



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:35 PM UTC

PDB ID : 5HYN / pdb_00005hyn
Title : Structure of Human Polycomb Repressive Complex 2 (PRC2) with oncogenic histone H3K27M peptide
Authors : Zhang, Y.; Justin, N.; Wilson, J.R.; Gamblin, S.J.
Deposited on : 2016-02-01
Resolution : 2.95 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

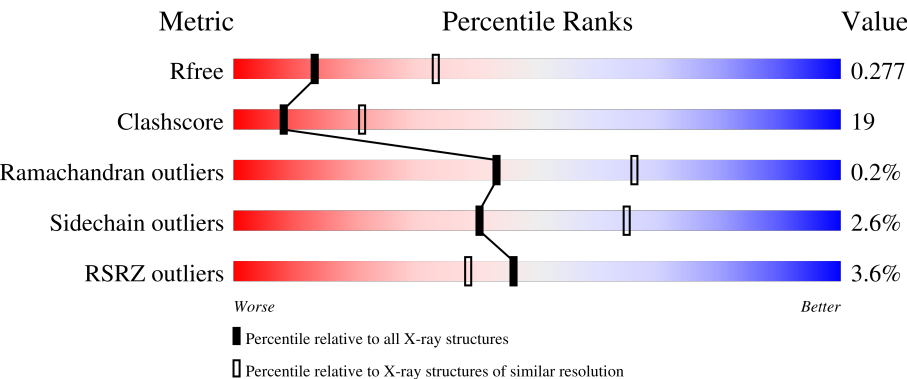
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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

Mol	Chain	Length	Quality of chain
1	A	746	4% 46% 29% .. 22%
1	F	746	4% 48% 26% . 24%
1	K	746	3% 49% 23% . 25%
1	Q	746	5% 45% 28% . 24%
2	B	367	2% 62% 37% ..

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Mol	Chain	Length	Quality of chain
2	G	367	
2	L	367	
2	R	367	
3	C	129	
3	H	129	
3	M	129	
3	S	129	
4	D	13	
4	I	13	
4	O	13	
4	T	13	
5	E	12	
5	J	12	
5	P	12	
5	U	12	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 35028 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 Histone-lysine N-methyltransferase EZH2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	581	Total	C	N	O	S	0	0	0
			4673	2932	825	874	42			
1	F	568	Total	C	N	O	S	0	0	0
			4567	2869	804	852	42			
1	K	562	Total	C	N	O	S	0	0	0
			4521	2836	799	844	42			
1	Q	565	Total	C	N	O	S	0	0	0
			4542	2850	801	849	42			

- Molecule 2 is a protein called Polycomb protein EED.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	365	Total	C	N	O	S	0	0	0
			2959	1873	521	543	22			
2	G	365	Total	C	N	O	S	0	0	0
			2959	1873	521	543	22			
2	L	365	Total	C	N	O	S	0	0	0
			2959	1873	521	543	22			
2	R	365	Total	C	N	O	S	0	0	0
			2959	1873	521	543	22			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	75	GLY	-	expression tag	UNP O75530
B	76	SER	-	expression tag	UNP O75530
G	75	GLY	-	expression tag	UNP O75530
G	76	SER	-	expression tag	UNP O75530
L	75	GLY	-	expression tag	UNP O75530
L	76	SER	-	expression tag	UNP O75530
R	75	GLY	-	expression tag	UNP O75530
R	76	SER	-	expression tag	UNP O75530

- Molecule 3 is a protein called Polycomb protein SUZ12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	125	Total	C	N	O	S	0	0	0
			1042	657	180	193	12			
3	H	124	Total	C	N	O	S	0	0	0
			1032	651	177	192	12			
3	M	125	Total	C	N	O	S	0	0	0
			1042	657	180	193	12			
3	S	125	Total	C	N	O	S	0	0	0
			1042	657	180	193	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	557	GLY	-	expression tag	UNP Q15022
H	557	GLY	-	expression tag	UNP Q15022
M	557	GLY	-	expression tag	UNP Q15022
S	557	GLY	-	expression tag	UNP Q15022

- Molecule 4 is a protein called H3K27M.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	9	Total	C	N	O	S	0	0	0
			63	38	13	11	1			
4	I	9	Total	C	N	O	S	0	0	0
			63	38	13	11	1			
4	O	9	Total	C	N	O	S	0	0	0
			63	38	13	11	1			
4	T	9	Total	C	N	O	S	0	0	0
			63	38	13	11	1			

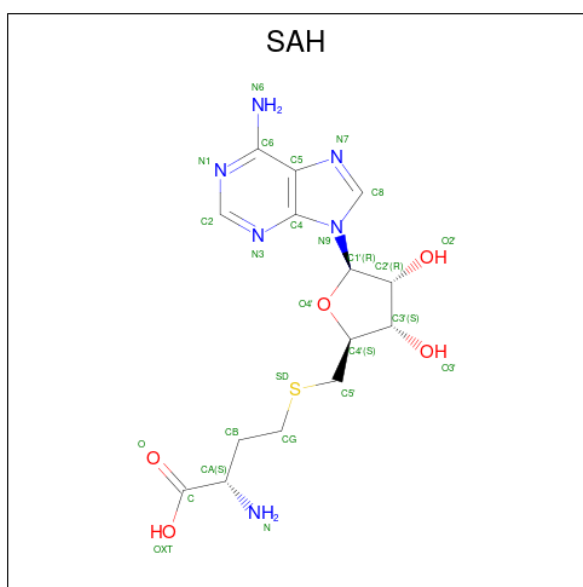
- Molecule 5 is a protein called JARID2 K116me3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	11	Total	C	N	O	0	0	0
			96	60	21	15			
5	J	10	Total	C	N	O	0	0	0
			85	54	17	14			
5	P	9	Total	C	N	O	0	0	0
			77	48	16	13			
5	U	10	Total	C	N	O	0	0	0
			85	54	17	14			

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	8	Total	Zn	0	0
			8	8		
6	F	8	Total	Zn	0	0
			8	8		
6	K	8	Total	Zn	0	0
			8	8		
6	Q	8	Total	Zn	0	0
			8	8		

- Molecule 7 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: C₁₄H₂₀N₆O₅S).

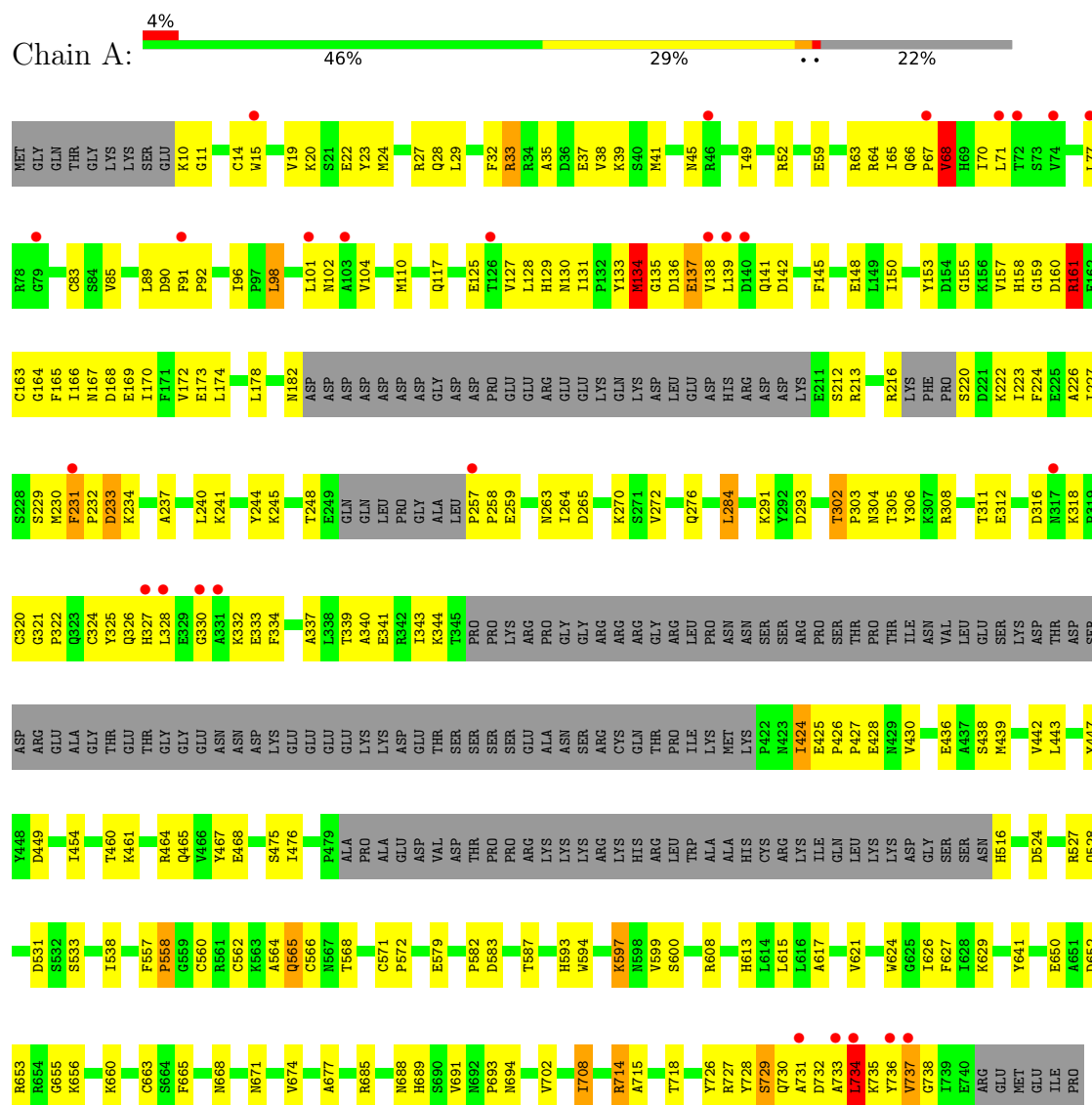


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
7	F	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
7	K	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
7	Q	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

3 Residue-property plots [i](#)

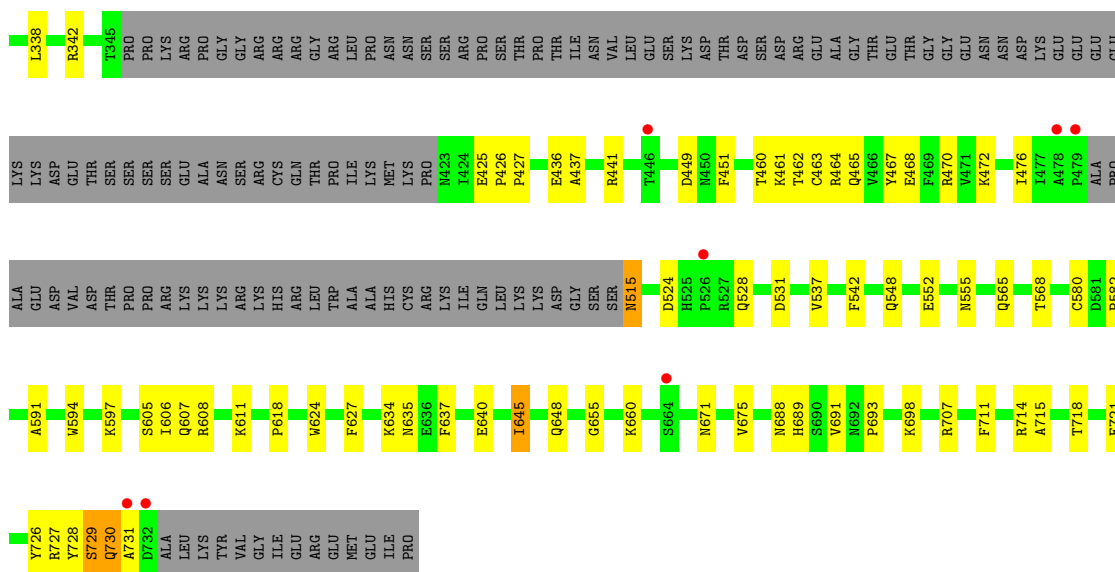
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: Histone-lysine N-methyltransferase EZH2

