
7:G:224:LEU:HB3	7:G:228:ASN:HB2	1.99	0.43
7:G:29:LYS:HD2	7:G:29:LYS:HA	1.79	0.43
11:K:111:TYR:CE1	11:K:121:LYS:HB2	2.53	0.43
1:O:55:SER:O	1:O:56:SER:HB2	2.19	0.43
4:R:215:ILE:HD12	4:R:216:THR:N	2.34	0.43
6:T:143:LYS:HG2	6:T:143:LYS:O	2.18	0.43
8:V:147:THR:HG23	8:V:150:GLU:CD	2.39	0.43
8:V:49:ALA:HB3	15:V:7710:SY2:H13A	2.01	0.43
10:X:74:LEU:HD22	10:X:78:ALA:HB1	1.99	0.43
11:Y:12:ILE:HD11	11:Y:109:THR:N	2.33	0.43
13:1:125:LEU:HA	16:1:218:HOH:O	2.17	0.43
12:Z:-8:PHE:HB2	13:1:-8:THR:HG23	2.01	0.43
1:A:8:TYR:HD2	7:G:128:TYR:HB3	1.83	0.43
7:G:192:PHE:CD1	7:G:192:PHE:C	2.91	0.43
7:G:8:TYR:C	7:G:10:ARG:N	2.72	0.43
14:N:66:TYR:CD2	14:N:74:PRO:HB3	2.54	0.43
1:O:5:THR:O	1:O:7:ARG:HG2	2.18	0.43
8:V:52:THR:O	8:V:56:THR:HB	2.18	0.43
12:Z:76:ILE:HG23	12:Z:77:ASN:N	2.33	0.43
1:A:78:TYR:HB3	1:A:85:TYR:CD1	2.54	0.43
3:C:46:VAL:HB	3:C:215:VAL:CG1	2.48	0.43
3:C:58:LEU:HA	3:C:58:LEU:HD12	1.82	0.43
4:D:40:ILE:CD1	4:D:193:VAL:HG23	2.47	0.43
5:E:35:SER:HB3	5:E:66:LYS:NZ	2.34	0.43
6:F:130:ARG:NH1	6:F:130:ARG:HG2	2.34	0.43
10:J:112:GLN:NE2	16:J:898:HOH:O	2.41	0.43
10:J:11:SER:HB2	10:J:178:VAL:O	2.19	0.43
11:K:15:ALA:HB2	11:K:175:LEU:HD23	2.00	0.43
12:L:21:ILE:C	12:L:21:ILE:CD1	2.87	0.43
13:M:104:VAL:CG2	13:M:178:ILE:HG22	2.46	0.43
14:N:3:ILE:HD13	14:N:46:SER:HB3	2.00	0.43
4:R:17:PRO:HG3	5:S:26:TYR:CZ	2.54	0.43
5:S:58:LEU:N	5:S:58:LEU:HD12	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:179:LEU:HD11	6:T:192:GLN:HG2	2.00	0.43
8:V:199:GLU:N	16:V:1207:HOH:O	2.31	0.43
11:Y:32:LYS:HD2	11:Y:32:LYS:N	2.33	0.43
12:Z:33:LYS:CD	12:Z:46:ASN:HD22	2.26	0.43
1:A:6:ASP:HB2	7:G:128:TYR:CE2	2.54	0.43
2:B:80:GLY:HA3	2:B:133:GLY:O	2.19	0.43
3:C:156:ILE:HD11	16:D:246:HOH:O	2.18	0.43
3:C:36:CYS:H	3:C:51:GLU:HG2	1.84	0.43
3:C:87:ILE:CD1	3:C:87:ILE:N	2.82	0.43
4:D:14:THR:HG22	4:D:15:PHE:N	2.33	0.43
6:F:205:ASN:O	6:F:20(B):GLU:N	2.52	0.43
8:H:81:GLN:NE2	16:H:747:HOH:O	2.51	0.43
10:J:104:TYR:CD1	10:J:180:LYS:HA	2.54	0.43
10:J:32:ASP:OD2	10:J:34:THR:HG22	2.18	0.43
11:K:32:LYS:N	11:K:32:LYS:HD2	2.34	0.43
1:O:159:PRO:O	2:P:59:LEU:HD12	2.18	0.43
3:Q:229:ILE:O	3:Q:233:VAL:HG23	2.18	0.43
3:Q:76:LEU:O	3:Q:76:LEU:HD23	2.18	0.43
4:R:17:PRO:HA	5:S:26:TYR:CD1	2.54	0.43
14:2:66:TYR:CD2	14:2:74:PRO:HB3	2.53	0.43
2:B:25:GLU:OE2	2:B:25:GLU:HA	2.19	0.43
5:E:4:PHE:CG	5:E:5:ARG:N	2.87	0.43
6:F:103:TYR:O	6:F:104:LYS:HB3	2.19	0.43
8:H:49:ALA:HB3	15:H:7710:SY2:H13A	2.00	0.43
12:L:29:ARG:NH1	12:L:171:ASP:OD1	2.49	0.43
13:M:-5:PRO:HD3	13:M:96:TRP:CE2	2.53	0.43
2:P:218:ASN:O	2:P:21(C):ASP:HB2	2.17	0.43
3:Q:224:LEU:H	3:Q:224:LEU:CD1	2.32	0.43
3:Q:225:SER:O	3:Q:229:ILE:HG13	2.18	0.43
4:R:121:LEU:HA	4:R:123:PHE:HE1	1.82	0.43
5:S:18(C):PHE:HA	5:S:18(F):ILE:CD1	2.49	0.43
5:S:47:VAL:CG1	5:S:48:LEU:N	2.82	0.43
6:T:107:ILE:HA	6:T:108:PRO:HD3	1.83	0.43
8:V:160:GLN:O	8:V:161:ALA:C	2.57	0.43
10:X:59:ILE:HD13	10:X:59:ILE:HA	1.86	0.43
11:Y:126:CYS:HB2	11:Y:135:TYR:CZ	2.53	0.43
11:Y:2:THR:HG22	11:Y:159:ILE:CD1	2.49	0.43
13:1:124:THR:O	13:1:125:LEU:HD23	2.19	0.42
2:B:209:ARG:HB3	2:B:209:ARG:CZ	2.48	0.42
4:D:81:LEU:HD12	4:D:133:GLY:HA3	2.00	0.42
7:G:150:LYS:O	7:G:157:TYR:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:18:THR:HB	8:H:30:ASN:HA	2.01	0.42
9:I:107:LYS:HA	9:I:108:PRO:HD3	1.80	0.42
10:J:3:ILE:HG22	10:J:100:LEU:CD1	2.49	0.42
10:J:45:PHE:HB3	10:J:99:VAL:HG12	2.01	0.42
12:L:14(E):GLU:HB2	12:L:14(I):THR:HG21	2.01	0.42
12:L:-9:GLN:NE2	12:L:-8:PHE:H	2.16	0.42
13:M:89:GLN:O	13:M:92(A):LYS:HG3	2.19	0.42
5:S:31:ILE:HD11	5:S:153:PRO:CD	2.49	0.42
5:S:226:GLY:HA3	5:S:227:GLU:OE2	2.19	0.42
6:T:69:VAL:HG12	16:T:811:HOH:O	2.18	0.42
9:W:143:GLU:CG	9:W:146:LEU:HD21	2.49	0.42
9:W:61:TYR:C	9:W:61:TYR:CD1	2.93	0.42
10:X:8:VAL:HG11	10:X:151:GLY:HA3	2.02	0.42
10:X:146:MET:HE1	10:X:154:LEU:HD22	2.00	0.42
11:Y:160:LEU:HD22	11:Y:199:VAL:HG21	2.00	0.42
13:1:157:ASN:ND2	16:1:905:HOH:O	2.51	0.42
1:A:77:VAL:HG12	1:A:137:LEU:HB2	2.01	0.42
1:A:7:ARG:HD3	5:E:127:TYR:CD2	2.53	0.42
2:B:141:TYR:CE2	2:B:145:GLY:HA2	2.54	0.42
3:C:225:SER:O	3:C:229:ILE:HG13	2.18	0.42
5:E:47:VAL:CG1	5:E:48:LEU:N	2.82	0.42
6:F:103:TYR:O	6:F:105:THR:HG22	2.19	0.42
7:G:217:LYS:CE	7:G:217:LYS:HA	2.46	0.42
8:H:124:TYR:O	8:H:125:LEU:HD23	2.20	0.42
12:L:76:ILE:HG23	12:L:77:ASN:N	2.33	0.42
2:P:235:LYS:N	2:P:235:LYS:HD3	2.34	0.42
3:Q:156:ILE:HG22	3:Q:157:TYR:N	2.32	0.42
4:R:170:GLU:N	4:R:170:GLU:OE1	2.51	0.42
5:S:137:LEU:CD2	5:S:150:GLU:HG3	2.49	0.42
5:S:160:LEU:HD13	5:S:163:THR:HB	2.01	0.42
5:S:2(B):THR:N	5:S:2(E):ASN:HD22	2.16	0.42
7:U:60:ASP:OD2	7:U:62:THR:OG1	2.36	0.42
10:X:137:LEU:CD1	10:X:158:CYS:HA	2.49	0.42
12:Z:109:ALA:HB2	12:Z:121:ARG:NH2	2.34	0.42
13:1:14(C):ARG:O	13:1:14(F):ASP:HB2	2.18	0.42
14:2:18(G):TYR:HA	14:2:18(J):LEU:HG	2.01	0.42
3:C:123:TYR:CD1	3:C:132:PHE:HE1	2.37	0.42
3:C:76:LEU:O	3:C:76:LEU:HD23	2.19	0.42
6:F:224:VAL:HG13	6:F:228:LEU:HD23	2.00	0.42
10:J:147:THR:OG1	10:J:150:GLU:HG3	2.20	0.42
13:M:160:ARG:HG3	13:M:192:VAL:HG11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:168:ARG:HD2	16:M:464:HOH:O	2.18	0.42
2:P:37:ALA:HB3	2:P:165:VAL:CG2	2.48	0.42
3:Q:62(A):ILE:HG13	3:Q:63:THR:N	2.34	0.42
3:Q:97:GLN:NE2	3:Q:97:GLN:HA	2.35	0.42
5:S:199:GLN:HE21	5:S:199:GLN:CA	2.32	0.42
6:T:203:GLU:OE1	6:T:203:GLU:HA	2.19	0.42
6:T:75:GLY:O	6:T:138:PHE:HA	2.19	0.42
7:U:14(A):GLU:HB2	16:U:915:HOH:O	2.19	0.42
7:U:217:LYS:HA	7:U:217:LYS:CE	2.45	0.42
10:X:148:THR:HG21	10:X:177:ILE:HD13	2.01	0.42
10:X:3:ILE:HD13	10:X:3:ILE:HA	1.83	0.42
10:X:52:THR:HG23	10:X:53:VAL:HG23	2.01	0.42
12:Z:31:GLU:OE1	13:1:120:TYR:HA	2.20	0.42
12:Z:55:LEU:CD2	12:Z:87:LEU:HD21	2.50	0.42
12:Z:93:PHE:N	12:Z:94:PRO:CD	2.80	0.42
2:B:122:GLY:C	2:B:124:THR:N	2.73	0.42
3:C:156:ILE:HG22	3:C:157:TYR:N	2.35	0.42
3:C:39:GLY:O	3:C:162:ALA:HA	2.20	0.42
3:C:238:GLN:O	3:C:242:GLU:HG3	2.19	0.42
4:D:12(D):ALA:HB3	4:D:126:ARG:CG	2.50	0.42
9:I:15:ALA:HB2	9:I:175:VAL:HG22	2.00	0.42
10:J:155:LEU:HD23	10:J:155:LEU:HA	1.89	0.42
2:P:122:GLY:C	2:P:124:THR:N	2.72	0.42
7:U:224:LEU:HB3	7:U:228:ASN:HB2	2.00	0.42
10:X:112:GLN:NE2	10:X:126:ALA:H	2.16	0.42
2:P:114:ARG:NH1	10:X:70:GLU:OE2	2.43	0.42
11:Y:25:TRP:CZ3	12:Z:132:SER:HA	2.54	0.42
13:1:14(A):VAL:O	13:1:14(A):VAL:HG23	2.20	0.42
13:1:42:VAL:HG23	13:1:178:ILE:HD11	2.00	0.42
13:1:19:LEU:HD12	13:1:28:PHE:O	2.20	0.42
3:C:57:LYS:HD2	3:C:58:LEU:N	2.34	0.42
5:E:137:LEU:CD2	5:E:150:GLU:HG3	2.49	0.42
6:F:37:SER:HB3	6:F:50:VAL:HG23	2.02	0.42
10:J:112:GLN:NE2	10:J:126:ALA:H	2.17	0.42
2:P:202:THR:CG2	2:P:204:SER:HB2	2.49	0.42
2:P:31:ILE:HG23	2:P:79:ALA:O	2.19	0.42
2:P:70:LEU:CD2	2:P:89:ILE:HG23	2.50	0.42
4:R:12(D):ALA:HB3	4:R:126:ARG:CG	2.49	0.42
6:T:179:LEU:HD11	6:T:192:GLN:HG3	2.01	0.42
6:T:50:VAL:HG12	6:T:211:GLU:HB3	2.01	0.42
7:U:18:GLU:HB2	7:U:20:ARG:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:V:197:ARG:NH2	9:W:139:GLU:O	2.52	0.42
11:Y:97:MET:HG2	11:Y:115:SER:HB3	2.02	0.42
13:1:191:GLN:HE21	13:1:191:GLN:HB3	1.60	0.42
1:A:77:VAL:CG1	1:A:137:LEU:HB2	2.50	0.42
2:B:69:LYS:HE2	2:B:221:GLN:OE1	2.20	0.42
5:E:199:GLN:NE2	5:E:199:GLN:CA	2.82	0.42
6:F:169:ARG:HB3	6:F:169:ARG:HE	1.59	0.42
7:G:38:LEU:HD23	7:G:197:MET:CE	2.50	0.42
10:J:161:GLU:HA	10:J:161:GLU:OE2	2.19	0.42
13:M:112:TYR:O	13:M:119:THR:HA	2.19	0.42
13:M:190:LEU:CD1	13:M:190:LEU:N	2.82	0.42
4:R:160:TYR:CE2	4:R:163:LYS:HD3	2.55	0.42
5:S:78:LEU:HD12	5:S:78:LEU:O	2.19	0.42
11:Y:156:LYS:HB2	11:Y:175:LEU:HD11	2.01	0.42
11:Y:9:GLN:HE21	11:Y:9:GLN:HB3	1.72	0.42
12:Z:166:HIS:CD2	12:Z:168:GLN:HB2	2.53	0.42
13:1:133:MET:O	13:1:136:PRO:HD2	2.19	0.42
1:A:55:SER:O	1:A:56:SER:HB2	2.20	0.42
2:B:186:VAL:HG21	2:B:216:ARG:HG2	2.01	0.42