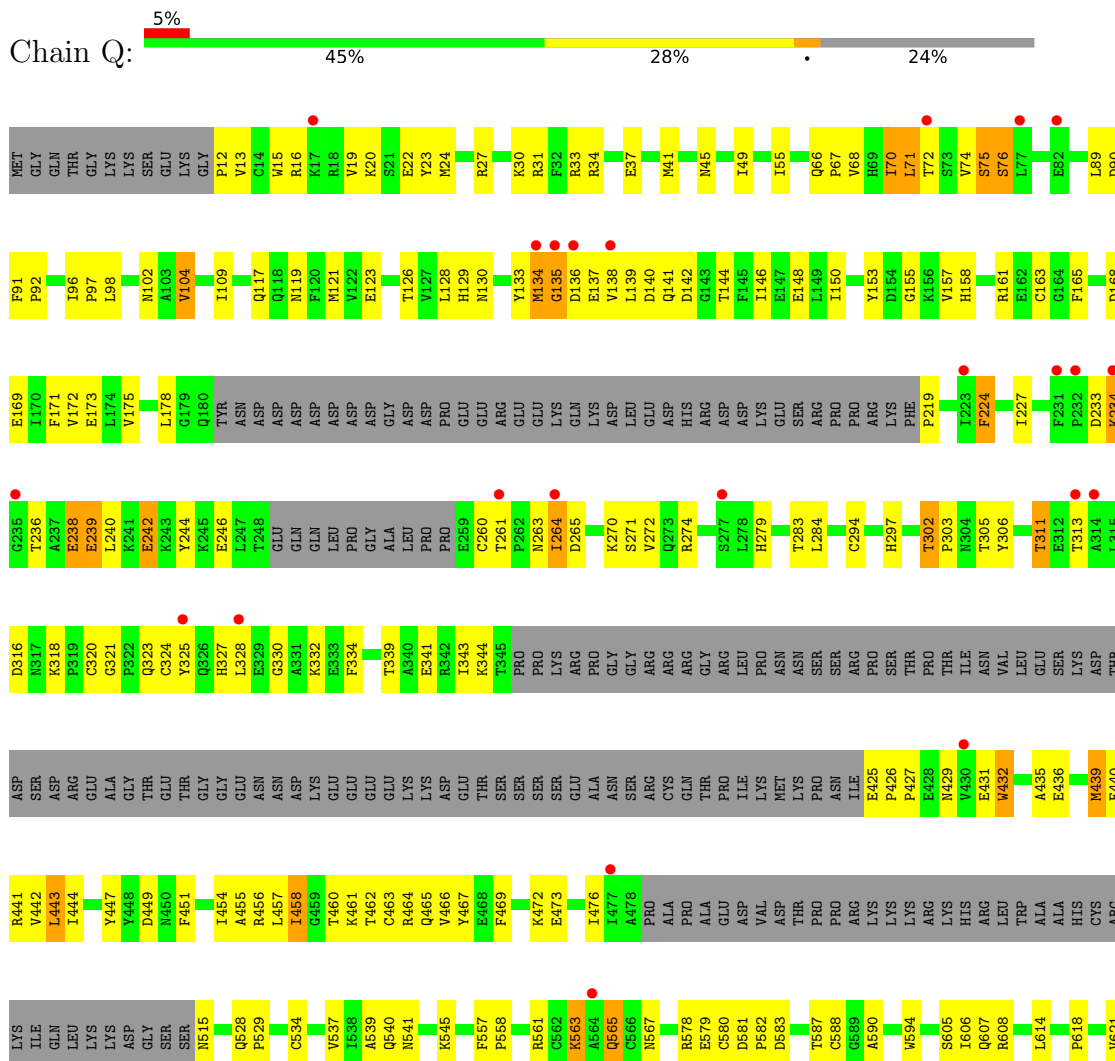


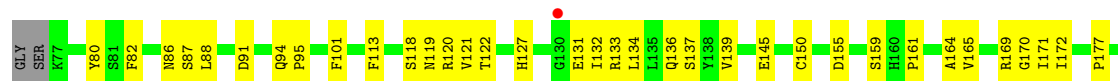
• Molecule 1: Histone-lysine N-methyltransferase EZH2





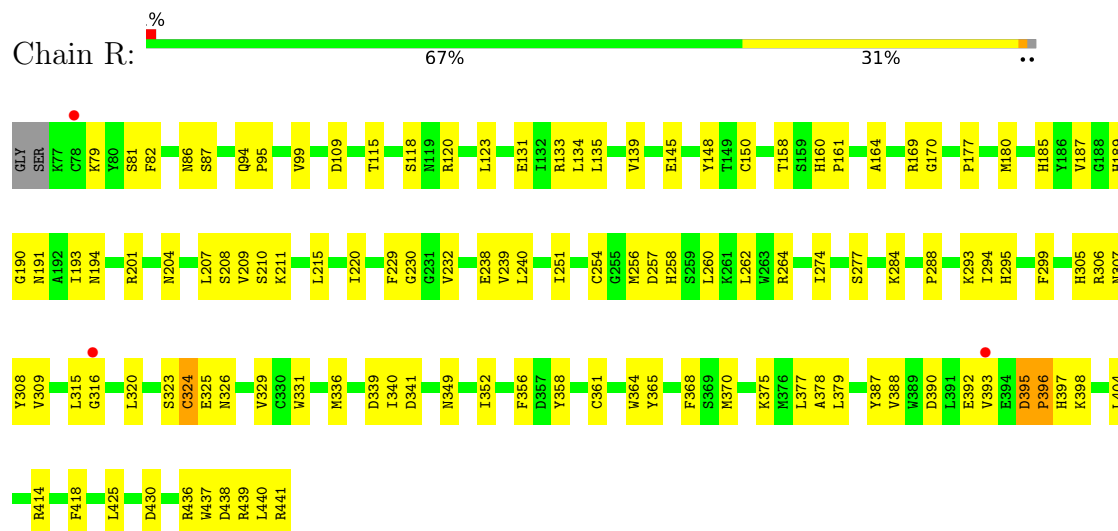
- Molecule 1: Histone-lysine N-methyltransferase EZH2



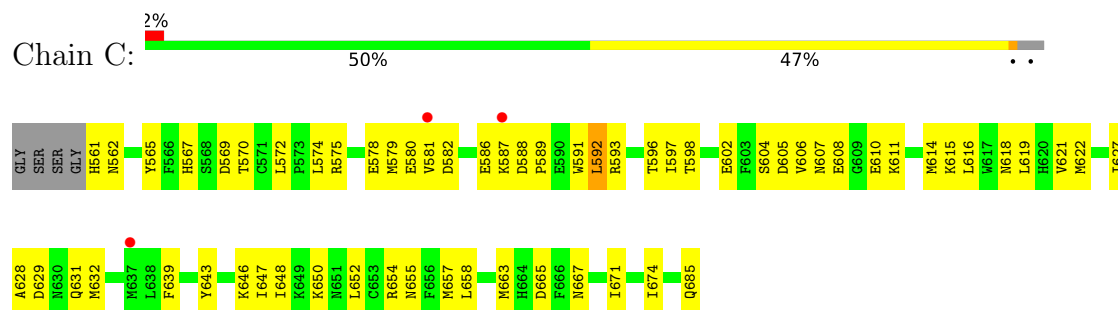




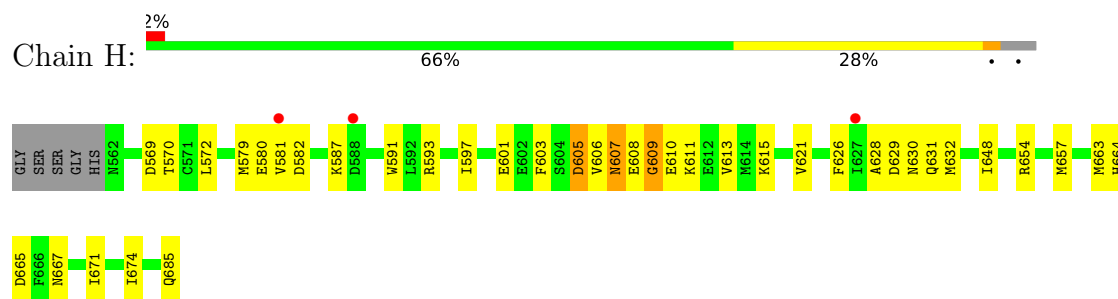
• Molecule 2: Polycomb protein EED



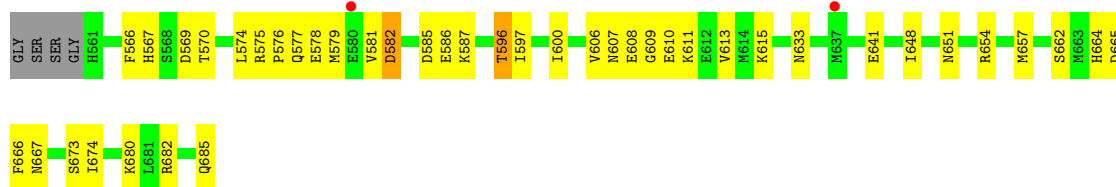
• Molecule 3: Polycomb protein SUZ12



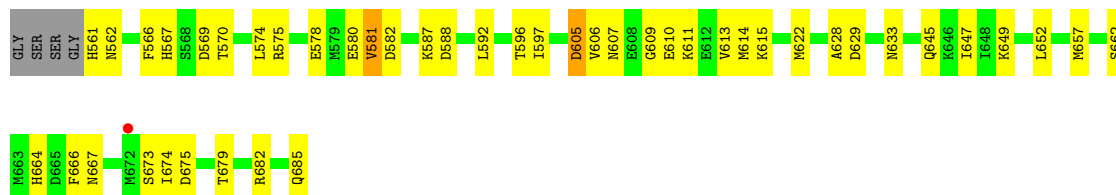
• Molecule 3: Polycomb protein SUZ12



• Molecule 3: Polycomb protein SUZ12



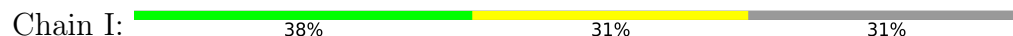
• Molecule 3: Polycomb protein SUZ12



• Molecule 4: H3K27M



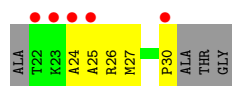
• Molecule 4: H3K27M



• Molecule 4: H3K27M



• Molecule 4: H3K27M

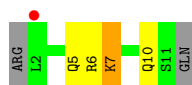


• Molecule 5: JARID2 K116me3

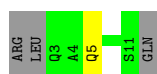




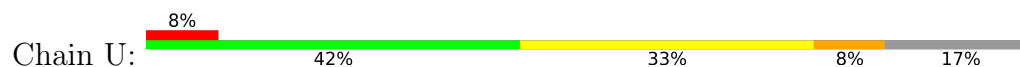
- Molecule 5: JARID2 K116me3



- Molecule 5: JARID2 K116me3



- Molecule 5: JARID2 K116me3



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	131.64Å 171.51Å 274.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	95.01 – 2.95 95.01 – 2.95	Depositor EDS
% Data completeness (in resolution range)	99.8 (95.01-2.95) 99.9 (95.01-2.95)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.96Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.219 , 0.273 0.226 , 0.277	Depositor DCC
R_{free} test set	6527 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	63.5	Xtriage
Anisotropy	0.627	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 82.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	35028	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.92 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.4013e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: M3L, SAH, ZN