10:J:93:ARG:HH11	10:J:93:ARG:HG2	1.84	0.42
11:K:99:THR:HG23	11:K:113:VAL:HB	2.02	0.42
12:L:14(Q):LEU:O	12:L:14(W):LYS:C	2.57	0.42
12:L:42:VAL:HG12	12:L:176:LEU:HD23	2.02	0.42
12:L:4:LEU:HD12	12:L:5:GLY:N	2.35	0.42
2:P:115:ARG:HG2	16:P:249:HOH:O	2.18	0.42
3:Q:100:ARG:HG3	3:Q:106:PRO:HA	2.01	0.42
3:Q:121:GLN:NE2	3:Q:122:ARG:N	2.66	0.42
4:R:117:CYS:SG	4:R:157:PHE:HB3	2.60	0.42
4:R:86:ARG:HD3	4:R:86:ARG:HA	1.87	0.42
5:S:188:GLU:OE1	5:S:188:GLU:HA	2.20	0.42
8:V:137:VAL:HG21	8:V:161:ALA:HB2	2.00	0.42
11:Y:200:LYS:HG2	16:Y:772:HOH:O	2.19	0.42
14:N:36:ARG:CD	13:1:211:ILE:HD11	2.49	0.42
3:C:46:VAL:HG22	3:C:146:PRO:HB2	2.01	0.42
6:F:169:ARG:O	6:F:173:LYS:HG3	2.20	0.42
9:I:192:ARG:HD3	16:I:1187:HOH:O	2.19	0.42
9:I:51:ASP:OD1	10:J:90(B):ARG:NH2	2.53	0.42
11:K:146:LEU:HD23	11:K:151:ALA:HA	2.01	0.42
12:L:133:LEU:O	9:W:136:GLY:HA3	2.19	0.42
13:M:6:MET:HA	13:M:124:THR:HA	2.01	0.42
1:O:124:THR:CG2	1:O:124:THR:O	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:186:VAL:HG11	2:P:216:ARG:CD	2.49	0.42
4:R:12(F):GLY:O	4:R:12(G):GLU:HB2	2.20	0.42
13:1:-5:PRO:HD3	13:1:96:TRP:CD2	2.54	0.42
14:2:3:ILE:HD13	14:2:46:SER:HB3	2.01	0.42
3:C:159:SER:O	4:D:59:LEU:HD22	2.20	0.42
10:J:83:VAL:HG21	10:J:101:ILE:HD11	2.02	0.42
1:O:38:LEU:HD12	1:O:38:LEU:O	2.19	0.42
3:Q:14:ILE:HB	4:R:23:GLN:HE22	1.84	0.42
5:S:201:LEU:HD11	5:S:207:LEU:CD2	2.39	0.42
5:S:4:PHE:CG	5:S:5:ARG:N	2.87	0.42
7:U:43:LYS:HB2	7:U:18(G):GLU:O	2.19	0.42
10:X:3:ILE:O	10:X:126:ALA:HA	2.20	0.42
13:1:94:PRO:HA	16:1:220:HOH:O	2.19	0.42
3:C:195:ARG:HG3	3:C:236:ILE:HD13	2.01	0.42
5:E:185:ASN:C	5:E:185:ASN:ND2	2.72	0.42
5:E:188:GLU:OE1	5:E:188:GLU:HA	2.20	0.42
6:F:18:ASP:N	6:F:18:ASP:OD2	2.38	0.42
1:A:8:TYR:CD2	7:G:128:TYR:HB3	2.55	0.42
9:I:103:GLY:O	9:I:109:PHE:N	2.52	0.42
9:I:143:GLU:CG	9:I:146:LEU:HD21	2.49	0.42
12:L:104:LEU:HD11	12:L:179:THR:C	2.40	0.42
13:M:157:ASN:ND2	16:M:1332:HOH:O	2.52	0.42
14:N:7:THR:HG22	14:N:110:VAL:HG23	2.02	0.42
1:O:221:PHE:C	1:O:221:PHE:CD2	2.93	0.42
2:P:233:LEU:HD12	2:P:233:LEU:HA	1.93	0.42
7:U:191:GLU:CG	7:U:232:ARG:HG3	2.50	0.42
12:Z:32:PRO:HD2	16:Z:1177:HOH:O	2.19	0.42
12:Z:58:ARG:HH11	12:Z:58:ARG:HG2	1.85	0.42
3:C:175:PHE:O	3:C:179:ASN:HB2	2.20	0.41
3:C:62(A):ILE:HG13	3:C:63:THR:N	2.35	0.41
5:E:139:ILE:HA	5:E:147:HIS:O	2.20	0.41
6:F:26:TYR:O	6:F:29:LYS:HB2	2.20	0.41
12:L:153:LYS:HG2	8:V:201:GLN:CG	2.50	0.41
14:N:18(G):TYR:HA	14:N:18(J):LEU:HG	2.00	0.41
1:O:202:VAL:HG21	1:O:206:PHE:HD1	1.84	0.41
1:O:36:THR:HG22	1:O:37:SER:N	2.34	0.41
5:S:90:ASN:O	5:S:94:GLN:HG3	2.20	0.41
12:L:24:TYR:HA	8:V:167:LEU:HD12	2.02	0.41
9:W:55:LEU:HD11	9:W:97:VAL:HG21	2.01	0.41
2:B:225:LYS:O	2:B:226:PRO:C	2.59	0.41
7:G:18(H):GLU:H	7:G:18(H):GLU:CD	2.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:167:LEU:HD12	12:Z:24:TYR:HA	2.00	0.41
10:J:129:TYR:O	10:J:130:SER:C	2.58	0.41
2:B:101:LYS:HZ2	10:J:85:GLN:HE22	1.67	0.41
13:M:18:ASN:HA	13:M:31:VAL:O	2.19	0.41
1:O:197:LEU:CD2	1:O:210:ILE:HD12	2.49	0.41
2:P:126:HIS:CB	3:Q:129:VAL:HG12	2.47	0.41
4:R:45:GLY:HA2	4:R:146:TYR:CD1	2.54	0.41
5:S:179:THR:HG22	5:S:179:THR:O	2.20	0.41
5:S:199:GLN:NE2	5:S:199:GLN:CA	2.82	0.41
7:U:171:GLU:OE1	7:U:171:GLU:N	2.51	0.41
7:U:26:TYR:N	7:U:26:TYR:CD1	2.86	0.41
11:Y:15:ALA:HA	11:Y:174:ASN:O	2.20	0.41
11:Y:16:VAL:HG21	11:Y:34:VAL:HG23	2.02	0.41
1:A:141:HIS:HB2	1:A:147:PHE:CD2	2.55	0.41
1:A:197:LEU:CD2	1:A:210:ILE:HD12	2.51	0.41
2:B:121:GLN:NE2	2:B:121:GLN:C	2.74	0.41
2:B:176:LEU:HD23	2:B:192:LEU:HD22	2.01	0.41
2:B:31:ILE:HG23	2:B:79:ALA:O	2.20	0.41
4:D:12(D):ALA:HA	5:E:129:GLY:HA2	2.02	0.41
5:E:18(C):PHE:HA	5:E:18(F):ILE:CD1	2.50	0.41
5:E:90:ASN:O	5:E:94:GLN:HG3	2.19	0.41
6:F:143:LYS:HG2	6:F:143:LYS:O	2.20	0.41
6:F:61:PRO:O	6:F:62:GLN:HB2	2.20	0.41
10:J:113:ILE:HG12	10:J:119:LYS:HG3	2.02	0.41
12:L:58:ARG:HH11	12:L:58:ARG:HG2	1.85	0.41
14:N:65:LEU:HG	14:N:69:GLN:NE2	2.34	0.41
9:W:187:ARG:HG3	9:W:187:ARG:HH11	1.85	0.41
10:X:166:MET:HA	10:X:167:PRO:HD3	1.74	0.41
16:Z:383:HOH:O	13:1:121:SER:HB2	2.19	0.41
13:1:14(E):SER:C	16:1:1126:HOH:O	2.59	0.41
13:1:17:ASP:C	13:1:17:ASP:OD2	2.59	0.41
4:D:12(F):GLY:O	4:D:12(G):GLU:HB2	2.19	0.41
5:E:179:THR:O	5:E:179:THR:HG22	2.21	0.41
5:E:172:ALA:CB	5:E:196:ALA:O	2.68	0.41
9:I:136:GLY:HA3	12:Z:133:LEU:O	2.20	0.41
9:I:165:ARG:HH22	12:Z:135:MET:HE2	1.83	0.41
13:M:205:GLY:HA2	16:2:194:HOH:O	2.19	0.41
14:N:105:ASP:HB2	16:N:980:HOH:O	2.20	0.41
4:R:137:LEU:HD23	4:R:137:LEU:HA	1.95	0.41
4:R:177:LEU:HD22	5:S:58:LEU:CD1	2.49	0.41
6:T:172:ALA:O	6:T:173:LYS:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:V:43:CYS:SG	8:V:99:LEU:HB3	2.61	0.41
1:A:221:PHE:C	1:A:221:PHE:CD2	2.93	0.41
4:D:117:CYS:SG	4:D:157:PHE:HB3	2.60	0.41
6:F:95:GLU:CG	6:F:115:ARG:HD2	2.51	0.41
9:I:55:LEU:HD11	9:I:97:VAL:HG21	2.01	0.41
10:J:52:THR:HG23	10:J:53:VAL:HG23	2.03	0.41
11:K:119:ARG:NH2	16:K:1295:HOH:O	2.48	0.41
12:L:14(Q):LEU:C	12:L:14(W):LYS:O	2.58	0.41
12:L:-7:ASN:ND2	12:L:-5:TYR:H	2.18	0.41
13:M:162:LEU:HB3	16:M:225:HOH:O	2.20	0.41
13:M:42:VAL:HG23	13:M:178:ILE:HD11	2.03	0.41
13:M:3:VAL:CG2	13:M:46:SER:HB3	2.49	0.41
2:P:6:ARG:HD2	4:R:9:ASP:N	2.36	0.41
3:Q:100:ARG:HH12	3:Q:106:PRO:HB3	1.78	0.41
4:R:185:THR:OG1	4:R:188:GLU:HG3	2.20	0.41
5:S:185:ASN:C	5:S:185:ASN:ND2	2.74	0.41
16:U:509:HOH:O	8:V:72:ARG:HA	2.21	0.41
11:Y:146:LEU:HD23	11:Y:151:ALA:HA	2.01	0.41
8:H:201:GLN:CG	12:Z:153:LYS:HG2	2.49	0.41
2:B:37:ALA:HB3	2:B:165:VAL:HG22	2.03	0.41
5:E:78:LEU:HD12	5:E:78:LEU:O	2.20	0.41
7:G:26:TYR:CD1	7:G:26:TYR:N	2.87	0.41
8:H:2:THR:O	8:H:16:ALA:HA	2.21	0.41
9:I:28:SER:CB	10:J:120:VAL:HG21	2.50	0.41
11:K:174:ASN:HD22	11:K:174:ASN:HA	1.65	0.41
12:L:14(C):GLN:HG2	8:V:210:THR:HG21	2.02	0.41
13:M:70:ASN:ND2	13:M:70(A):ALA:HA	2.36	0.41
14:N:8:PHE:CE2	14:N:13:ILE:HG13	2.55	0.41
6:T:184:LEU:CD1	6:T:188:GLU:HB3	2.49	0.41
9:W:28:SER:CB	10:X:120:VAL:HG21	2.49	0.41
10:X:69:ARG:HD2	16:X:553:HOH:O	2.21	0.41
11:Y:86:LEU:O	11:Y:89:GLN:HB2	2.21	0.41
12:Z:33:LYS:HE2	12:Z:33:LYS:HB3	1.78	0.41
13:1:89:GLN:O	13:1:92(A):LYS:HG3	2.21	0.41
1:A:21(G):LEU:HA	1:A:21(G):LEU:HD12	1.85	0.41
2:B:134:VAL:O	2:B:153:PRO:HD3	2.21	0.41
2:B:207:TYR:CG	2:B:208:ASP:N	2.88	0.41
6:F:39:GLY:C	6:F:148:LEU:HD21	2.41	0.41
7:G:39:ALA:HB2	7:G:48:VAL:HG12	2.03	0.41
8:H:139:GLU:HA	8:H:139:GLU:OE2	2.20	0.41
11:K:6:PHE:HB2	11:K:124:ILE:HG12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:55:LEU:HD22	12:L:87:LEU:HD21	2.02	0.41
13:M:-1:GLY:HA2	16:M:213:HOH:O	2.21	0.41
2:P:80:GLY:HA3	2:P:133:GLY:O	2.21	0.41
6:T:70:VAL:HG11	6:T:112:PHE:CE1	2.56	0.41
7:U:38:LEU:HD23	7:U:197:MET:CE	2.49	0.41
10:X:83:VAL:HG21	10:X:101:ILE:HD11	2.02	0.41
11:Y:174:ASN:HA	11:Y:174:ASN:HD22	1.67	0.41
11:Y:39:PRO:HG3	16:Y:1267:HOH:O	2.21	0.41
1:A:233:LEU:O	1:A:236:LEU:HB2	2.21	0.41
2:B:174:THR:O	2:B:178:MET:HB2	2.20	0.41
3:C:27:ALA:O	3:C:30:ALA:HB3	2.21	0.41
4:D:31:ILE:HD13	4:D:135:ALA:HB2	2.03	0.41
5:E:58:LEU:HD12	5:E:58:LEU:N	2.35	0.41
10:J:138:LEU:HD21	10:J:158:CYS:SG	2.61	0.41
10:J:85:GLN:HG2	10:J:89:LYS:HE3	2.03	0.41
10:J:90(A):ILE:HD12	10:J:90(A):ILE:HA	1.89	0.41
10:J:88:ALA:O	10:J:90(A):ILE:HG22	2.20	0.41
1:O:137:LEU:HD23	1:O:137:LEU:HA	1.91	0.41
1:O:78:TYR:HB3	1:O:85:TYR:CD1	2.55	0.41
2:P:69:LYS:HE2	2:P:221:GLN:OE1	2.20	0.41
3:Q:134:VAL:HG12	3:Q:135:SER:N	2.36	0.41
4:R:189:ALA:O	4:R:193:VAL:HG23	2.21	0.41
9:W:80:THR:HG1	9:W:109:PHE:HE2	1.68	0.41
10:X:191:GLN:O	10:X:192:ALA:HB2	2.20	0.41
11:Y:114:ASP:C	11:Y:116:ASP:H	2.24	0.41
12:Z:42:VAL:HG12	12:Z:176:LEU:HD23	2.02	0.41
12:Z:4:LEU:HD12	12:Z:5:GLY:N	2.36	0.41
12:Z:98:HIS:ND1	12:Z:98:HIS:C	2.74	0.41
13:1:190:LEU:N	13:1:190:LEU:HD12	2.36	0.41
1:A:67:VAL:HG23	1:A:211:GLU:HG2	2.02	0.41
6:F:75:GLY:O	6:F:138:PHE:HA	2.21	0.41
5:E:161:TYR:CE2	6:F:60:VAL:HA	2.55	0.41
7:G:78:VAL:HG22	7:G:136:LEU:CD2	2.50	0.41
7:G:17(C):LYS:HE3	7:G:17(C):LYS:HB2	1.77	0.41
10:J:191:GLN:O	10:J:192:ALA:HB2	2.21	0.41
1:O:67:VAL:CG2	1:O:211:GLU:HG2	2.51	0.41
3:Q:55:THR:C	3:Q:56:LEU:HD22	2.41	0.41
8:V:105:ASP:HB2	8:V:10(A):PRO:HD2	2.01	0.41
2:B:186:VAL:HG11	2:B:216:ARG:CD	2.51	0.41
3:C:157:TYR:N	16:C:1013:HOH:O	2.42	0.41
4:D:148:LEU:HB3	4:D:160:TYR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:72:ARG:HG3	16:D:662:HOH:O	2.21	0.41
6:F:95:GLU:CG	6:F:115:ARG:HB3	2.46	0.41
9:I:36:HIS:HB3	9:I:42:PHE:CD2	2.56	0.41
11:K:4:LEU:CD1	11:K:15:ALA:HB3	2.51	0.41
3:Q:57:LYS:HD2	3:Q:58:LEU:N	2.36	0.41
5:S:22:PHE:O	5:S:25:GLU:N	2.54	0.41
7:U:8:TYR:C	7:U:10:ARG:N	2.73	0.41
9:W:103:GLY:O	9:W:109:PHE:N	2.49	0.41
9:W:15:ALA:HB2	9:W:175:VAL:HG22	2.03	0.41
9:W:81:GLN:CA	9:W:81:GLN:NE2	2.83	0.41
12:Z:14(Q):LEU:O	12:Z:14(W):LYS:C	2.59	0.41
12:Z:32:PRO:N	16:Z:1177:HOH:O	2.53	0.41
1:A:185:GLU:OE1	1:A:187:GLU:HB2	2.21	0.41
5:E:148:LEU:HB3	5:E:160:LEU:O	2.22	0.41
7:G:119:LEU:HA	7:G:119:LEU:HD12	1.91	0.41
7:G:55:PRO:HG2	7:G:56:ASP:N	2.36	0.41
8:H:63:ILE:HD13	8:H:63:ILE:HA	1.98	0.41
9:I:15:ALA:HB1	9:I:175:VAL:HG22	2.02	0.41
9:I:66:TYR:CZ	9:I:70:GLU:HG3	2.55	0.41
10:J:64:GLN:O	10:J:67:SER:HB2	2.20	0.41
1:O:112:LEU:O	1:O:115:GLU:HB2	2.21	0.41
1:O:77:VAL:CG1	1:O:137:LEU:HB2	2.51	0.41
2:P:184:MET:HE2	2:P:188:ASP:CB	2.51	0.41
2:P:40:ILE:HD12	2:P:193:ALA:HB2	2.02	0.41
3:Q:238:GLN:O	3:Q:242:GLU:HG3	2.21	0.41
3:Q:38:VAL:HG22	3:Q:39:GLY:N	2.36	0.41
5:S:148:LEU:O	5:S:149:LEU:HD12	2.21	0.41
4:R:177:LEU:HA	5:S:58:LEU:HD11	2.02	0.41
6:T:148:LEU:HB3	6:T:160:TYR:O	2.21	0.41
6:T:194:ALA:O	6:T:198:TYR:HD1	2.04	0.41
7:U:82:ILE:N	7:U:83:PRO:HD2	2.36	0.41
11:Y:97:MET:O	11:Y:114:ASP:HA	2.21	0.41
11:Y:13:ILE:HG13	11:Y:151:ALA:HB1	2.02	0.41
11:Y:50:ALA:CB	12:Z:116:VAL:HG23	2.51	0.41
13:1:80:PHE:CE1	13:1:111:ARG:HD3	2.56	0.40
1:A:62:GLU:O	1:A:64:LEU:N	2.52	0.40
9:I:133:GLN:OE1	9:I:133:GLN:N	2.44	0.40
10:J:3:ILE:O	10:J:126:ALA:HA	2.20	0.40
11:K:25:TRP:CZ3	12:L:132:SER:HA	2.56	0.40
13:M:7:LYS:HD2	13:M:14(G):ILE:HD13	2.02	0.40
1:O:15:PHE:HB2	2:P:23:GLN:HE22	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:197:LEU:HD23	1:O:210:ILE:HD12	2.03	0.40
1:O:31:VAL:HG13	1:O:79:SER:O	2.21	0.40
2:P:53:LYS:HG2	2:P:54:VAL:HG23	2.03	0.40
4:R:140:GLY:HA2	4:R:215:ILE:HG12	2.01	0.40
4:R:24:VAL:O	4:R:28:LEU:HD13	2.20	0.40
6:T:151:LEU:HD12	6:T:157:TYR:HB3	2.02	0.40
6:T:172:ALA:O	6:T:175:GLU:N	2.55	0.40
7:U:55:PRO:HG2	7:U:56:ASP:N	2.36	0.40
12:Z:55:LEU:HD22	12:Z:87:LEU:HD21	2.02	0.40
13:1:133:MET:HE2	13:1:133:MET:HB3	1.94	0.40
4:D:215:ILE:HD12	4:D:216:THR:N	2.36	0.40
9:I:80:THR:HG1	9:I:109:PHE:HE2	1.67	0.40
10:J:22:ARG:HD3	10:J:22:ARG:HA	1.96	0.40
10:J:85:GLN:HB3	16:J:202:HOH:O	2.21	0.40
10:J:8:VAL:HG11	10:J:151:GLY:HA3	2.03	0.40
11:K:102:CYS:SG	11:K:110:ILE:HG23	2.61	0.40
11:K:45:MET:HE1	11:K:53:GLN:HB2	2.04	0.40
1:O:141:HIS:HB2	1:O:147:PHE:CD2	2.55	0.40
1:O:67:VAL:HG23	1:O:211:GLU:HG2	2.03	0.40
1:O:39:GLY:O	1:O:162:ALA:HA	2.21	0.40
1:O:62:GLU:O	1:O:64:LEU:N	2.49	0.40
1:O:94:LYS:O	1:O:97:HIS:N	2.54	0.40
2:P:121:GLN:NE2	16:P:462:HOH:O	2.54	0.40
2:P:134:VAL:HG12	2:P:135:SER:N	2.36	0.40
2:P:239:THR:OXT	2:P:239:THR:CG2	2.68	0.40
3:Q:195:ARG:HG3	3:Q:236:ILE:HD13	2.02	0.40
6:T:26:TYR:O	6:T:29:LYS:HB2	2.21	0.40
8:V:144:GLN:O	8:V:145:ASP:HB2	2.20	0.40
8:V:84:LYS:HE2	8:V:119:THR:CG2	2.52	0.40
9:W:123:ASP:OD1	9:W:124:PHE:N	2.45	0.40
14:2:104:TYR:OH	14:2:180:ALA:HB2	2.21	0.40
2:B:184:MET:HE3	2:B:188:ASP:HB3	2.03	0.40
2:B:235:LYS:HD3	2:B:235:LYS:N	2.36	0.40
3:C:100:ARG:HG3	3:C:106:PRO:HA	2.03	0.40
3:C:224:LEU:H	3:C:224:LEU:CD1	2.35	0.40
4:D:160:TYR:CE2	4:D:163:LYS:HD3	2.57	0.40
8:H:103:GLY:HA2	8:H:178:MET:SD	2.61	0.40
13:M:211:ILE:HD11	14:2:36:ARG:HD3	2.03	0.40
13:M:95:LEU:O	13:M:97:ASN:N	2.54	0.40
1:O:77:VAL:HG12	1:O:137:LEU:HB2	2.02	0.40
2:P:184:MET:HE3	2:P:188:ASP:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:201:VAL:HG21	3:Q:210:ILE:CG1	2.52	0.40
6:T:61:PRO:O	6:T:62:GLN:HB2	2.21	0.40
10:X:120:VAL:HG13	10:X:122:LEU:HG	2.03	0.40
10:X:138:LEU:C	10:X:140:HIS:N	2.74	0.40
11:Y:77:ALA:HA	11:Y:111:TYR:CE2	2.56	0.40
3:C:163:GLN:HE21	3:C:164:THR:N	2.05	0.40
4:D:224:TYR:N	4:D:224:TYR:CD2	2.90	0.40
6:F:70:VAL:HG11	6:F:112:PHE:CE1	2.56	0.40
7:G:143:GLU:HG2	16:G:532:HOH:O	2.20	0.40
7:G:152:ASP:HB2	7:G:153:PRO:CD	2.51	0.40
10:J:137:LEU:CD1	10:J:158:CYS:HA	2.51	0.40
10:J:193:GLN:OXT	10:J:193:GLN:HG2	2.21	0.40
10:J:85:GLN:CG	16:J:202:HOH:O	2.70	0.40
12:L:70(A):ASN:O	12:L:72:LYS:N	2.55	0.40
2:P:174:THR:O	2:P:178:MET:HB2	2.21	0.40
2:P:231:ASP:O	2:P:235:LYS:HG2	2.21	0.40
3:Q:224:LEU:N	3:Q:224:LEU:CD1	2.84	0.40
5:S:172:ALA:HB2	5:S:196:ALA:O	2.21	0.40
5:S:199:GLN:HE21	5:S:199:GLN:N	2.19	0.40
5:S:67:ILE:HD13	5:S:213:ALA:HB2	2.03	0.40
7:U:123:TYR:CE1	7:U:129:MET:HE2	2.56	0.40
7:U:39:ALA:HB2	7:U:48:VAL:HG12	2.03	0.40
8:V:148:LYS:HE3	8:V:177:VAL:HG11	2.03	0.40
8:V:2:THR:OG1	8:V:130:GLY:HA3	2.22	0.40
16:V:1181:HOH:O	9:W:150:ASP:HA	2.21	0.40
10:X:93:ARG:NH2	11:Y:91:LYS:HD3	2.37	0.40
2:B:50:ALA:HB1	2:B:66:LYS:HD3	2.03	0.40
3:C:57:LYS:HG2	3:C:208:LYS:HZ3	1.86	0.40
4:D:16:SER:HA	4:D:22:PHE:CZ	2.56	0.40
3:C:14:ILE:HB	4:D:23:GLN:HE22	1.86	0.40
4:D:24:VAL:O	4:D:28:LEU:HD13	2.22	0.40
10:J:110:LEU:O	10:J:121:GLU:HG2	2.21	0.40
10:J:120:VAL:HG13	10:J:122:LEU:HG	2.02	0.40
10:J:143:ARG:HA	10:J:144:PRO:HD3	1.81	0.40
11:K:15:ALA:HA	11:K:174:ASN:O	2.22	0.40
12:L:114:ASP:CB	12:L:118:SER:HB3	2.51	0.40
14:N:133:PHE:CE2	14:N:166:ASP:HB2	2.57	0.40
1:O:21(G):LEU:HG	1:O:21(I):TYR:CE1	2.55	0.40
2:P:186:VAL:HG21	2:P:216:ARG:CG	2.51	0.40
3:Q:36:CYS:H	3:Q:51:GLU:HG2	1.87	0.40
4:R:17:PRO:HG3	5:S:26:TYR:CE2	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:73:HIS:HE1	5:S:107:LEU:O	2.04	0.40
7:U:222:PHE:N	7:U:222:PHE:CD2	2.89	0.40
7:U:78:VAL:HG22	7:U:136:LEU:CD2	2.52	0.40
11:Y:111:TYR:CE1	11:Y:121:LYS:HB2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/250 (99%)	220 (89%)	23 (9%)	5 (2%)	7	19
1	O	248/250 (99%)	222 (90%)	21 (8%)	5 (2%)	7	19
2	B	242/244 (99%)	215 (89%)	23 (10%)	4 (2%)	9	23
2	P	242/244 (99%)	215 (89%)	23 (10%)	4 (2%)	9	23
3	C	239/241 (99%)	220 (92%)	14 (6%)	5 (2%)	7	18
3	Q	239/241 (99%)	220 (92%)	14 (6%)	5 (2%)	7	18
4	D	240/242 (99%)	217 (90%)	17 (7%)	6 (2%)	5	14
4	R	240/242 (99%)	216 (90%)	18 (8%)	6 (2%)	5	14
5	E	231/233 (99%)	204 (88%)	23 (10%)	4 (2%)	9	23
5	S	231/233 (99%)	205 (89%)	23 (10%)	3 (1%)	12	30
6	F	242/244 (99%)	229 (95%)	11 (4%)	2 (1%)	19	43
6	T	242/244 (99%)	229 (95%)	11 (4%)	2 (1%)	19	43
7	G	241/243 (99%)	223 (92%)	17 (7%)	1 (0%)	34	60
7	U	241/243 (99%)	221 (92%)	19 (8%)	1 (0%)	34	60
8	H	220/222 (99%)	197 (90%)	19 (9%)	4 (2%)	8	21
8	V	220/222 (99%)	197 (90%)	18 (8%)	5 (2%)	6	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	202/204 (99%)	191 (95%)	10 (5%)	1 (0%)	29	54
9	W	202/204 (99%)	190 (94%)	11 (5%)	1 (0%)	29	54
10	J	196/198 (99%)	180 (92%)	15 (8%)	1 (0%)	29	54
10	X	196/198 (99%)	180 (92%)	15 (8%)	1 (0%)	29	54
11	K	210/212 (99%)	191 (91%)	18 (9%)	1 (0%)	29	54
11	Y	210/212 (99%)	192 (91%)	17 (8%)	1 (0%)	29	54
12	L	220/222 (99%)	201 (91%)	16 (7%)	3 (1%)	11	28
12	Z	220/222 (99%)	202 (92%)	13 (6%)	5 (2%)	6	16
13	1	231/233 (99%)	208 (90%)	20 (9%)	3 (1%)	12	30
13	M	231/233 (99%)	208 (90%)	20 (9%)	3 (1%)	12	30
14	2	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
14	N	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
All	All	6312/6368 (99%)	5769 (91%)	461 (7%)	82 (1%)	12	30