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	0.62	3/4777 (0.1%)	0.87	9/6443 (0.1%)
1	F	0.61	1/4667 (0.0%)	0.91	7/6293 (0.1%)
1	K	0.63	1/4621 (0.0%)	1.01	20/6232 (0.3%)
1	Q	0.68	1/4641 (0.0%)	1.01	15/6258 (0.2%)
2	B	0.47	0/3034	0.79	0/4107
2	G	0.55	1/3034 (0.0%)	0.84	6/4107 (0.1%)
2	L	0.56	0/3034	0.84	1/4107 (0.0%)
2	R	0.59	0/3034	0.87	1/4107 (0.0%)
3	C	0.52	0/1063	0.93	1/1427 (0.1%)
3	H	0.56	0/1052	0.88	2/1412 (0.1%)
3	M	0.67	2/1063 (0.2%)	0.86	3/1427 (0.2%)
3	S	0.50	0/1063	0.84	4/1427 (0.3%)
4	D	0.54	0/63	0.86	0/83
4	I	0.50	0/63	0.82	0/83
4	O	0.72	0/63	0.91	0/83
4	T	0.50	0/63	0.84	0/83
5	E	0.64	0/84	1.01	0/110
5	J	0.81	0/73	1.35	0/96
5	P	0.50	0/65	0.61	0/85
5	U	0.93	0/73	1.42	0/96
All	All	0.60	9/35630 (0.0%)	0.91	69/48066 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	F	0	1
1	K	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	Q	0	4
2	G	0	2
2	L	0	3
2	R	0	1
3	H	0	1
All	All	0	15

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	33	ARG	NE-CZ	-14.53	1.17	1.33
1	K	11	GLY	CA-C	-13.92	1.42	1.51
1	A	564	ALA	CA-C	9.72	1.65	1.52
2	G	396	PRO	N-CD	7.52	1.58	1.47
1	F	181	TYR	CB-CG	-7.10	1.36	1.51
3	M	582	ASP	C-O	6.79	1.32	1.24
3	M	574	LEU	CG-CD1	5.40	1.70	1.52
1	Q	224	PHE	CB-CG	-5.12	1.38	1.50
1	A	161	ARG	CZ-NH2	-5.03	1.26	1.33

All (69) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	11	GLY	O-C-N	-23.42	112.64	121.07
3	C	608	GLU	N-CA-C	11.93	123.83	111.07
1	Q	134	MET	N-CA-C	10.71	128.13	114.31
1	Q	264	ILE	N-CA-C	10.45	120.45	110.42
1	K	11	GLY	CA-C-N	9.53	129.16	119.82
1	K	11	GLY	C-N-CA	9.53	129.16	119.82
1	F	302	THR	N-CA-C	9.05	126.01	113.16
1	F	181	TYR	CA-CB-CG	-8.50	98.60	113.90
1	K	321	GLY	N-CA-C	-8.16	95.69	112.34
1	Q	729	SER	N-CA-C	7.90	119.52	111.07
3	S	581	VAL	CA-C-N	7.69	135.55	121.70
3	S	581	VAL	C-N-CA	7.69	135.55	121.70
1	K	66	GLN	CA-C-N	-7.64	112.14	119.85
1	K	66	GLN	C-N-CA	-7.64	112.14	119.85
1	Q	443	LEU	CB-CG-CD1	-7.50	88.20	110.70
1	K	12	PRO	N-CA-C	7.29	123.38	113.98
1	Q	70	ILE	CG1-CB-CG2	-7.24	88.99	110.70
1	K	67	PRO	CA-C-N	7.07	134.42	121.70
1	K	67	PRO	C-N-CA	7.07	134.42	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	236	THR	CA-C-N	7.07	130.05	120.44
1	K	236	THR	C-N-CA	7.07	130.05	120.44
2	G	324	CYS	CA-CB-SG	-7.00	98.31	114.40
3	H	570	THR	CA-C-N	-6.98	110.56	122.56
3	H	570	THR	C-N-CA	-6.98	110.56	122.56
1	A	33	ARG	CA-CB-CG	-6.95	100.19	114.10
1	Q	264	ILE	CA-C-N	6.95	134.22	121.70
1	Q	264	ILE	C-N-CA	6.95	134.22	121.70
2	L	180	MET	CB-CG-SD	-6.94	91.88	112.70
3	S	570	THR	CA-C-N	-6.42	112.00	122.65
3	S	570	THR	C-N-CA	-6.42	112.00	122.65
2	R	324	CYS	CA-CB-SG	-6.34	99.82	114.40
1	Q	163	CYS	N-CA-C	-6.21	99.69	109.50
1	Q	134	MET	CA-CB-CG	-6.14	101.81	114.10
1	K	72	THR	CA-C-N	6.08	132.65	121.70
1	K	72	THR	C-N-CA	6.08	132.65	121.70
1	A	734	LEU	CA-C-N	6.06	132.60	121.70
1	A	734	LEU	C-N-CA	6.06	132.60	121.70
1	K	302	THR	N-CA-C	6.03	123.14	109.81
1	K	140	ASP	N-CA-C	5.93	125.42	113.31
1	K	319	PRO	CA-C-O	-5.92	114.73	122.19
1	Q	302	THR	N-CA-C	5.77	122.56	109.81
1	A	729	SER	CA-C-N	5.60	131.78	121.70
1	A	729	SER	C-N-CA	5.60	131.78	121.70
1	A	302	THR	N-CA-C	5.58	122.13	109.81
2	G	421	ASP	CA-C-N	-5.57	111.25	122.55
2	G	421	ASP	C-N-CA	-5.57	111.25	122.55
1	A	729	SER	N-CA-C	5.51	116.96	111.07
3	M	570	THR	CA-C-N	-5.41	113.67	122.65
3	M	570	THR	C-N-CA	-5.41	113.67	122.65
1	F	65	ILE	CA-CB-CG1	-5.37	101.28	110.40
1	Q	135	GLY	N-CA-C	-5.36	97.75	113.30
1	Q	728	TYR	CA-CB-CG	5.34	123.51	113.90
1	F	729	SER	CA-C-N	5.33	131.30	121.70
1	F	729	SER	C-N-CA	5.33	131.30	121.70
1	F	729	SER	CA-C-O	-5.30	115.43	121.00
1	F	140	ASP	N-CA-C	5.27	117.03	111.28
1	Q	33	ARG	NE-CZ-NH2	-5.18	114.54	119.20
1	K	68	VAL	N-CA-C	-5.17	96.52	111.00
3	M	582	ASP	CA-C-O	-5.14	113.16	120.51
2	G	209	VAL	CA-C-N	-5.10	113.95	122.21
2	G	209	VAL	C-N-CA	-5.10	113.95	122.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	729	SER	CA-C-N	5.09	130.87	121.70
1	K	729	SER	C-N-CA	5.09	130.87	121.70
1	Q	71	LEU	CA-C-N	5.07	130.83	121.70
1	Q	71	LEU	C-N-CA	5.07	130.83	121.70
1	A	558	PRO	CA-C-N	-5.06	111.50	121.41
1	A	558	PRO	C-N-CA	-5.06	111.50	121.41
2	G	118	SER	CB-CA-C	-5.05	110.73	116.54
1	K	68	VAL	N-CA-CB	5.02	120.03	111.50

There are no chirality outliers.

All (15) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	102	ASN	Peptide
1	A	134	MET	Peptide
1	F	564	ALA	Peptide
2	G	392	GLU	Peptide
2	G	395	ASP	Peptide
3	H	608	GLU	Peptide
1	K	730	GLN	Peptide
2	L	355	ARG	Mainchain
2	L	393	VAL	Peptide
2	L	396	PRO	Peptide
1	Q	102	ASN	Peptide
1	Q	311	THR	Peptide
1	Q	327	HIS	Peptide
1	Q	76	SER	Peptide
2	R	396	PRO	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4673	0	4524	255	1
1	F	4567	0	4427	203	1
1	K	4521	0	4373	186	1
1	Q	4542	0	4400	240	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2959	0	2881	148	0
2	G	2959	0	2881	101	0
2	L	2959	0	2881	99	0
2	R	2959	0	2881	100	0
3	C	1042	0	1021	60	0
3	H	1032	0	1014	39	0
3	M	1042	0	1021	50	0
3	S	1042	0	1021	38	0
4	D	63	0	68	3	0
4	I	63	0	68	4	0
4	O	63	0	68	4	0
4	T	63	0	68	13	0
5	E	96	0	106	3	0
5	J	85	0	90	5	0
5	P	77	0	79	1	0
5	U	85	0	90	8	0
6	A	8	0	0	0	0
6	F	8	0	0	0	0
6	K	8	0	0	0	0
6	Q	8	0	0	0	0
7	A	26	0	19	6	0
7	F	26	0	19	2	0
7	K	26	0	19	1	0
7	Q	26	0	19	1	0
All	All	35028	0	34038	1335	2

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 19.