All (82) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	167	LYS
3	C	58	LEU
3	C	203	THR
4	D	12(G)	GLU
7	G	220	LYS
10	J	192	ALA
11	K	39	PRO
12	L	71	ASP
12	L	14(I)	THR
13	M	96	TRP
1	O	167	LYS
3	Q	58	LEU
3	Q	203	THR
4	R	12(G)	GLU
7	U	220	LYS
10	X	192	ALA
11	Y	39	PRO
12	Z	71	ASP
12	Z	14(I)	THR
1	A	56	SER

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Mol	Chain	Res	Type
2	B	54	VAL
2	B	21(B)	GLY
2	B	21(C)	ASP
3	C	183	PRO
4	D	18(D)	SER
5	E	202	ARG
5	E	227	GLU
6	F	205	ASN
6	F	206	LYS
8	H	91	GLN
8	H	96	GLY
1	O	5	THR
1	O	56	SER
2	P	54	VAL
2	P	21(B)	GLY
2	P	21(C)	ASP
3	Q	183	PRO
4	R	18(D)	SER
5	S	202	ARG
5	S	227	GLU
6	T	205	ASN
6	T	206	LYS
8	V	91	GLN
8	V	96	GLY
13	1	96	TRP
1	A	6	ASP
1	A	63	THR
4	D	12(F)	GLY
4	D	128	MET
5	E	180	LEU
13	M	2	SER
1	O	6	ASP
1	O	63	THR
4	R	12(F)	GLY
4	R	128	MET
5	S	180	LEU
13	1	2	SER
2	B	22	TYR
3	C	53	ARG
3	C	242	GLU
4	D	169	SER
8	H	115	ALA