All (1335) 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)
1:Q:432:TRP:CH2	1:Q:461:LYS:HG3	1.65	1.32
1:Q:318:LYS:NZ	1:Q:324:CYS:SG	2.26	1.08
1:Q:432:TRP:HD1	1:Q:469:PHE:CD1	1.75	1.05
1:Q:432:TRP:HH2	1:Q:461:LYS:CG	1.70	1.04
1:A:430:VAL:HG21	1:A:465:GLN:HE21	1.19	1.03
3:S:596:THR:HG21	3:S:622:MET:HE1	1.42	1.01
1:Q:652:ASP:OD1	4:T:26:ARG:NH2	1.93	1.00
2:L:120:ARG:HG2	2:L:139:VAL:HG22	1.42	1.00
1:Q:71:LEU:HB3	1:Q:72:THR:HA	1.45	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:691:VAL:H	1:A:737:VAL:HG21	1.32	0.95
1:F:45:ASN:HD21	2:G:317:ASP:H	1.03	0.93
1:F:23:TYR:OH	1:F:165:PHE:O	1.87	0.93
1:K:117:GLN:HA	1:K:117:GLN:HE21	1.33	0.92
1:F:42:PHE:HB3	2:G:393:VAL:HB	1.52	0.90
1:K:320:CYS:O	1:K:324:CYS:HB2	1.72	0.90
1:A:330:GLY:HA2	1:A:334:PHE:H	1.35	0.89
2:R:305:HIS:ND1	2:R:325:GLU:OE1	2.05	0.89
1:K:427:PRO:HA	1:K:464:ARG:HH22	1.37	0.89
2:L:131:GLU:OE2	2:L:133:ARG:NH2	2.05	0.88
1:Q:128:LEU:HD21	1:Q:157:VAL:HG12	1.55	0.87
1:F:436:GLU:OE2	1:F:460:THR:OG1	1.92	0.87
1:A:10:LYS:HG3	1:A:15:TRP:HE1	1.37	0.87
1:A:68:VAL:HG21	2:B:110:PRO:HG2	1.56	0.87
1:Q:432:TRP:HA	1:Q:432:TRP:CE3	2.09	0.87
1:A:41:MET:HG3	2:B:336:MET:HE2	1.57	0.87
3:H:580:GLU:HB3	3:H:581:VAL:HA	1.54	0.87
1:F:688:ASN:OD1	7:F:1009:SAH:N	2.07	0.87
1:F:161:ARG:NH2	1:F:233:ASP:OD2	2.07	0.86
2:L:82:PHE:HZ	2:L:376:MET:HE1	1.41	0.85
1:Q:541:ASN:HD21	1:Q:701:MET:HE3	1.40	0.85
1:F:175:VAL:HG21	1:F:244:TYR:CE2	2.11	0.85
1:Q:432:TRP:CD1	1:Q:469:PHE:CD1	2.62	0.85
1:Q:727:ARG:HH21	4:T:30:PRO:HG3	1.41	0.85
1:K:72:THR:HA	1:K:73:SER:HB3	1.59	0.85
1:A:71:LEU:HB3	2:B:180:MET:HE1	1.56	0.84
3:S:645:GLN:HE21	3:S:649:LYS:HE2	1.41	0.84
1:A:263:ASN:HD21	3:C:655:ASN:HD21	1.24	0.84
1:K:83:CYS:HB2	1:K:98:LEU:HD13	1.61	0.83
1:K:65:ILE:HB	1:K:67:PRO:HD3	1.57	0.83
1:Q:260:CYS:HB3	1:Q:261:THR:HA	1.61	0.82
1:K:729:SER:N	1:K:730:GLN:HB2	1.94	0.82
1:F:175:VAL:HG21	1:F:244:TYR:HE2	1.45	0.82
1:K:655:GLY:HA3	4:O:24:ALA:HB2	1.61	0.82
1:Q:41:MET:HG3	2:R:336:MET:HE2	1.62	0.81
1:K:437:ALA:HB1	1:K:441:ARG:HH12	1.45	0.81
1:F:150:ILE:HG22	1:F:155:GLY:HA2	1.61	0.81
1:K:611:LYS:NZ	3:M:586:GLU:OE2	2.13	0.81
1:Q:136:ASP:OD2	5:U:7:M3L:N	2.13	0.81
1:Q:460:THR:O	1:Q:461:LYS:HE3	1.81	0.81
1:Q:23:TYR:OH	1:Q:165:PHE:O	1.99	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:655:GLY:HA3	4:I:24:ALA:HB1	1.61	0.80
1:F:237:ALA:HA	1:F:240:LEU:HD12	1.64	0.79
1:Q:323:GLN:HG2	1:Q:462:THR:HB	1.64	0.79
1:F:731:ALA:C	1:F:733:ALA:HA	2.08	0.78
1:A:161:ARG:HH11	1:A:164:GLY:N	1.82	0.77
1:F:234:LYS:HB3	1:F:240:LEU:HD21	1.65	0.77
2:B:197:LYS:NZ	2:B:242:ALA:O	2.17	0.77
2:G:324:CYS:SG	5:J:5:GLN:NE2	2.57	0.77
1:F:525:HIS:HB2	1:F:528:GLN:HG2	1.65	0.77
1:Q:440:PHE:CE2	1:Q:444:ILE:HD13	2.20	0.77
1:Q:655:GLY:HA3	4:T:24:ALA:CB	2.15	0.77
1:K:45:ASN:HD21	2:L:317:ASP:H	1.32	0.76
1:A:135:GLY:HA2	1:A:138:VAL:HB	1.66	0.76
1:F:430:VAL:HG21	1:F:465:GLN:HE21	1.50	0.76
1:F:655:GLY:HA3	4:I:24:ALA:CB	2.14	0.76
2:B:282:PRO:HB3	3:C:575:ARG:HH12	1.51	0.75
1:Q:175:VAL:HG21	1:Q:244:TYR:CE1	2.21	0.75
2:G:322:LYS:HE2	2:G:366:MET:O	1.87	0.75
1:Q:624:TRP:O	7:Q:1009:SAH:N	2.18	0.75
2:B:125:GLU:HB2	2:B:135:LEU:HD11	1.68	0.75
1:F:451:PHE:HD2	1:F:466:VAL:HG12	1.52	0.75
2:G:79:LYS:NZ	2:G:392:GLU:OE2	2.16	0.74
1:A:150:ILE:HG22	1:A:155:GLY:HA2	1.67	0.74
1:F:315:LEU:HD21	1:F:450:ASN:HB2	1.67	0.74
1:K:236:THR:O	1:K:240:LEU:HD22	1.87	0.74
1:A:130:ASN:ND2	2:B:237:ASP:OD2	2.20	0.74
1:F:714:ARG:NH2	1:F:720:GLU:OE1	2.20	0.74
1:A:476:ILE:HD13	1:Q:55:ILE:HG23	1.69	0.74
1:K:689:HIS:HD2	1:K:726:TYR:H	1.34	0.74
2:G:274:ILE:O	2:G:277:SER:OG	2.06	0.74
2:L:362:ASP:O	5:P:5:GLN:NE2	2.20	0.74
1:K:279:HIS:O	1:K:283:THR:HG22	1.88	0.74
1:Q:150:ILE:HG22	1:Q:155:GLY:HA2	1.69	0.73
2:R:396:PRO:HD2	2:R:397:HIS:HD2	1.51	0.73
1:Q:328:LEU:HG	1:Q:425:GLU:HG2	1.70	0.73
2:G:404:LEU:HB3	2:G:437:TRP:CZ3	2.23	0.73
2:L:396:PRO:HD2	2:L:397:HIS:HD2	1.54	0.73
1:A:729:SER:N	1:A:730:GLN:HB2	2.04	0.73
1:A:284:LEU:HD21	1:A:293:ASP:HB2	1.70	0.72
3:S:567:HIS:CE1	3:S:574:LEU:HD12	2.25	0.72
2:B:120:ARG:HB3	2:B:139:VAL:HG22	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:133:TYR:OH	1:F:136:ASP:HB2	1.87	0.72
1:K:15:TRP:HZ3	1:K:223:ILE:HG22	1.55	0.72
3:M:586:GLU:HB2	3:M:587:LYS:HB3	1.69	0.72
1:Q:662:MET:HE3	1:Q:732:ASP:HB2	1.70	0.72
2:B:396:PRO:HB2	2:B:398:LYS:HG2	1.70	0.72
1:K:67:PRO:HB2	1:K:68:VAL:HG23	1.72	0.72
2:B:225:LEU:HD23	3:C:570:THR:HG23	1.71	0.72
1:A:597:LYS:HD3	1:A:608:ARG:HB3	1.72	0.72
1:F:153:TYR:O	1:F:156:LYS:HG2	1.88	0.71
1:F:233:ASP:OD1	1:F:233:ASP:N	2.22	0.71
1:A:233:ASP:OD1	1:A:233:ASP:N	2.23	0.71
2:G:125:GLU:HB2	2:G:135:LEU:HD11	1.72	0.71
1:A:167:ASN:ND2	2:B:350:VAL:O	2.24	0.71
2:L:358:TYR:CE1	2:L:361:CYS:HB3	2.25	0.71
1:Q:30:LYS:HE2	1:Q:34:ARG:HE	1.56	0.71
1:K:127:VAL:HG12	1:K:156:LYS:HB3	1.71	0.71
2:R:256:MET:O	2:R:258:HIS:HD2	1.74	0.71
1:A:302:THR:HG22	1:A:305:THR:HG22	1.72	0.71
1:A:691:VAL:HG23	1:A:737:VAL:HG11	1.71	0.70
3:S:561:HIS:N	3:S:562:ASN:HA	2.04	0.70
1:A:263:ASN:ND2	3:C:655:ASN:HD21	1.89	0.70
1:F:732:ASP:N	1:F:733:ALA:HA	2.06	0.70
1:K:135:GLY:O	1:K:141:GLN:HG3	1.91	0.70
1:F:652:ASP:OD1	4:I:26:ARG:NH2	2.23	0.70
1:Q:563:LYS:HB3	1:Q:587:THR:HG22	1.72	0.70
1:F:82:GLU:HG2	1:F:97:PRO:HA	1.72	0.70
1:F:321:GLY:HA2	1:F:324:CYS:HB2	1.73	0.70
1:A:328:LEU:HD23	1:A:424:ILE:HG23	1.73	0.70
1:Q:457:LEU:HD12	1:Q:458:ILE:N	2.06	0.70
1:K:263:ASN:CA	3:M:607:ASN:HD21	2.03	0.69
1:K:265:ASP:OD1	3:M:654:ARG:NH1	2.25	0.69
1:Q:45:ASN:ND2	2:R:316:GLY:O	2.25	0.69
1:Q:134:MET:N	1:Q:135:GLY:HA3	2.05	0.69
1:A:318:LYS:NZ	1:A:325:TYR:O	2.25	0.69
1:Q:334:PHE:HD2	1:Q:467:TYR:OH	1.76	0.69
2:R:307:ASN:HD21	5:U:5:GLN:HG3	1.58	0.69
2:L:191:ASN:HB3	2:L:211:LYS:HB3	1.73	0.69
1:Q:432:TRP:HA	1:Q:432:TRP:HE3	1.58	0.69
1:Q:441:ARG:NH2	1:Q:473:GLU:OE1	2.26	0.69
2:R:254:CYS:HB3	2:R:260:LEU:HD23	1.75	0.69
1:A:306:TYR:O	3:C:665:ASP:HB3	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:GLY:HA2	1:A:334:PHE:N	2.06	0.69
1:K:308:ARG:HD2	3:M:664:HIS:CE1	2.26	0.69
1:K:451:PHE:HE2	1:K:467:TYR:HD1	1.40	0.69
2:L:355:ARG:O	2:L:397:HIS:HB2	1.94	0.68
1:Q:650:GLU:OE1	1:Q:653:ARG:NH1	2.26	0.68
3:H:587:LYS:HE2	3:H:593:ARG:HH12	1.58	0.68
1:K:77:LEU:HD12	1:K:77:LEU:H	1.59	0.68
1:Q:320:CYS:HB3	1:Q:321:GLY:HA2	1.75	0.68
1:A:68:VAL:HG23	2:B:112:VAL:HG22	1.76	0.68
1:A:731:ALA:C	1:A:733:ALA:HA	2.18	0.68
1:A:425:GLU:CD	1:A:426:PRO:HD2	2.18	0.68
1:K:22:GLU:OE2	1:K:181:TYR:OH	2.10	0.68
1:Q:142:ASP:OD1	1:Q:144:THR:OG1	2.12	0.68
1:Q:472:LYS:O	1:Q:476:ILE:HG12	1.94	0.68
1:K:91:PHE:N	1:K:92:PRO:HA	2.08	0.67
1:Q:71:LEU:CB	1:Q:72:THR:HA	2.23	0.67
1:A:615:LEU:HD21	3:C:581:VAL:HG11	1.75	0.67
1:F:61:LYS:O	1:F:64:ARG:NH1	2.24	0.67
3:H:601:GLU:HA	3:H:611:LYS:HD3	1.74	0.67
1:Q:691:VAL:O	1:Q:693:PRO:HD3	1.94	0.67
3:C:570:THR:HG22	3:C:572:LEU:HD13	1.77	0.67
1:A:234:LYS:HB3	1:A:240:LEU:HD21	1.76	0.67
2:B:269:ARG:NE	2:B:292:GLN:OE1	2.21	0.67
1:K:284:LEU:HD11	3:M:606:VAL:HG11	1.77	0.67
2:B:232:VAL:HG21	3:C:591:TRP:CE3	2.30	0.67
1:Q:140:ASP:N	1:Q:141:GLN:HA	2.08	0.67
1:A:19:VAL:HG11	1:A:227:ILE:HG22	1.77	0.67
2:B:88:LEU:HD11	2:B:434:ILE:HD12	1.75	0.67
2:G:189:HIS:NE2	2:G:208:SER:OG	2.27	0.67
1:Q:104:VAL:O	2:R:169:ARG:NH2	2.28	0.67
1:Q:432:TRP:HD1	1:Q:469:PHE:CE1	2.13	0.67
2:B:256:MET:O	2:B:258:HIS:HD2	1.78	0.67
1:Q:334:PHE:HD2	1:Q:467:TYR:HH	1.43	0.67
1:Q:655:GLY:HA3	4:T:24:ALA:HB2	1.76	0.67
2:B:399:ALA:HB1	2:B:400:LYS:HB2	1.77	0.66
1:A:212:SER:HB2	1:A:213:ARG:HG2	1.75	0.66
1:A:216:ARG:HH12	1:A:245:LYS:HE2	1.61	0.66
2:G:256:MET:O	2:G:258:HIS:HD2	1.78	0.66
2:L:396:PRO:HD2	2:L:397:HIS:CD2	2.30	0.66
2:R:315:LEU:HD13	2:R:370:MET:HE1	1.77	0.66
1:F:464:ARG:NH1	1:F:468:GLU:OE1	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:199:HIS:CE1	2:G:248:GLY:HA3	2.30	0.66
1:A:621:VAL:HG13	1:A:736:TYR:HD1	1.60	0.66
2:B:285:THR:OG1	2:B:287:ARG:HG2	1.96	0.66
1:A:96:ILE:HG13	2:B:134:LEU:HG	1.76	0.66
3:H:628:ALA:HB3	3:H:631:GLN:HG3	1.77	0.66
2:L:127:HIS:HB2	2:L:131:GLU:HG3	1.78	0.66
3:S:581:VAL:HA	3:S:582:ASP:HB2	1.78	0.65
1:A:67:PRO:HG3	2:B:105:SER:CB	2.27	0.65
1:A:691:VAL:N	1:A:737:VAL:HG21	2.09	0.65
1:K:161:ARG:HH21	1:K:233:ASP:CG	2.04	0.65
1:Q:129:HIS:CD2	1:Q:129:HIS:H	2.14	0.65
1:F:729:SER:N	1:F:730:GLN:HB2	2.11	0.65
1:Q:71:LEU:HD13	2:R:180:MET:SD	2.37	0.65
1:Q:462:THR:N	1:Q:465:GLN:OE1	2.28	0.65
1:K:324:CYS:SG	1:K:325:TYR:N	2.70	0.65
1:K:688:ASN:OD1	7:K:1009:SAH:N	2.29	0.65
1:A:655:GLY:HA3	4:D:24:ALA:CB	2.27	0.65
2:G:268:LYS:O	2:G:272:ASN:ND2	2.29	0.65
1:K:328:LEU:HG	1:K:331:ALA:HB2	1.77	0.65
2:B:394:GLU:OE1	2:B:394:GLU:N	2.26	0.65
1:A:28:GLN:HB3	1:A:32:PHE:HE2	1.60	0.65
1:K:314:ALA:HB1	1:K:315:LEU:HB2	1.79	0.65
1:A:734:LEU:HA	1:A:735:LYS:HB3	1.80	0.64
1:K:42:PHE:CZ	2:L:396:PRO:HG3	2.31	0.64
1:K:265:ASP:OD2	3:M:654:ARG:N	2.24	0.64
1:Q:432:TRP:CD1	1:Q:469:PHE:CG	2.85	0.64
1:A:174:LEU:O	1:A:178:LEU:HG	1.98	0.64
1:A:303:PRO:HB2	1:A:306:TYR:CZ	2.32	0.64
1:A:37:GLU:CD	2:B:336:MET:HG2	2.22	0.64
2:B:125:GLU:HB2	2:B:135:LEU:HD21	1.78	0.64
3:C:598:THR:O	3:C:602:GLU:HG2	1.97	0.64
2:L:422:SER:HB2	2:L:439:ARG:NH1	2.13	0.64
1:K:303:PRO:HB2	1:K:306:TYR:CZ	2.32	0.64
1:A:220:SER:HB2	1:A:223:ILE:HG23	1.78	0.64
1:A:730:GLN:HG3	1:A:732:ASP:H	1.63	0.64
2:B:254:CYS:HB3	2:B:260:LEU:HD23	1.80	0.64
1:F:528:GLN:N	1:F:528:GLN:OE1	2.31	0.64
3:M:682:ARG:HA	3:M:685:GLN:HG3	1.79	0.64
1:K:71:LEU:HD11	1:K:97:PRO:HG2	1.79	0.63
1:Q:655:GLY:HA3	4:T:24:ALA:HB1	1.80	0.63
1:K:582:PRO:HB2	1:K:594:TRP:HH2	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:618:PRO:HD3	3:M:566:PHE:CE1	2.33	0.63
1:F:154:ASP:HB3	1:F:156:LYS:HE2	1.79	0.63
2:G:118:SER:OG	2:G:119:ASN:N	2.31	0.63
2:G:211:LYS:HG3	2:G:238:GLU:HG2	1.81	0.63
2:B:189:HIS:HD2	2:B:212:ASP:OD2	1.81	0.62
1:K:10:LYS:HG2	1:K:11:GLY:H	1.64	0.62
1:Q:456:ARG:NH2	3:S:679:THR:OG1	2.32	0.62
2:B:88:LEU:CD1	2:B:434:ILE:HD12	2.29	0.62
1:F:19:VAL:HG22	1:F:178:LEU:HD21	1.80	0.62
1:A:339:THR:OG1	1:A:449:ASP:OD2	2.17	0.62
1:F:128:LEU:HD21	1:F:157:VAL:HG12	1.80	0.62
1:K:104:VAL:O	2:L:169:ARG:NH2	2.32	0.62
1:Q:23:TYR:CZ	1:Q:27:ARG:HD2	2.34	0.62
1:Q:432:TRP:HH2	1:Q:461:LYS:HG3	0.74	0.62
2:B:104:HIS:NE2	2:B:153:THR:HA	2.14	0.62
1:K:436:GLU:OE2	1:K:460:THR:OG1	2.17	0.62
1:Q:726:TYR:CD1	4:T:27:MET:HG2	2.35	0.62
1:A:430:VAL:HG21	1:A:465:GLN:NE2	2.04	0.62
1:K:515:ASN:HA	1:K:671:ASN:HD21	1.65	0.62
2:R:189:HIS:NE2	2:R:208:SER:OG	2.33	0.62
1:F:430:VAL:HG21	1:F:465:GLN:NE2	2.14	0.62
2:L:197:LYS:NZ	2:L:242:ALA:O	2.33	0.62
2:R:86:ASN:HD22	2:R:87:SER:H	1.46	0.62
1:A:136:ASP:OD2	5:E:7:M3L:N	2.32	0.62
3:C:616:LEU:HD22	3:C:643:TYR:HD2	1.64	0.62
1:Q:150:ILE:CG2	1:Q:155:GLY:HA2	2.30	0.62
2:R:264:ARG:NH2	2:R:340:ILE:O	2.31	0.62
1:Q:139:LEU:HG	1:Q:140:ASP:HA	1.81	0.61
1:K:597:LYS:HD3	1:K:608:ARG:HB3	1.82	0.61
2:R:207:LEU:HD22	2:R:251:ILE:HD13	1.82	0.61
1:A:324:CYS:SG	1:A:325:TYR:N	2.72	0.61
3:C:596:THR:OG1	3:C:622:MET:HE1	2.00	0.61
2:G:232:VAL:HG22	2:G:295:HIS:HB3	1.83	0.61
2:L:170:GLY:HA2	2:L:193:ILE:HG13	1.83	0.61
1:Q:128:LEU:H	1:Q:128:LEU:HD23	1.65	0.61
1:Q:432:TRP:HZ3	1:Q:461:LYS:HZ2	1.46	0.61
2:R:209:VAL:HG13	2:R:239:VAL:HB	1.81	0.61
3:H:607:ASN:O	3:H:611:LYS:N	2.28	0.61
1:A:161:ARG:HH11	1:A:164:GLY:C	2.08	0.61
1:A:291:LYS:HG2	3:C:621:VAL:HG21	1.81	0.61
2:G:118:SER:O	2:G:146:ASN:HA	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:427:PRO:HA	1:K:464:ARG:NH2	2.14	0.61
1:Q:640:GLU:OE1	1:Q:707:ARG:HD3	2.01	0.61
1:F:16:ARG:HG3	1:F:17:LYS:N	2.14	0.61
1:F:730:GLN:HE21	1:F:731:ALA:H	1.46	0.61
1:K:220:SER:O	1:K:223:ILE:HG13	2.00	0.61
1:K:308:ARG:HG2	1:K:309:LYS:H	1.65	0.61
1:K:96:ILE:HG13	2:L:134:LEU:HG	1.83	0.61
1:Q:137:GLU:N	1:Q:139:LEU:HD13	2.16	0.61
2:G:207:LEU:HD22	2:G:251:ILE:HD13	1.83	0.61
2:L:232:VAL:HG12	2:L:295:HIS:HB3	1.82	0.61
2:R:150:CYS:HA	2:R:164:ALA:O	2.01	0.61
3:S:580:GLU:OE1	3:S:580:GLU:N	2.34	0.61