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Mol	Chain	Res	Type
8	H	171	SER
9	I	93	GLY
2	P	22	TYR
3	Q	53	ARG
3	Q	242	GLU
4	R	169	SER
8	V	171	SER
9	W	93	GLY
12	Z	96	TYR
13	1	72	ALA
4	D	12(C)	GLY
5	E	18(A)	ASP
12	L	96	TYR
13	M	72	ALA
4	R	12(C)	GLY
8	V	115	ALA
8	V	9	ASN
12	Z	32	PRO
12	Z	93	PHE

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%)	42	71
1	O	209/209 (100%)	204 (98%)	5 (2%)	49	77
2	B	203/203 (100%)	190 (94%)	13 (6%)	17	39
2	P	203/203 (100%)	190 (94%)	13 (6%)	17	39
3	C	213/213 (100%)	202 (95%)	11 (5%)	23	49
3	Q	213/213 (100%)	202 (95%)	11 (5%)	23	49
4	D	198/198 (100%)	189 (96%)	9 (4%)	27	55
4	R	198/198 (100%)	190 (96%)	8 (4%)	31	60
5	E	192/192 (100%)	176 (92%)	16 (8%)	11	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	S	192/192 (100%)	176 (92%)	16 (8%)	11	25
6	F	201/201 (100%)	182 (90%)	19 (10%)	8	20
6	T	201/201 (100%)	182 (90%)	19 (10%)	8	20
7	G	207/207 (100%)	197 (95%)	10 (5%)	25	53
7	U	207/207 (100%)	197 (95%)	10 (5%)	25	53
8	H	181/181 (100%)	176 (97%)	5 (3%)	43	73
8	V	181/181 (100%)	175 (97%)	6 (3%)	38	67
9	I	172/172 (100%)	168 (98%)	4 (2%)	50	78
9	W	172/172 (100%)	168 (98%)	4 (2%)	50	78
10	J	175/175 (100%)	169 (97%)	6 (3%)	37	66
10	X	175/175 (100%)	169 (97%)	6 (3%)	37	66
11	K	169/169 (100%)	160 (95%)	9 (5%)	22	48
11	Y	169/169 (100%)	159 (94%)	10 (6%)	19	43
12	L	185/185 (100%)	175 (95%)	10 (5%)	22	47
12	Z	185/185 (100%)	175 (95%)	10 (5%)	22	47
13	1	199/199 (100%)	189 (95%)	10 (5%)	24	51
13	M	199/199 (100%)	189 (95%)	10 (5%)	24	51
14	2	162/162 (100%)	154 (95%)	8 (5%)	25	52
14	N	162/162 (100%)	153 (94%)	9 (6%)	21	45
All	All	5332/5332 (100%)	5059 (95%)	273 (5%)	24	50

All (273) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	64	LEU
1	A	124	THR
1	A	135	SER
1	A	158	PHE
1	A	179	ARG
2	B	5	SER
2	B	58	LEU
2	B	71	ASN
2	B	91	THR
2	B	121	GLN

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Mol	Chain	Res	Type
2	B	150	THR
2	B	156	ASN
2	B	183	ASP
2	B	185	LYS
2	B	187	ASP
2	B	192	LEU
2	B	218	ASN
2	B	224	PHE
3	C	10	ARG
3	C	25	GLU
3	C	57	LYS
3	C	66	LYS
3	C	100	ARG
3	C	121	GLN
3	C	135	SER
3	C	150	GLN
3	C	163	GLN
3	C	174	GLU
3	C	208	LYS
4	D	28	LEU
4	D	76	CYS
4	D	126	ARG
4	D	170	GLU
4	D	177	LEU
4	D	191	LEU
4	D	215	ILE
4	D	237	LEU
4	D	244	GLU
5	E	12	THR
5	E	13	VAL
5	E	32	LYS
5	E	56	ASP
5	E	57	GLU
5	E	76	LEU
5	E	97	ASN
5	E	104	ASN
5	E	121	GLN
5	E	185	ASN
5	E	189	LEU
5	E	199	GLN
5	E	207	LEU
5	E	2(C)	VAL

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Mol	Chain	Res	Type
5	E	227	GLU
5	E	231	LYS
6	F	11	SER
6	F	35	THR
6	F	43	ASN
6	F	44	ASP
6	F	56	SER
6	F	98	SER
6	F	105	THR
6	F	121	GLN
6	F	127	ASN
6	F	144	ASN
6	F	169	ARG
6	F	18(E)	GLU
6	F	187	ARG
6	F	203	GLU
6	F	204	ASP
6	F	205	ASN
6	F	208	PHE
6	F	214	TRP
6	F	21(C)	ASN
7	G	40	VAL
7	G	72	ARG
7	G	87	ASN
7	G	121	GLN
7	G	169	GLN
7	G	184	ASN
7	G	197	MET
7	G	217	LYS
7	G	232	ARG
7	G	233	LEU
8	H	56	THR
8	H	68	LEU
8	H	144	GLN
8	H	194	PRO
8	H	197	ARG
9	I	29	ASN
9	I	90	ARG
9	I	160	LEU
9	I	171	TRP
10	J	34	THR
10	J	70	GLU

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Mol	Chain	Res	Type
10	J	77	GLN
10	J	121	GLU
10	J	155	LEU
10	J	168	MET
11	K	4	LEU
11	K	8	PHE
11	K	9	GLN
11	K	39	PRO
11	K	65	LEU
11	K	73	ARG
11	K	87	VAL
11	K	100	MET
11	K	104	TYR
12	L	-7	ASN
12	L	14	LEU
12	L	40	ASN
12	L	58	ARG
12	L	70(A)	ASN
12	L	98	HIS
12	L	99	THR
12	L	115	PRO
12	L	1(I)	ASN
12	L	145	TYR
13	M	40	ASN
13	M	62	LEU
13	M	71(A)	ASP
13	M	91	ARG
13	M	93	ASN
13	M	96	TRP
13	M	129	PHE
13	M	14(C)	ARG
13	M	149	GLN
13	M	204	LYS
14	N	36	ARG
14	N	70	TYR
14	N	84	LYS
14	N	89	GLU
14	N	10(A)	ASP
14	N	119	VAL
14	N	149	GLU
14	N	178	LEU
14	N	18(I)	GLN

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Mol	Chain	Res	Type
1	O	33	GLN
1	O	64	LEU
1	O	124	THR
1	O	158	PHE
1	O	179	ARG
2	P	5	SER
2	P	58	LEU
2	P	71	ASN
2	P	91	THR
2	P	121	GLN
2	P	150	THR
2	P	156	ASN
2	P	183	ASP
2	P	185	LYS
2	P	187	ASP
2	P	192	LEU
2	P	218	ASN
2	P	224	PHE
3	Q	10	ARG
3	Q	25	GLU
3	Q	57	LYS
3	Q	66	LYS
3	Q	100	ARG
3	Q	121	GLN
3	Q	135	SER
3	Q	150	GLN
3	Q	163	GLN
3	Q	174	GLU
3	Q	208	LYS
4	R	28	LEU
4	R	126	ARG
4	R	170	GLU
4	R	177	LEU
4	R	191	LEU
4	R	215	ILE
4	R	237	LEU
4	R	244	GLU
5	S	12	THR
5	S	13	VAL
5	S	32	LYS
5	S	56	ASP
5	S	57	GLU

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Mol	Chain	Res	Type
5	S	76	LEU
5	S	97	ASN
5	S	104	ASN
5	S	121	GLN
5	S	185	ASN
5	S	189	LEU
5	S	199	GLN
5	S	207	LEU
5	S	2(C)	VAL
5	S	227	GLU
5	S	231	LYS
6	T	11	SER
6	T	35	THR
6	T	43	ASN
6	T	44	ASP
6	T	56	SER
6	T	98	SER
6	T	105	THR
6	T	121	GLN
6	T	127	ASN
6	T	144	ASN
6	T	169	ARG
6	T	18(E)	GLU
6	T	187	ARG
6	T	203	GLU
6	T	204	ASP
6	T	205	ASN
6	T	208	PHE
6	T	214	TRP
6	T	21(C)	ASN
7	U	40	VAL
7	U	72	ARG
7	U	87	ASN
7	U	121	GLN
7	U	169	GLN
7	U	184	ASN
7	U	197	MET
7	U	217	LYS
7	U	232	ARG
7	U	233	LEU
8	V	55	VAL
8	V	56	THR

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Mol	Chain	Res	Type
8	V	68	LEU
8	V	144	GLN
8	V	194	PRO
8	V	197	ARG
9	W	29	ASN
9	W	90	ARG
9	W	160	LEU
9	W	171	TRP
10	X	35	ARG
10	X	70	GLU
10	X	77	GLN
10	X	121	GLU
10	X	155	LEU
10	X	168	MET
11	Y	4	LEU
11	Y	7	ARG
11	Y	8	PHE
11	Y	9	GLN
11	Y	39	PRO
11	Y	65	LEU
11	Y	73	ARG
11	Y	87	VAL
11	Y	100	MET
11	Y	104	TYR
12	Z	-7	ASN
12	Z	14	LEU
12	Z	40	ASN
12	Z	58	ARG
12	Z	70(A)	ASN
12	Z	98	HIS
12	Z	99	THR
12	Z	115	PRO
12	Z	1(I)	ASN
12	Z	145	TYR
13	1	40	ASN
13	1	62	LEU
13	1	71(A)	ASP
13	1	91	ARG
13	1	93	ASN
13	1	96	TRP
13	1	129	PHE
13	1	14(C)	ARG

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Mol	Chain	Res	Type
13	1	149	GLN
13	1	204	LYS
14	2	36	ARG
14	2	70	TYR
14	2	84	LYS
14	2	89	GLU
14	2	10(A)	ASP
14	2	119	VAL
14	2	178	LEU
14	2	18(I)	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (221) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	97	HIS
1	A	191	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
3	C	163	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	211	GLN
4	D	218	GLN
4	D	226	ASN
5	E	7	ASN

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Mol	Chain	Res	Type
5	E	33	GLN
5	E	64	GLN
5	E	73	HIS
5	E	97	ASN
5	E	104	ASN
5	E	121	GLN
5	E	123	ASN
5	E	125	GLN
5	E	156	ASN
5	E	185	ASN
5	E	199	GLN
5	E	2(E)	ASN
6	F	23	GLN
6	F	43	ASN
6	F	87	HIS
6	F	90	ASN
6	F	121	GLN
6	F	127	ASN
6	F	192	GLN
7	G	34(A)	ASN
7	G	87	ASN
7	G	118	ASN
7	G	121	GLN
7	G	125	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	91	GLN
8	H	116	HIS
8	H	144	GLN
8	H	165	ASN
8	H	172	ASN
8	H	190	ASN
8	H	195	ASN
9	I	29	ASN
9	I	81	GLN
10	J	54	GLN
10	J	77	GLN
10	J	85	GLN

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Mol	Chain	Res	Type
10	J	112	GLN
10	J	186	GLN
10	J	193	GLN
11	K	9	GLN
11	K	53	GLN
11	K	85	ASN
11	K	174	ASN
11	K	190	HIS
11	K	207	ASN
11	K	208	ASN
12	L	-9	GLN
12	L	-7	ASN
12	L	-2	ASN
12	L	20	ASN
12	L	27	ASN
12	L	40	ASN
12	L	46	ASN
12	L	61	ASN
12	L	70(A)	ASN
12	L	82	ASN
12	L	123	GLN
12	L	140	ASN
12	L	14(B)	ASN
12	L	1(I)	ASN
12	L	166	HIS
12	L	168	GLN
13	M	-7	GLN
13	M	10	ASN
13	M	18	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	69	GLN
14	N	145	ASN
14	N	157	HIS
14	N	161	GLN
1	O	33	GLN
1	O	97	HIS

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Mol	Chain	Res	Type
1	O	191	HIS
2	P	23	GLN
2	P	71	ASN
2	P	97	GLN
2	P	121	GLN
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	97	GLN
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	161	ASN
4	R	199	GLN
4	R	211	GLN
4	R	218	GLN
4	R	226	ASN
5	S	7	ASN
5	S	33	GLN
5	S	64	GLN
5	S	73	HIS
5	S	97	ASN
5	S	104	ASN
5	S	114	HIS
5	S	121	GLN
5	S	123	ASN
5	S	125	GLN
5	S	156	ASN
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

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Mol	Chain	Res	Type
6	T	121	GLN
6	T	127	ASN
6	T	147	HIS
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	170	GLN
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	29	ASN
9	W	81	GLN
10	X	54	GLN
10	X	77	GLN
10	X	85	GLN
10	X	112	GLN
10	X	186	GLN
10	X	193	GLN
11	Y	9	GLN
11	Y	53	GLN
11	Y	66	HIS
11	Y	85	ASN
11	Y	174	ASN
11	Y	190	HIS
11	Y	207	ASN
11	Y	208	ASN
12	Z	-9	GLN
12	Z	-7	ASN
12	Z	-2	ASN
12	Z	27	ASN
12	Z	40	ASN
12	Z	46	ASN
12	Z	61	ASN