3:C:579:MET:HG3	3:C:581:VAL:HG12	1.83	0.60
2:L:189:HIS:CE1	2:L:216:ARG:HG3	2.35	0.60
2:R:215:LEU:HB2	2:R:229:PHE:HB2	1.82	0.60
2:R:288:PRO:HB3	3:S:578:GLU:OE2	2.00	0.60
3:C:604:SER:O	3:C:605:ASP:OD1	2.19	0.60
1:K:308:ARG:HG3	3:M:667:ASN:ND2	2.16	0.60
1:K:437:ALA:HB1	1:K:441:ARG:NH1	2.17	0.60
1:A:330:GLY:CA	1:A:334:PHE:HB2	2.32	0.60
1:F:318:LYS:HG2	1:F:319:PRO:HA	1.84	0.60
1:K:117:GLN:HA	1:K:117:GLN:NE2	2.09	0.60
1:Q:432:TRP:CH2	1:Q:461:LYS:CG	2.59	0.60
1:Q:515:ASN:HA	1:Q:671:ASN:HD21	1.67	0.60
1:A:330:GLY:HA2	1:A:334:PHE:HB2	1.83	0.60
1:K:10:LYS:C	1:K:12:PRO:HD2	2.26	0.60
1:Q:328:LEU:HD22	1:Q:330:GLY:H	1.66	0.60
1:A:23:TYR:OH	1:A:165:PHE:O	2.13	0.60
1:A:128:LEU:HD21	1:A:157:VAL:HG22	1.82	0.60
2:B:215:LEU:HB2	2:B:229:PHE:HB2	1.83	0.60
1:F:306:TYR:O	3:H:665:ASP:HB3	2.01	0.60
2:L:358:TYR:HE1	2:L:361:CYS:HB3	1.66	0.60
2:R:215:LEU:HD11	2:R:239:VAL:HG11	1.83	0.60
1:K:515:ASN:HA	1:K:671:ASN:ND2	2.17	0.60
1:Q:270:LYS:C	1:Q:272:VAL:HG23	2.26	0.60
2:R:161:PRO:O	2:R:177:PRO:HD2	2.01	0.60
1:A:161:ARG:NH2	1:A:231:PHE:CE2	2.70	0.59
2:B:386:LEU:HD11	2:B:427:ALA:HB2	1.84	0.59
2:L:306:ARG:N	2:L:325:GLU:OE2	2.33	0.59
2:B:125:GLU:CB	2:B:135:LEU:HD21	2.32	0.59
1:Q:270:LYS:O	1:Q:272:VAL:HG23	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:ASP:O	1:A:172:VAL:HG23	2.02	0.59
2:G:395:ASP:OD1	2:G:398:LYS:HG3	2.02	0.59
1:K:11:GLY:N	1:K:12:PRO:HD2	2.17	0.59
1:Q:426:PRO:O	1:Q:464:ARG:NH2	2.35	0.59
1:Q:440:PHE:CZ	1:Q:444:ILE:HG21	2.38	0.59
1:A:655:GLY:HA3	4:D:24:ALA:HB1	1.83	0.59
1:F:130:ASN:ND2	2:G:237:ASP:OD2	2.34	0.59
2:G:232:VAL:HG11	3:H:591:TRP:CE3	2.37	0.59
1:Q:728:TYR:HB3	1:Q:730:GLN:HB2	1.83	0.59
1:A:101:LEU:N	2:B:139:VAL:O	2.24	0.59
2:B:322:LYS:HD3	2:B:366:MET:O	2.02	0.59
1:Q:67:PRO:HG3	2:R:109:ASP:CG	2.28	0.59
1:Q:614:LEU:HB3	1:Q:626:ILE:HD11	1.84	0.59
3:C:628:ALA:HB3	3:C:631:GLN:HG3	1.84	0.59
1:F:140:ASP:N	1:F:141:GLN:HA	2.18	0.59
1:A:263:ASN:ND2	1:A:265:ASP:H	2.01	0.59
1:A:284:LEU:O	1:A:284:LEU:HD23	2.03	0.59
1:Q:236:THR:OG1	1:Q:239:GLU:HB3	2.02	0.59
1:K:67:PRO:HB3	2:L:161:PRO:HG2	1.85	0.59
1:Q:161:ARG:NH2	1:Q:233:ASP:OD2	2.35	0.59
2:B:400:LYS:HD2	2:B:401:CYS:H	1.68	0.59
3:C:588:ASP:OD2	3:C:593:ARG:NH1	2.35	0.59
1:K:41:MET:HG3	2:L:336:MET:HE2	1.84	0.59
1:Q:22:GLU:HG3	1:Q:178:LEU:HD23	1.85	0.59
1:A:33:ARG:HG2	1:A:33:ARG:O	2.03	0.59
2:B:170:GLY:HA2	2:B:193:ILE:HD12	1.85	0.59
1:Q:172:VAL:O	1:Q:175:VAL:HG22	2.03	0.59
3:C:618:ASN:HB3	3:C:622:MET:HE3	1.85	0.58
1:K:67:PRO:CB	1:K:68:VAL:HG23	2.32	0.58
1:K:171:PHE:O	1:K:175:VAL:HG22	2.03	0.58
3:M:607:ASN:O	3:M:611:LYS:HG3	2.02	0.58
1:Q:590:ALA:O	1:Q:608:ARG:NH2	2.35	0.58
1:A:272:VAL:HG12	1:A:276:GLN:HB2	1.85	0.58
1:F:22:GLU:OE2	1:F:177:ALA:HB1	2.03	0.58
1:F:629:LYS:O	1:F:718:THR:HG23	2.03	0.58
1:K:68:VAL:HG12	1:K:69:HIS:N	2.17	0.58
1:Q:563:LYS:HA	1:Q:588:CYS:HA	1.84	0.58
1:K:728:TYR:HB3	1:K:730:GLN:CB	2.34	0.58
2:R:396:PRO:HD2	2:R:397:HIS:CD2	2.36	0.58
1:F:128:LEU:CD2	1:F:157:VAL:HG12	2.33	0.58
1:F:144:THR:HG22	1:F:148:GLU:HG3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:617:ALA:HB3	1:F:627:PHE:CE1	2.38	0.58
2:L:86:ASN:HD22	2:L:87:SER:H	1.50	0.58
1:Q:75:SER:OG	1:Q:76:SER:N	2.37	0.58
2:B:390:ASP:HB3	2:B:393:VAL:HG23	1.84	0.58
1:F:109:ILE:HD12	1:F:109:ILE:H	1.68	0.58
1:F:150:ILE:CG2	1:F:155:GLY:HA2	2.33	0.58
3:H:605:ASP:OD1	3:H:605:ASP:N	2.36	0.58
1:Q:665:PHE:HD2	1:Q:678:THR:HG22	1.67	0.58
1:A:68:VAL:HG23	2:B:112:VAL:CG2	2.34	0.58
1:A:101:LEU:HB2	2:B:140:ASP:HA	1.85	0.58
3:M:579:MET:O	3:M:581:VAL:HG12	2.03	0.58
1:Q:264:ILE:O	1:Q:435:ALA:HB2	2.03	0.58
1:F:265:ASP:OD1	3:H:654:ARG:HB2	2.03	0.58
1:F:302:THR:HG1	1:F:305:THR:H	1.52	0.58
1:K:13:VAL:O	1:K:17:LYS:HG2	2.04	0.58
1:A:63:ARG:NE	2:B:154:TYR:OH	2.32	0.58
1:A:91:PHE:CD1	1:A:92:PRO:HD2	2.39	0.58
1:A:320:CYS:HB3	1:A:321:GLY:HA2	1.85	0.58
1:F:77:LEU:O	1:F:78:ARG:HB3	2.03	0.58
3:M:577:GLN:OE1	3:M:577:GLN:N	2.27	0.58
1:Q:284:LEU:HD12	3:S:614:MET:HE1	1.85	0.58
2:B:199:HIS:CE1	2:B:248:GLY:HA3	2.39	0.57
2:B:145:GLU:OE2	2:B:169:ARG:HB2	2.04	0.57
3:C:561:HIS:HB2	3:C:562:ASN:HA	1.86	0.57
1:F:677:ALA:O	1:F:685:ARG:NH2	2.38	0.57
2:G:237:ASP:HB3	2:G:256:MET:HB2	1.86	0.57
2:B:318:LEU:HD13	2:B:353:LEU:HD12	1.86	0.57
1:F:42:PHE:HB3	2:G:393:VAL:CB	2.31	0.57
1:F:304:ASN:HB2	1:F:524:ASP:OD2	2.04	0.57
1:F:324:CYS:HA	1:F:463:CYS:HB3	1.85	0.57
2:L:136:GLN:NE2	2:L:180:MET:HG2	2.20	0.57
3:S:575:ARG:N	3:S:578:GLU:OE1	2.35	0.57
2:R:260:LEU:HD21	2:R:309:VAL:HG11	1.86	0.57
1:A:20:LYS:HE2	1:A:24:MET:HE2	1.86	0.57
1:A:23:TYR:CZ	1:A:27:ARG:HD2	2.40	0.57
1:A:734:LEU:HB3	7:A:1009:SAH:N1	2.20	0.57
1:F:324:CYS:SG	1:F:325:TYR:N	2.78	0.57
2:L:288:PRO:HG3	3:M:567:HIS:HE1	1.69	0.57
1:Q:339:THR:O	1:Q:343:ILE:HG13	2.05	0.57
1:F:133:TYR:HH	1:F:136:ASP:HB2	1.70	0.57
2:G:285:THR:OG1	2:G:287:ARG:HG2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:121:MET:HE1	1:Q:673:PHE:CE1	2.39	0.57
1:F:128:LEU:HB3	1:F:153:TYR:CE2	2.39	0.57
1:A:65:ILE:HG22	2:B:161:PRO:HG3	1.87	0.57
1:A:732:ASP:N	1:A:733:ALA:HA	2.20	0.57
1:K:168:ASP:O	1:K:172:VAL:HG23	2.05	0.57
1:K:645:ILE:HG22	1:K:675:VAL:HG22	1.86	0.57
2:B:194:ASN:ND2	2:B:240:LEU:HD23	2.19	0.57
1:Q:629:LYS:O	1:Q:718:THR:HG23	2.05	0.57
1:A:629:LYS:O	1:A:718:THR:HG23	2.05	0.56
2:B:118:SER:OG	2:B:119:ASN:N	2.37	0.56
1:F:284:LEU:CD2	1:F:292:TYR:HB3	2.35	0.56
2:G:194:ASN:ND2	2:G:240:LEU:HD23	2.19	0.56
1:K:317:ASN:ND2	1:K:332:LYS:HD2	2.20	0.56
1:Q:728:TYR:CE1	4:T:25:ALA:HB1	2.39	0.56
3:S:645:GLN:NE2	3:S:649:LYS:HE2	2.16	0.56
2:L:80:TYR:O	2:L:402:THR:HG21	2.05	0.56
1:A:85:VAL:HG23	2:B:134:LEU:HD22	1.86	0.56
1:A:439:MET:HE2	3:C:657:MET:SD	2.45	0.56
1:K:20:LYS:O	1:K:24:MET:HG2	2.05	0.56
3:M:585:ASP:CB	3:M:586:GLU:HB3	2.35	0.56
1:Q:303:PRO:HB2	1:Q:306:TYR:CZ	2.39	0.56
1:A:320:CYS:HB3	1:A:324:CYS:HB2	1.86	0.56
1:A:650:GLU:OE1	1:A:653:ARG:NH1	2.39	0.56
1:F:531:ASP:C	1:F:531:ASP:OD1	2.49	0.56
1:Q:582:PRO:CB	1:Q:594:TRP:HH2	2.18	0.56