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Mol	Chain	Res	Type
12	Z	67	HIS
12	Z	70	HIS
12	Z	70(A)	ASN
12	Z	85	HIS
12	Z	123	GLN
12	Z	140	ASN
12	Z	14(B)	ASN
12	Z	1(I)	ASN
12	Z	166	HIS
12	Z	168	GLN
13	1	-7	GLN
13	1	10	ASN
13	1	18	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	69	GLN
14	2	106	ASN
14	2	145	ASN
14	2	157	HIS
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 ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
15	SY2	K	7710	11	31,35,35	2.33	4 (12%)	42,47,47	2.16	9 (21%)
15	SY2	H	7710	8	31,35,35	2.28	4 (12%)	42,47,47	2.23	11 (26%)
15	SY2	Y	7710	11	31,35,35	2.20	4 (12%)	42,47,47	2.17	9 (21%)
15	SY2	V	7710	8	31,35,35	2.35	4 (12%)	42,47,47	2.27	11 (26%)

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	SY2	K	7710	11	-	14/49/53/53	0/0/1/1
15	SY2	H	7710	8	-	19/49/53/53	0/0/1/1
15	SY2	Y	7710	11	-	18/49/53/53	0/0/1/1
15	SY2	V	7710	8	-	19/49/53/53	0/0/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	V	7710	SY2	C27-C26	10.42	1.56	1.32
15	H	7710	SY2	C27-C26	10.36	1.56	1.32
15	K	7710	SY2	C27-C26	10.06	1.56	1.32
15	Y	7710	SY2	C27-C26	9.98	1.55	1.32
15	K	7710	SY2	C23-C22	3.90	1.60	1.54
15	V	7710	SY2	C23-C22	3.73	1.60	1.54
15	H	7710	SY2	C27-C28	2.57	1.53	1.48
15	K	7710	SY2	C11-N36	2.53	1.51	1.45
15	Y	7710	SY2	C23-C22	2.49	1.58	1.54
15	H	7710	SY2	C22-C26	2.42	1.56	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	K	7710	SY2	C8-N7	2.25	1.40	1.35
15	H	7710	SY2	C23-C22	2.23	1.58	1.54
15	V	7710	SY2	C27-C28	2.21	1.52	1.48
15	Y	7710	SY2	C11-N36	2.13	1.50	1.45
15	V	7710	SY2	C22-C26	2.08	1.55	1.49
15	Y	7710	SY2	C8-N7	2.04	1.40	1.35

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	H	7710	SY2	C22-C26-C27	-8.91	110.72	126.78
15	Y	7710	SY2	C22-C26-C27	-8.86	110.81	126.78
15	K	7710	SY2	C22-C26-C27	-8.60	111.28	126.78
15	V	7710	SY2	C22-C26-C27	-8.39	111.67	126.78
15	V	7710	SY2	C27-C28-N30	5.98	126.23	114.97
15	Y	7710	SY2	C27-C28-N30	5.61	125.55	114.97
15	H	7710	SY2	C27-C28-N30	5.59	125.50	114.97
15	K	7710	SY2	C27-C28-N30	5.50	125.34	114.97
15	K	7710	SY2	C26-C27-C28	-4.36	111.80	122.69
15	Y	7710	SY2	C26-C27-C28	-4.27	112.00	122.69
15	V	7710	SY2	C26-C27-C28	-4.06	112.53	122.69
15	H	7710	SY2	N36-C8-N7	4.03	120.91	115.25
15	V	7710	SY2	N36-C8-N7	3.97	120.82	115.25
15	H	7710	SY2	C26-C27-C28	-3.59	113.71	122.69
15	V	7710	SY2	C5-C4-C3	-3.32	108.03	111.24
15	H	7710	SY2	C3-N7-C8	-3.28	119.25	122.75
15	V	7710	SY2	O29-C28-C27	-3.18	115.77	123.03
15	H	7710	SY2	O29-C28-C27	-2.99	116.22	123.03
15	Y	7710	SY2	O29-C28-C27	-2.93	116.34	123.03
15	K	7710	SY2	C18-N17-C15	-2.88	115.49	121.67
15	H	7710	SY2	C6-C4-C3	2.87	114.00	111.24
15	V	7710	SY2	C3-N7-C8	-2.84	119.72	122.75
15	K	7710	SY2	N36-C8-N7	2.83	119.23	115.25
15	Y	7710	SY2	C18-N17-C15	-2.81	115.65	121.67
15	Y	7710	SY2	N36-C8-N7	2.79	119.16	115.25
15	K	7710	SY2	O29-C28-C27	-2.77	116.72	123.03
15	Y	7710	SY2	C11-N36-C8	2.74	126.50	121.94
15	H	7710	SY2	C5-C4-C3	-2.69	108.64	111.24
15	Y	7710	SY2	C31-N30-C28	2.63	126.40	122.54
15	K	7710	SY2	C11-N36-C8	2.62	126.30	121.94
15	K	7710	SY2	O29-C28-N30	-2.59	117.94	122.23
15	V	7710	SY2	O29-C28-N30	-2.56	118.00	122.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	V	7710	SY2	C6-C4-C3	2.50	113.64	111.24
15	Y	7710	SY2	O29-C28-N30	-2.49	118.10	122.23
15	V	7710	SY2	C31-N30-C28	2.46	126.15	122.54
15	K	7710	SY2	C31-N30-C28	2.39	126.04	122.54
15	H	7710	SY2	O29-C28-N30	-2.39	118.28	122.23
15	H	7710	SY2	O9-C8-N7	-2.35	118.35	122.62
15	H	7710	SY2	C31-N30-C28	2.34	125.97	122.54
15	V	7710	SY2	O9-C8-N7	-2.27	118.49	122.62

There are no chirality outliers.

All (70) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	K	7710	SY2	O29-C28-N30-C31
15	K	7710	SY2	C27-C28-N30-C31
15	K	7710	SY2	C22-C26-C27-C28
15	K	7710	SY2	C23-C22-C26-C27
15	K	7710	SY2	N21-C22-C26-C27
15	H	7710	SY2	O29-C28-N30-C31
15	H	7710	SY2	C27-C28-N30-C31
15	H	7710	SY2	C22-C26-C27-C28
15	H	7710	SY2	C23-C22-C26-C27
15	H	7710	SY2	N21-C22-C26-C27
15	Y	7710	SY2	O29-C28-N30-C31
15	Y	7710	SY2	C27-C28-N30-C31
15	Y	7710	SY2	C22-C26-C27-C28
15	Y	7710	SY2	C23-C22-C26-C27
15	Y	7710	SY2	N21-C22-C26-C27
15	V	7710	SY2	O29-C28-N30-C31
15	V	7710	SY2	C27-C28-N30-C31
15	V	7710	SY2	C22-C26-C27-C28
15	V	7710	SY2	C23-C22-C26-C27
15	V	7710	SY2	N21-C22-C26-C27
15	V	7710	SY2	C26-C22-C23-C24
15	V	7710	SY2	N21-C22-C23-C25
15	Y	7710	SY2	N30-C31-C32-C33
15	K	7710	SY2	N30-C31-C32-C33
15	V	7710	SY2	C26-C27-C28-O29
15	V	7710	SY2	C26-C27-C28-N30
15	H	7710	SY2	C26-C27-C28-N30
15	H	7710	SY2	C26-C27-C28-O29
15	K	7710	SY2	C31-C32-C33-C34

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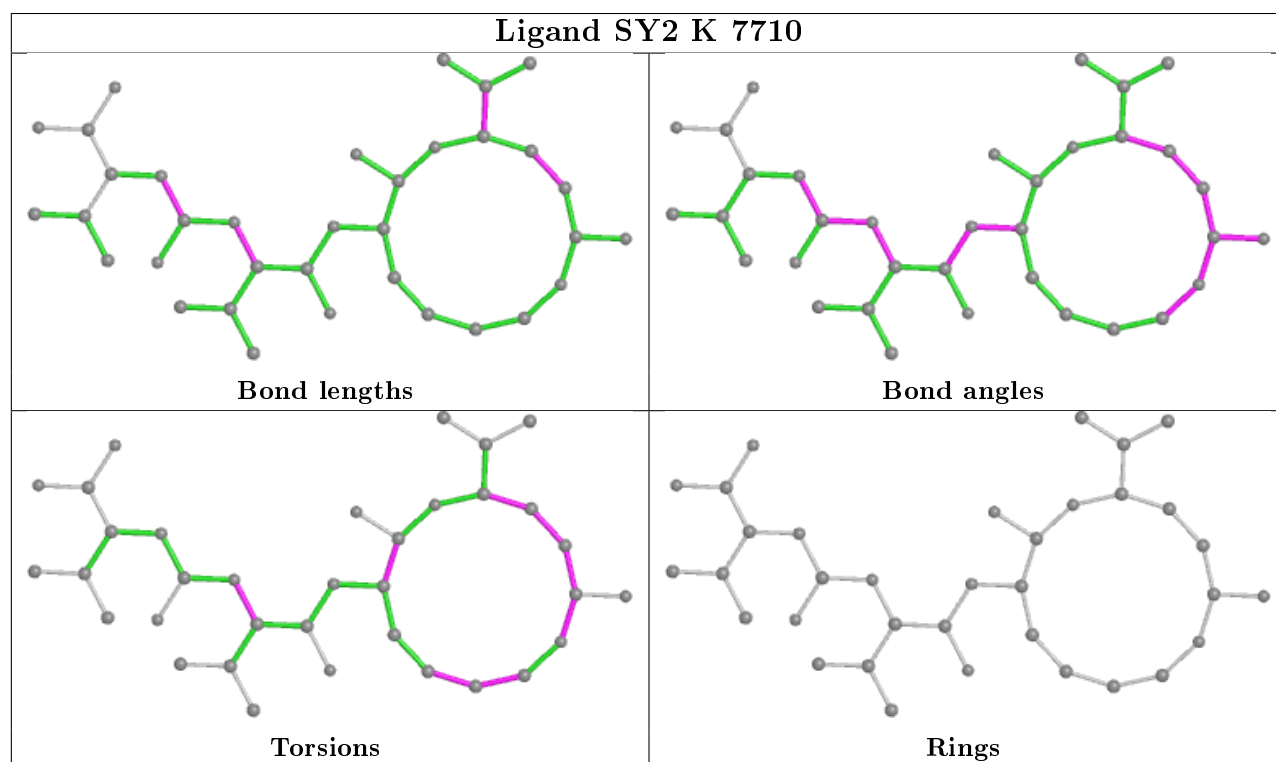
Mol	Chain	Res	Type	Atoms
15	Y	7710	SY2	C31-C32-C33-C34
15	K	7710	SY2	C12-C11-N36-C8
15	H	7710	SY2	C12-C11-N36-C8
15	Y	7710	SY2	C12-C11-N36-C8
15	V	7710	SY2	C12-C11-N36-C8
15	K	7710	SY2	C26-C27-C28-O29
15	K	7710	SY2	C26-C27-C28-N30
15	V	7710	SY2	N30-C31-C32-C33
15	H	7710	SY2	N30-C31-C32-C33
15	V	7710	SY2	N17-C18-C19-O20
15	H	7710	SY2	N17-C18-C19-O20
15	K	7710	SY2	N17-C18-C19-O20
15	Y	7710	SY2	N17-C18-C19-O20
15	V	7710	SY2	N17-C18-C19-N21
15	H	7710	SY2	N17-C18-C19-N21
15	Y	7710	SY2	C26-C27-C28-N30
15	Y	7710	SY2	C26-C27-C28-O29
15	K	7710	SY2	N17-C18-C19-N21
15	H	7710	SY2	C26-C22-C23-C25
15	Y	7710	SY2	C26-C22-C23-C24
15	V	7710	SY2	C26-C22-C23-C25
15	Y	7710	SY2	N17-C18-C19-N21
15	H	7710	SY2	N21-C22-C23-C25
15	Y	7710	SY2	N21-C22-C23-C25
15	V	7710	SY2	N21-C22-C23-C24
15	V	7710	SY2	N17-C18-C34-C33
15	H	7710	SY2	N17-C18-C34-C33
15	K	7710	SY2	C34-C18-C19-O20
15	Y	7710	SY2	C34-C18-C19-O20
15	V	7710	SY2	C34-C18-C19-O20
15	H	7710	SY2	C34-C18-C19-O20
15	V	7710	SY2	C19-C18-C34-C33
15	H	7710	SY2	C19-C18-C34-C33
15	H	7710	SY2	C26-C22-C23-C24
15	Y	7710	SY2	C26-C22-C23-C25
15	V	7710	SY2	C34-C18-C19-N21
15	H	7710	SY2	N21-C22-C23-C24
15	Y	7710	SY2	N21-C22-C23-C24
15	H	7710	SY2	C34-C18-C19-N21
15	K	7710	SY2	C34-C18-C19-N21
15	Y	7710	SY2	C34-C18-C19-N21

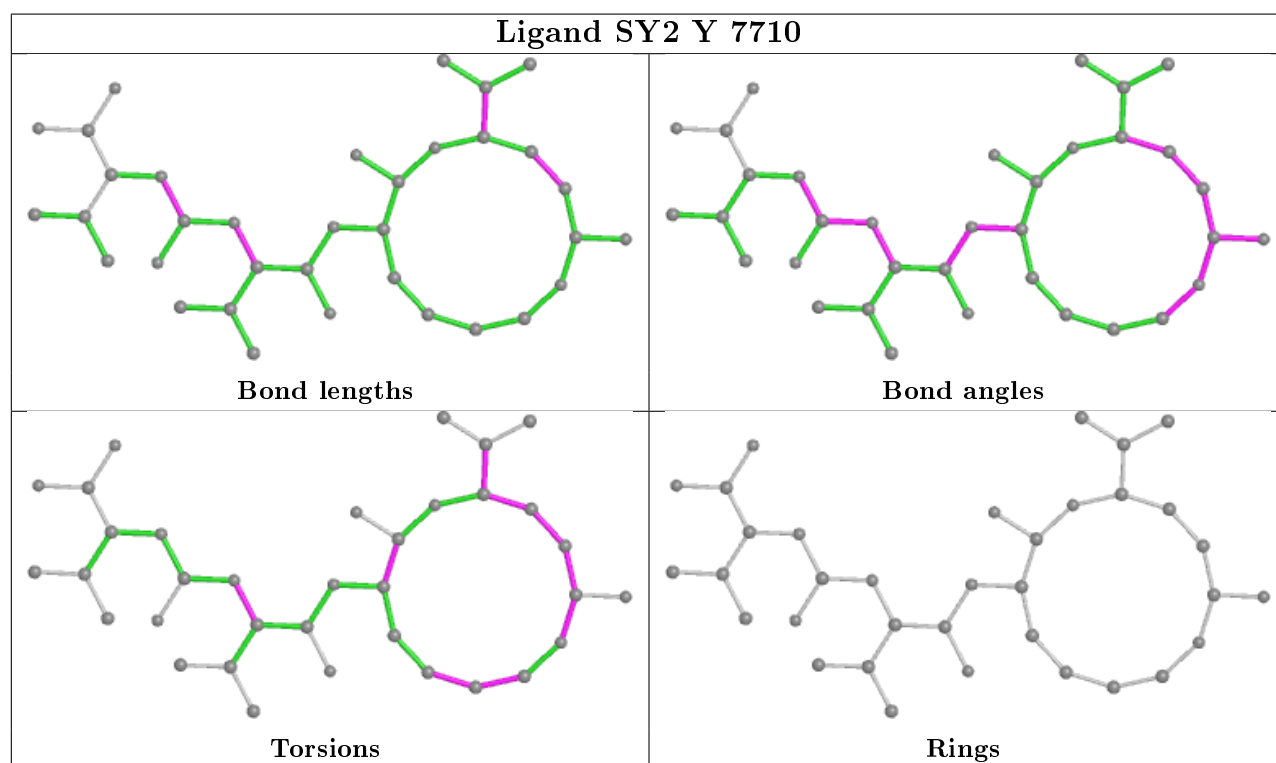
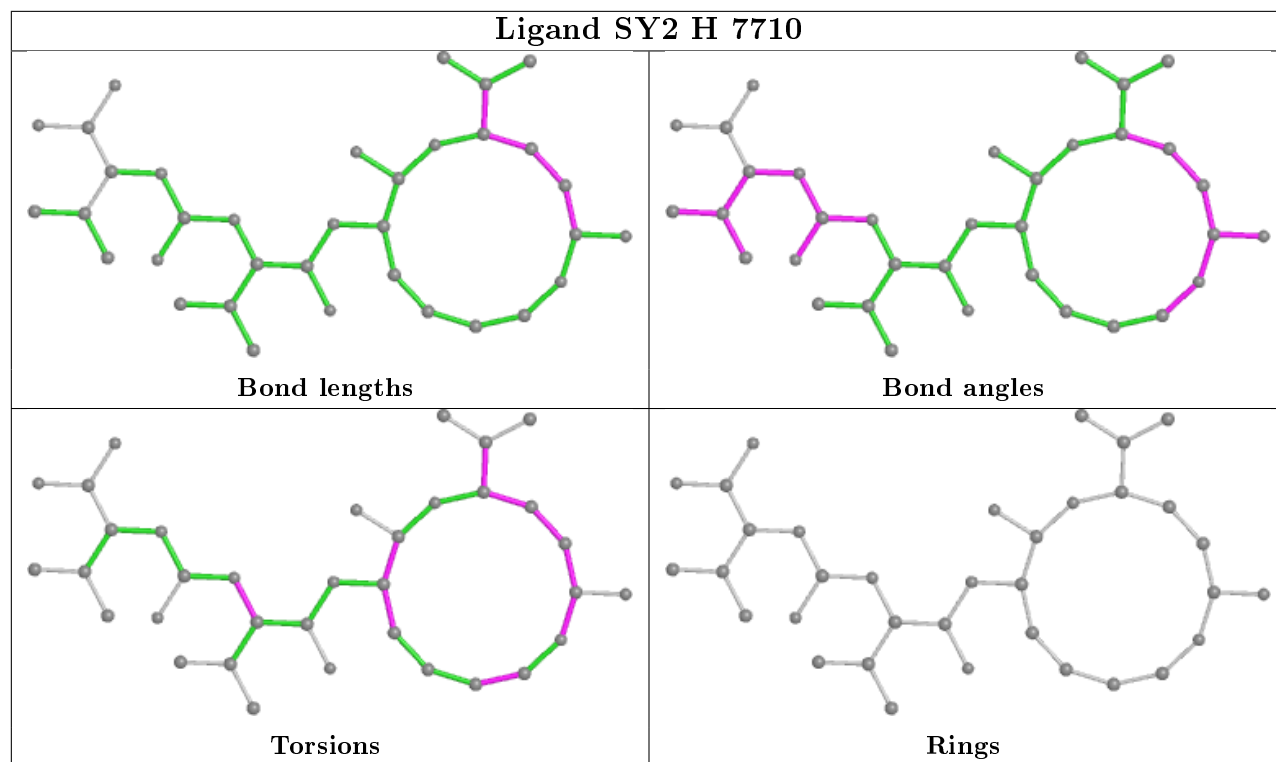
There are no ring outliers.

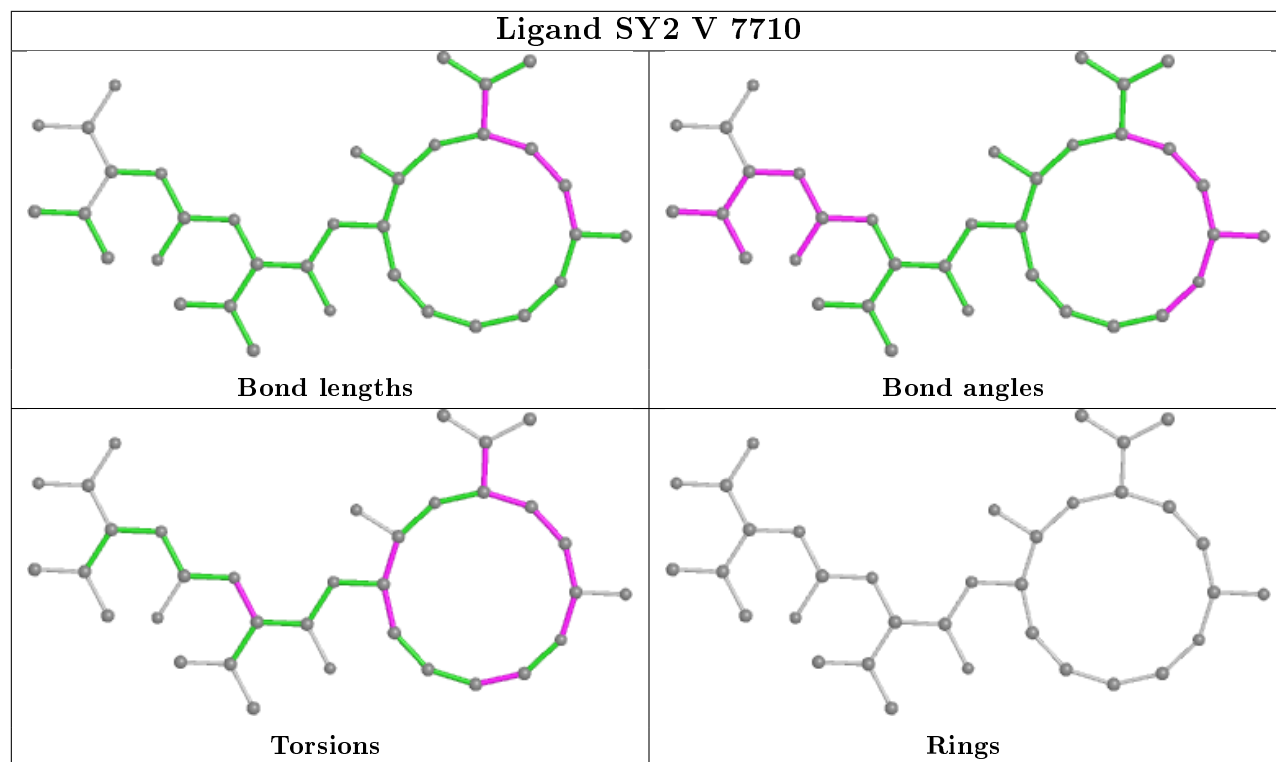
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	H	7710	SY2	2	0
15	V	7710	SY2	2	0