2:B:211:LYS:HG3	2:B:238:GLU:CD	2.30	0.56
3:H:580:GLU:CB	3:H:581:VAL:HA	2.31	0.56
1:K:319:PRO:HA	1:K:320:CYS:HB3	1.87	0.56
1:Q:279:HIS:O	1:Q:283:THR:HG22	2.05	0.56
1:Q:146:ILE:O	1:Q:150:ILE:HG12	2.06	0.56
2:R:230:GLY:O	2:R:293:LYS:HE2	2.05	0.56
1:F:41:MET:HG3	2:G:336:MET:HE2	1.88	0.56
1:F:98:LEU:HB3	2:G:139:VAL:CG2	2.36	0.56
1:F:104:VAL:O	2:G:169:ARG:NH2	2.37	0.56
1:F:125:GLU:HG2	1:F:650:GLU:OE2	2.05	0.56
1:F:339:THR:O	1:F:343:ILE:HG12	2.05	0.56
2:R:404:LEU:HB3	2:R:437:TRP:CZ3	2.41	0.56
1:K:26:LEU:HD22	1:K:173:GLU:OE2	2.06	0.56
1:K:263:ASN:HB3	3:M:607:ASN:HD21	1.70	0.56
3:M:577:GLN:H	3:M:577:GLN:CD	2.14	0.56
1:Q:545:LYS:HD3	1:Q:581:ASP:OD2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:ASN:HD21	3:C:655:ASN:ND2	2.00	0.56
1:A:621:VAL:HG13	1:A:736:TYR:CD1	2.40	0.56
1:A:91:PHE:CG	1:A:92:PRO:HD2	2.41	0.55
2:B:323:SER:C	2:B:325:GLU:H	2.14	0.55
2:B:331:TRP:HB3	2:B:352:ILE:HD13	1.87	0.55
2:L:95:PRO:HB3	2:L:430:ASP:HA	1.88	0.55
1:Q:219:PRO:HD2	1:Q:244:TYR:HE2	1.71	0.55
1:Q:665:PHE:HB2	1:Q:678:THR:HG23	1.89	0.55
1:A:579:GLU:HG3	1:A:702:VAL:HG22	1.87	0.55
1:A:689:HIS:HD2	1:A:726:TYR:H	1.55	0.55
1:K:312:GLU:N	1:K:312:GLU:OE1	2.38	0.55
2:R:260:LEU:HD13	2:R:331:TRP:CZ2	2.41	0.55
1:K:640:GLU:OE1	1:K:707:ARG:HD3	2.07	0.55
1:A:129:HIS:H	1:A:129:HIS:CD2	2.24	0.55
1:K:464:ARG:NH1	1:K:468:GLU:HB2	2.22	0.55
2:L:215:LEU:HB2	2:L:229:PHE:HB2	1.86	0.55
2:L:287:ARG:O	2:L:287:ARG:HG3	2.07	0.55
1:Q:316:ASP:HB3	1:Q:332:LYS:HE2	1.88	0.55
2:R:307:ASN:HD21	5:U:5:GLN:CG	2.19	0.55
1:A:104:VAL:HG11	2:B:171:ILE:HG21	1.89	0.55
1:A:624:TRP:N	7:A:1009:SAH:OXT	2.40	0.55
1:F:728:TYR:HB3	1:F:730:GLN:CB	2.36	0.55
1:Q:730:GLN:NE2	1:Q:732:ASP:H	2.05	0.55
3:S:597:ILE:HG23	3:S:615:LYS:HD2	1.89	0.55
1:Q:324:CYS:SG	1:Q:325:TYR:N	2.79	0.55
1:Q:325:TYR:HE1	1:Q:463:CYS:SG	2.29	0.55
1:A:28:GLN:HB3	1:A:32:PHE:CE2	2.41	0.55
1:A:167:ASN:HD21	2:B:350:VAL:H	1.53	0.55
1:K:460:THR:O	1:K:461:LYS:HD2	2.07	0.55
3:M:651:ASN:O	3:M:651:ASN:ND2	2.40	0.55
1:Q:139:LEU:CD1	1:Q:140:ASP:HA	2.35	0.55
1:Q:168:ASP:HB2	2:R:349:ASN:ND2	2.21	0.55
1:Q:323:GLN:HG2	1:Q:462:THR:CB	2.37	0.55
2:B:280:TYR:OH	3:C:575:ARG:NH2	2.40	0.55
1:Q:606:ILE:CG2	1:Q:707:ARG:HD2	2.37	0.55
1:A:85:VAL:HG11	2:B:88:LEU:HD13	1.88	0.55
2:B:82:PHE:HA	2:B:438:ASP:O	2.06	0.55
1:F:82:GLU:HG2	1:F:97:PRO:CA	2.37	0.55
2:G:211:LYS:HD2	2:G:238:GLU:CD	2.32	0.55
1:Q:339:THR:HG21	1:Q:449:ASP:OD2	2.06	0.55
1:A:728:TYR:HB3	1:A:730:GLN:CB	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:646:LYS:O	3:C:650:LYS:HG3	2.07	0.55
2:G:132:ILE:HD11	2:G:436:ARG:HB2	1.88	0.55
1:K:175:VAL:HG21	1:K:244:TYR:CD2	2.42	0.55
1:Q:130:ASN:OD1	2:R:257:ASP:HA	2.07	0.55
1:K:648:GLN:HE22	4:O:26:ARG:NH1	2.05	0.54
1:K:655:GLY:HA3	4:O:24:ALA:CB	2.36	0.54
1:Q:730:GLN:HG3	1:Q:731:ALA:N	2.22	0.54
2:R:148:TYR:HB3	2:R:365:TYR:OH	2.07	0.54
2:R:307:ASN:ND2	2:R:308:TYR:H	2.05	0.54
2:L:331:TRP:HB3	2:L:352:ILE:HD13	1.88	0.54
2:L:395:ASP:OD2	2:L:399:ALA:N	2.40	0.54
2:R:397:HIS:ND1	2:R:398:LYS:HG3	2.22	0.54
1:A:641:TYR:HB3	1:A:708:ILE:HB	1.90	0.54
2:G:125:GLU:HB2	2:G:135:LEU:HD21	1.89	0.54
1:A:263:ASN:HD22	1:A:264:ILE:N	2.06	0.54
2:B:315:LEU:HD13	2:B:370:MET:HE1	1.89	0.54
2:G:186:TYR:HE2	2:G:220:ILE:HG22	1.71	0.54
1:K:548:GLN:OE1	1:K:548:GLN:HA	2.06	0.54
1:A:39:LYS:HE3	2:B:394:GLU:HB3	1.89	0.54
1:K:302:THR:N	1:K:303:PRO:HA	2.23	0.54
1:A:326:GLN:HB2	1:A:327:HIS:HB3	1.88	0.54
2:B:396:PRO:HA	2:B:397:HIS:CG	2.42	0.54
1:Q:541:ASN:ND2	1:Q:701:MET:HE3	2.17	0.54
3:C:569:ASP:OD1	3:C:569:ASP:N	2.40	0.54
1:Q:431:GLU:O	1:Q:432:TRP:HE3	1.91	0.54
1:Q:728:TYR:HE1	4:T:25:ALA:HB1	1.72	0.54
2:G:88:LEU:HD12	2:G:434:ILE:HB	1.88	0.54
1:Q:224:PHE:HZ	1:Q:244:TYR:CB	2.21	0.54
1:A:272:VAL:CG1	1:A:276:GLN:HB2	2.38	0.54
1:Q:582:PRO:HB3	1:Q:594:TRP:HH2	1.73	0.54
1:A:68:VAL:HG21	2:B:110:PRO:CG	2.35	0.53
1:A:101:LEU:O	2:B:141:ALA:N	2.41	0.53
1:F:67:PRO:HB3	2:G:109:ASP:OD2	2.07	0.53
2:L:230:GLY:O	2:L:293:LYS:HE2	2.08	0.53
2:L:326:ASN:HA	2:L:358:TYR:CE1	2.43	0.53
2:B:422:SER:HB2	2:B:439:ARG:HH11	1.74	0.53
1:A:131:ILE:HG21	5:E:4:ALA:HB2	1.90	0.53
1:A:427:PRO:HA	1:A:464:ARG:HH12	1.74	0.53
1:A:694:ASN:HB3	1:A:714:ARG:HH21	1.72	0.53
1:F:63:ARG:HD3	2:G:154:TYR:CZ	2.43	0.53
2:G:395:ASP:OD2	2:G:398:LYS:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:169:GLU:OE2	2:L:335:LYS:HG2	2.09	0.53
1:K:308:ARG:HG3	3:M:667:ASN:HD21	1.73	0.53
1:Q:119:ASN:HB3	1:Q:645:ILE:HG13	1.90	0.53
1:A:29:LEU:HA	1:A:32:PHE:HD2	1.73	0.53
2:B:140:ASP:OD2	2:B:173:ARG:NE	2.42	0.53
1:F:531:ASP:OD1	1:F:533:SER:N	2.37	0.53
1:K:263:ASN:CB	3:M:607:ASN:HD21	2.21	0.53
1:A:52:ARG:HD3	2:B:247:LEU:HG	1.91	0.53
2:B:211:LYS:HG3	2:B:238:GLU:HG2	1.91	0.53
1:K:96:ILE:HG22	1:K:97:PRO:O	2.08	0.53
1:K:580:CYS:O	1:K:607:GLN:NE2	2.41	0.53
1:K:689:HIS:CD2	1:K:726:TYR:H	2.20	0.53
1:Q:161:ARG:HG3	2:R:306:ARG:HH11	1.74	0.53
1:Q:728:TYR:CB	1:Q:730:GLN:HB2	2.39	0.53
1:A:562:CYS:SG	1:A:566:CYS:HB3	2.49	0.53
1:A:728:TYR:HB3	1:A:730:GLN:HB2	1.90	0.53
2:B:358:TYR:HE1	2:B:361:CYS:HB3	1.73	0.53
1:F:102:ASN:O	2:G:173:ARG:NH2	2.36	0.53
1:Q:515:ASN:HA	1:Q:671:ASN:ND2	2.22	0.53
2:R:339:ASP:OD1	2:R:341:ASP:N	2.42	0.53
1:K:338:LEU:O	1:K:342:ARG:HB2	2.09	0.53
1:Q:129:HIS:H	1:Q:129:HIS:HD2	1.55	0.53
1:Q:726:TYR:HD1	4:T:27:MET:HG2	1.74	0.53
1:A:460:THR:O	1:A:461:LYS:HD2	2.09	0.53
1:A:582:PRO:HB2	3:C:628:ALA:HB2	1.90	0.53
1:Q:161:ARG:HG3	2:R:306:ARG:NH1	2.24	0.53
1:Q:171:PHE:O	1:Q:175:VAL:HG13	2.08	0.53
1:F:728:TYR:HB3	1:F:730:GLN:HB2	1.91	0.53
1:K:728:TYR:HB3	1:K:730:GLN:HB2	1.91	0.53
1:A:35:ALA:HA	1:A:38:VAL:HG22	1.91	0.52
2:G:385:LYS:HE2	2:G:403:THR:HB	1.90	0.52
3:C:579:MET:HA	3:C:580:GLU:C	2.35	0.52
1:K:542:PHE:HB3	1:K:555:ASN:O	2.10	0.52
2:B:389:TRP:CD1	2:B:401:CYS:HB2	2.44	0.52
1:F:175:VAL:CG2	1:F:244:TYR:HE2	2.21	0.52
1:F:303:PRO:HB2	1:F:306:TYR:CZ	2.44	0.52
1:Q:98:LEU:HD22	2:R:139:VAL:HG23	1.91	0.52