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







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	250/250 (100%)	-0.01	4 (1%) 72 74	17, 35, 65, 90	0
1	O	250/250 (100%)	-0.08	3 (1%) 79 80	16, 36, 66, 89	0
2	B	244/244 (100%)	0.09	3 (1%) 79 80	19, 40, 71, 96	0
2	P	244/244 (100%)	0.11	4 (1%) 72 74	20, 40, 70, 96	0
3	C	241/241 (100%)	0.21	5 (2%) 63 65	24, 46, 90, 112	0
3	Q	241/241 (100%)	0.25	10 (4%) 37 36	25, 47, 90, 111	0
4	D	242/242 (100%)	0.21	7 (2%) 51 52	23, 43, 74, 105	0
4	R	242/242 (100%)	0.13	7 (2%) 51 52	23, 44, 76, 105	0
5	E	233/233 (100%)	0.02	1 (0%) 92 93	23, 40, 66, 86	0
5	S	233/233 (100%)	0.06	5 (2%) 63 65	24, 40, 66, 86	0
6	F	244/244 (100%)	-0.08	1 (0%) 92 93	16, 34, 69, 90	0
6	T	244/244 (100%)	-0.03	1 (0%) 92 93	16, 34, 69, 90	0
7	G	243/243 (100%)	-0.05	4 (1%) 72 74	15, 32, 59, 96	0
7	U	243/243 (100%)	-0.03	3 (1%) 79 80	17, 32, 59, 96	0
8	H	222/222 (100%)	-0.12	2 (0%) 84 85	14, 28, 46, 92	0
8	V	222/222 (100%)	-0.14	1 (0%) 91 92	14, 28, 47, 92	0
9	I	204/204 (100%)	-0.16	0 100 100	16, 32, 48, 64	0
9	W	204/204 (100%)	-0.10	1 (0%) 91 92	17, 31, 48, 63	0
10	J	198/198 (100%)	-0.06	3 (1%) 73 76	21, 35, 52, 108	0
10	X	198/198 (100%)	-0.03	3 (1%) 73 76	21, 35, 52, 109	0
11	K	212/212 (100%)	0.04	4 (1%) 66 69	16, 35, 61, 71	0
11	Y	212/212 (100%)	-0.03	3 (1%) 75 77	17, 36, 61, 70	0
12	L	222/222 (100%)	-0.08	2 (0%) 84 85	19, 32, 56, 71	0
12	Z	222/222 (100%)	-0.08	2 (0%) 84 85	21, 32, 56, 71	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
13	1	233/233 (100%)	-0.16	0	100	100	14, 28, 42, 50	0
13	M	233/233 (100%)	-0.19	0	100	100	15, 28, 43, 50	0
14	2	196/196 (100%)	-0.17	0	100	100	18, 26, 47, 68	0
14	N	196/196 (100%)	-0.15	0	100	100	17, 26, 47, 68	0
All	All	6368/6368 (100%)	-0.02	79 (1%)	79	80	14, 35, 67, 112	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	12(D)	ALA	10.2
4	R	12(E)	SER	8.5
10	X	193	GLN	8.2
4	D	12(E)	SER	7.5
3	C	55	THR	6.6
4	D	12(C)	GLY	6.6
7	U	240	ASP	6.5
4	D	12(F)	GLY	6.2
4	R	12(D)	ALA	5.6
10	X	192	ALA	4.9
6	F	5	GLY	4.8
1	A	236	LEU	4.8
12	L	145	TYR	4.5
3	Q	56	LEU	4.4
7	G	6	ALA	4.4
3	Q	236	ILE	4.2
3	Q	55	THR	4.1
2	P	21(A)	LYS	4.1
2	B	54	VAL	4.0
7	G	240	ASP	4.0
4	R	12(F)	GLY	3.9
6	T	240	ILE	3.8
12	Z	145	TYR	3.8
4	D	126	ARG	3.7
3	C	56	LEU	3.7
5	S	127	TYR	3.6
7	U	6	ALA	3.5
10	J	193	GLN	3.4
1	O	5	THR	3.3
2	B	218	ASN	3.3
1	O	236	LEU	3.3
10	J	192	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
10	J	191	GLN	3.2
4	R	12(C)	GLY	3.1
11	Y	210	ILE	3.1
5	S	233	ILE	2.8
4	R	126	ARG	2.8
9	W	-8	SER	2.8
1	A	5	THR	2.8
3	Q	240	LYS	2.7
12	L	14(W)	LYS	2.7
1	O	4	MET	2.7
3	Q	203	THR	2.7
7	G	7	GLY	2.6
5	S	207	LEU	2.6
5	S	4	PHE	2.6
1	A	4	MET	2.6
2	P	54	VAL	2.6
3	C	240	LYS	2.5
11	Y	211	GLY	2.5
8	V	223	ASP	2.5
3	Q	206	GLY	2.4
3	Q	210	ILE	2.4
2	P	217	ALA	2.4
12	Z	14(W)	LYS	2.4
11	Y	104	TYR	2.3
5	S	5	ARG	2.3
4	D	207	LEU	2.3
3	C	203	THR	2.3
11	K	211	GLY	2.3
2	P	6	ARG	2.3
2	B	21(A)	LYS	2.3
11	K	143	LYS	2.3
11	K	210	ILE	2.3
10	X	133	TYR	2.2
3	Q	197	LEU	2.2
4	R	121	LEU	2.2
11	K	40	PHE	2.2
7	G	8	TYR	2.1
8	H	219	VAL	2.1
3	Q	88	LEU	2.1
4	D	12(G)	GLU	2.1
7	U	239	GLN	2.1
3	Q	54	SER	2.1

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Mol	Chain	Res	Type	RSRZ
8	H	223	ASP	2.1
5	E	233	ILE	2.0
4	R	127	LEU	2.0
1	A	202	VAL	2.0
3	C	236	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

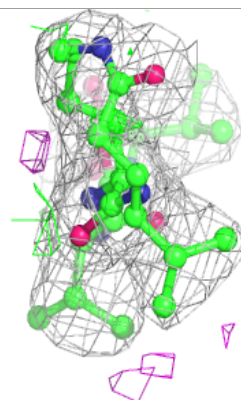
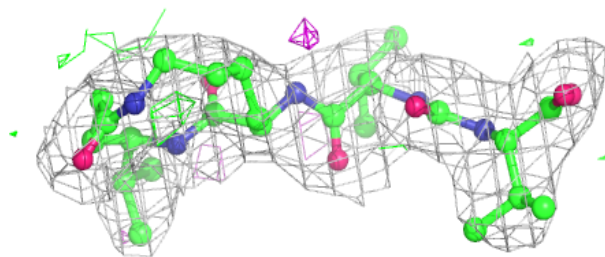
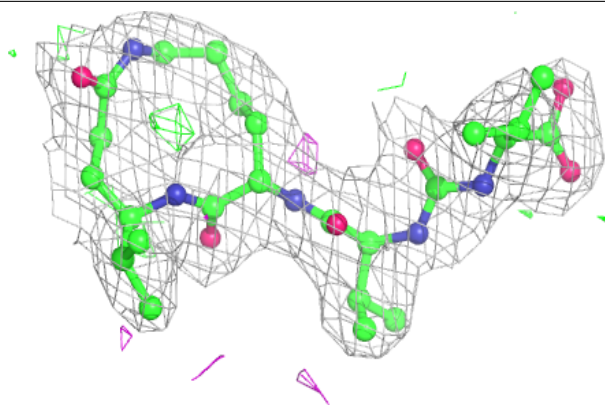
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
15	SY2	K	7710	35/35	0.95	0.20	23,33,51,54	0
15	SY2	H	7710	35/35	0.95	0.23	32,37,50,51	0
15	SY2	Y	7710	35/35	0.95	0.21	24,34,52,54	0
15	SY2	V	7710	35/35	0.95	0.23	30,37,49,51	0

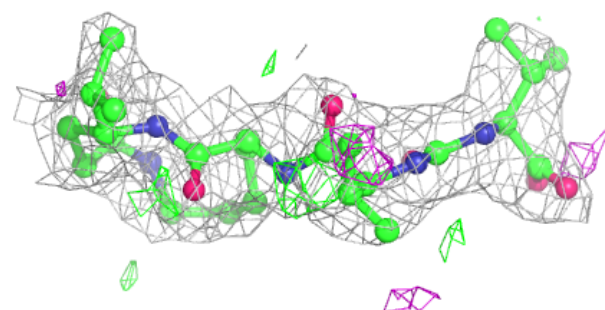
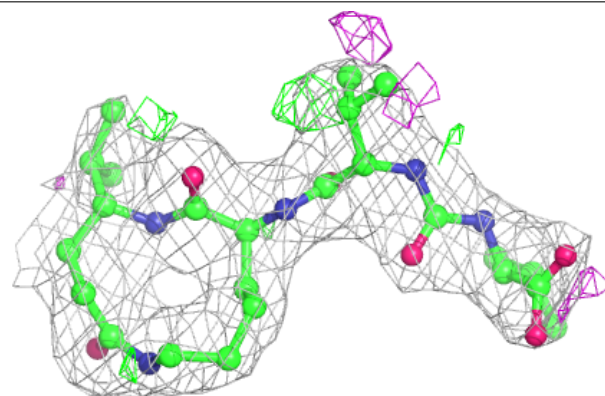
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SY2 K 7710:

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

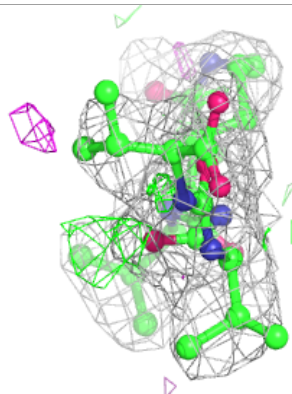
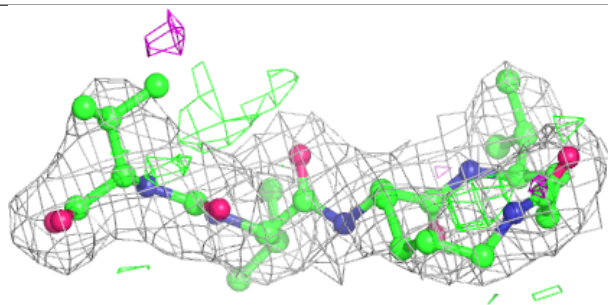
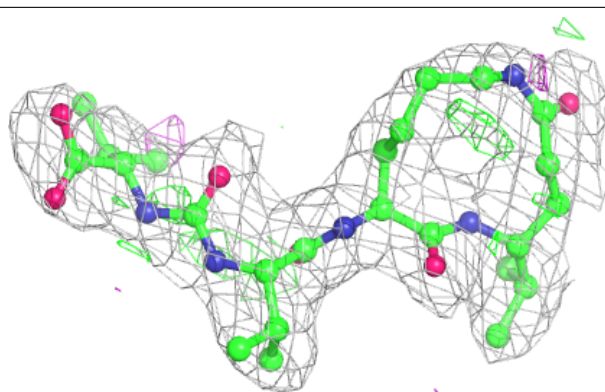
**Electron density around SY2 H 7710:**

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

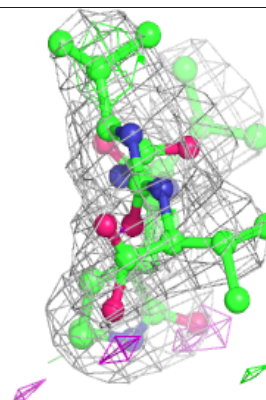
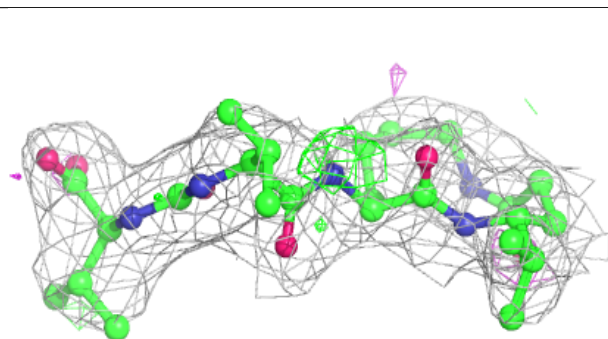
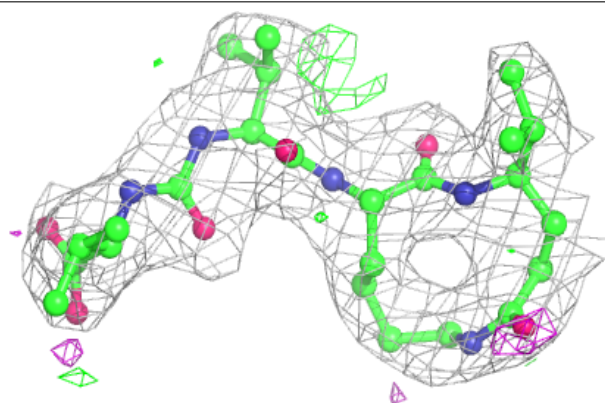


Electron density around SY2 Y 7710:

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

**Electron density around SY2 V 7710:**

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



6.5 Other polymers ⓘ

There are no such residues in this entry.