1:Q:171:PHE:HZ	1:Q:224:PHE:HE2	1.57	0.52
1:Q:451:PHE:HD2	1:Q:466:VAL:HG12	1.74	0.52
1:A:688:ASN:OD1	7:A:1009:SAH:N	2.39	0.52
1:Q:67:PRO:HG3	2:R:109:ASP:OD2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:ASN:HB2	1:A:524:ASP:OD2	2.09	0.52
1:A:617:ALA:HB3	1:A:627:PHE:CE1	2.45	0.52
2:G:148:TYR:HB3	2:G:365:TYR:OH	2.09	0.52
1:K:89:LEU:HD12	1:K:91:PHE:N	2.24	0.52
1:K:342:ARG:HD2	1:K:470:ARG:HH22	1.74	0.52
2:L:404:LEU:HB3	2:L:437:TRP:CZ3	2.43	0.52
2:R:191:ASN:HB3	2:R:211:LYS:HB3	1.92	0.52
1:F:730:GLN:HG3	1:F:731:ALA:N	2.25	0.52
1:Q:74:VAL:HB	1:Q:75:SER:O	2.10	0.52
2:R:145:GLU:OE1	2:R:169:ARG:HB2	2.09	0.52
2:R:204:ASN:O	2:R:220:ILE:HG12	2.10	0.52
2:B:197:LYS:O	2:B:206:LEU:HD12	2.09	0.52
3:M:585:ASP:HB3	3:M:586:GLU:HB3	1.92	0.52
2:R:94:GLN:HB2	2:R:118:SER:HB2	1.91	0.52
1:K:150:ILE:HG22	1:K:155:GLY:HA2	1.92	0.52
1:K:582:PRO:CB	1:K:594:TRP:HH2	2.22	0.52
2:R:414:ARG:NH1	5:U:8:PHE:CD1	2.78	0.52
1:A:231:PHE:HB3	1:A:234:LYS:HG2	1.92	0.51
1:A:322:PRO:HB2	1:F:58:GLN:HB3	1.91	0.51
1:K:175:VAL:HG21	1:K:244:TYR:HD2	1.75	0.51
2:L:88:LEU:O	2:L:434:ILE:N	2.39	0.51
1:Q:128:LEU:HD23	1:Q:128:LEU:N	2.22	0.51
1:K:119:ASN:HB3	1:K:645:ILE:HG23	1.93	0.51
2:B:106:LYS:O	2:B:109:ASP:HB2	2.09	0.51
2:B:389:TRP:NE1	2:B:401:CYS:HB2	2.26	0.51
3:C:586:GLU:HB3	3:C:587:LYS:HB2	1.93	0.51
1:F:629:LYS:NZ	3:H:581:VAL:O	2.43	0.51
1:Q:462:THR:O	1:Q:466:VAL:HG23	2.10	0.51
5:U:6:ARG:HH11	5:U:10:GLN:NE2	2.07	0.51
2:G:262:LEU:HB3	2:G:299:PHE:HB3	1.92	0.51
2:G:315:LEU:HD13	2:G:370:MET:HE1	1.93	0.51
1:K:306:TYR:O	3:M:665:ASP:HB3	2.10	0.51
1:Q:539:ALA:O	1:Q:540:GLN:HB2	2.09	0.51
3:C:570:THR:CG2	3:C:572:LEU:HD13	2.39	0.51
2:G:194:ASN:HD22	2:G:240:LEU:HA	1.74	0.51
1:Q:70:ILE:CG2	2:R:135:LEU:HD22	2.40	0.51
2:B:237:ASP:HB3	2:B:256:MET:HB2	1.92	0.51
1:F:67:PRO:HG2	1:F:69:HIS:CE1	2.46	0.51
1:F:117:GLN:HA	1:F:117:GLN:NE2	2.26	0.51
2:G:238:GLU:HB2	2:G:256:MET:HG3	1.92	0.51
1:K:20:LYS:HG2	1:K:24:MET:HE2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:134:MET:H	1:Q:135:GLY:HA3	1.75	0.51
1:A:161:ARG:NH1	1:A:164:GLY:C	2.68	0.51
2:G:199:HIS:HB2	2:G:205:LEU:HB2	1.92	0.51
2:B:225:LEU:HD23	3:C:570:THR:CG2	2.39	0.51
1:F:175:VAL:HG21	1:F:244:TYR:CD2	2.46	0.51
2:G:102:ASN:HB2	2:G:152:TRP:CE2	2.46	0.51
1:K:67:PRO:HB3	2:L:161:PRO:CG	2.40	0.51
1:K:691:VAL:O	1:K:693:PRO:HD3	2.11	0.51
1:A:528:GLN:OE1	1:A:528:GLN:N	2.38	0.51
1:K:71:LEU:HD12	1:K:73:SER:HB2	1.93	0.51
3:M:607:ASN:OD1	3:M:608:GLU:N	2.43	0.51
1:A:230:MET:HB2	1:A:231:PHE:CD1	2.46	0.51
1:A:615:LEU:HD21	3:C:581:VAL:CG1	2.42	0.51
1:F:129:HIS:HA	1:F:158:HIS:HB3	1.93	0.51
1:F:302:THR:HG1	1:F:305:THR:N	2.07	0.51
1:K:127:VAL:HG12	1:K:156:LYS:CB	2.41	0.51
1:Q:49:ILE:HG12	2:R:316:GLY:HA3	1.93	0.51
1:Q:469:PHE:CE1	1:Q:473:GLU:OE2	2.64	0.51
1:A:264:ILE:HD12	3:C:658:LEU:HD11	1.92	0.50
1:A:340:ALA:O	1:A:343:ILE:HG22	2.12	0.50
1:F:125:GLU:OE1	2:G:236:ARG:NH2	2.44	0.50
2:G:186:TYR:CE2	2:G:220:ILE:HG22	2.46	0.50
1:K:130:ASN:OD1	2:L:257:ASP:HA	2.11	0.50
1:K:462:THR:OG1	1:K:465:GLN:OE1	2.11	0.50
3:M:576:PRO:HG2	3:M:577:GLN:OE1	2.12	0.50
1:Q:242:GLU:O	1:Q:246:GLU:HG3	2.10	0.50
1:A:241:LYS:O	1:A:245:LYS:HG3	2.11	0.50
1:A:694:ASN:HB3	1:A:714:ARG:NH2	2.25	0.50
1:K:618:PRO:HD3	3:M:566:PHE:HE1	1.74	0.50
1:Q:565:GLN:HG3	1:Q:567:ASN:OD1	2.10	0.50
1:Q:580:CYS:O	1:Q:607:GLN:NE2	2.44	0.50
2:R:145:GLU:HB2	2:R:169:ARG:HD3	1.93	0.50
1:A:161:ARG:NH1	1:A:165:PHE:N	2.59	0.50
1:A:665:PHE:HB3	1:A:677:ALA:HB3	1.94	0.50
1:K:129:HIS:H	1:K:129:HIS:CD2	2.29	0.50
2:L:127:HIS:HB2	2:L:131:GLU:CG	2.42	0.50
1:Q:224:PHE:CZ	1:Q:244:TYR:CB	2.94	0.50
1:Q:579:GLU:HG3	1:Q:702:VAL:HG22	1.93	0.50
1:Q:621:VAL:HG21	1:Q:737:VAL:HG22	1.94	0.50
1:Q:736:TYR:OH	1:Q:739:ILE:O	2.26	0.50
1:A:464:ARG:NH1	1:A:468:GLU:OE2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:404:LEU:HB2	2:B:437:TRP:CZ3	2.46	0.50
1:F:302:THR:N	1:F:303:PRO:HA	2.26	0.50
1:K:121:MET:HA	1:K:645:ILE:HG13	1.93	0.50
1:K:138:VAL:HB	1:K:141:GLN:HG2	1.94	0.50
1:K:552:GLU:O	1:K:552:GLU:HG3	2.11	0.50
1:Q:20:LYS:O	1:Q:24:MET:HG2	2.11	0.50
1:Q:219:PRO:HD2	1:Q:244:TYR:CE2	2.46	0.50
1:Q:284:LEU:HD11	3:S:606:VAL:HG21	1.93	0.50
2:R:86:ASN:HD22	2:R:87:SER:N	2.09	0.50
2:R:288:PRO:HD3	3:S:578:GLU:HG2	1.93	0.50
3:C:607:ASN:O	3:C:611:LYS:HG3	2.12	0.50
1:K:449:ASP:HA	1:K:451:PHE:CE1	2.46	0.50
3:M:569:ASP:OD1	3:M:569:ASP:N	2.45	0.50
3:M:607:ASN:HB3	3:M:610:GLU:HB2	1.94	0.50
2:B:95:PRO:HB3	2:B:430:ASP:HA	1.92	0.50
2:B:136:GLN:NE2	2:B:180:MET:HE2	2.26	0.50
1:F:303:PRO:HB2	1:F:306:TYR:CE2	2.46	0.50
1:F:592:ASP:HB3	1:F:593:HIS:ND1	2.26	0.50
1:F:691:VAL:O	1:F:693:PRO:HD3	2.12	0.50
2:G:120:ARG:HE	2:G:139:VAL:HG13	1.77	0.50
1:K:726:TYR:O	4:O:27:MET:HA	2.12	0.50
1:A:19:VAL:HG22	1:A:178:LEU:CD2	2.42	0.50
1:A:161:ARG:HH11	1:A:164:GLY:CA	2.23	0.50
1:A:263:ASN:CG	3:C:607:ASN:HD21	2.19	0.50
1:F:640:GLU:OE1	1:F:707:ARG:HD2	2.11	0.50
2:G:120:ARG:HG2	2:G:139:VAL:HG13	1.93	0.50
2:G:229:PHE:HD2	2:G:263:TRP:CE3	2.30	0.50
3:H:621:VAL:HG12	3:H:626:PHE:HD2	1.76	0.50
1:A:70:ILE:HG13	2:B:135:LEU:HB3	1.93	0.50
1:A:212:SER:HB2	1:A:213:ARG:CG	2.42	0.50
1:F:314:ALA:H	1:F:315:LEU:HD12	1.77	0.50
2:L:82:PHE:CZ	2:L:376:MET:HE1	2.33	0.50
2:L:94:GLN:HB2	2:L:118:SER:HB2	1.94	0.50
2:R:262:LEU:HB3	2:R:299:PHE:HB3	1.92	0.50
1:A:308:ARG:NH1	3:C:667:ASN:HA	2.27	0.49
1:A:652:ASP:OD1	4:D:26:ARG:NH2	2.45	0.49
1:F:89:LEU:HD11	1:F:91:PHE:CD1	2.47	0.49
2:G:150:CYS:HA	2:G:164:ALA:O	2.12	0.49
2:G:364:TRP:CE3	2:G:365:TYR:HB2	2.47	0.49
1:Q:12:PRO:O	1:Q:15:TRP:N	2.43	0.49
1:Q:23:TYR:CE1	1:Q:27:ARG:HD2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:81:SER:HB2	2:R:440:LEU:HD11	1.93	0.49
1:A:11:GLY:HA3	1:A:14:CYS:SG	2.52	0.49
1:A:428:GLU:N	1:A:468:GLU:OE2	2.36	0.49
3:C:586:GLU:CB	3:C:587:LYS:HB2	2.42	0.49
3:C:607:ASN:HB3	3:C:610:GLU:CG	2.41	0.49
1:F:432:TRP:CH2	1:F:461:LYS:HG2	2.47	0.49
3:H:603:PHE:O	3:H:611:LYS:NZ	2.39	0.49
1:A:168:ASP:OD2	2:B:348:SER:HB3	2.11	0.49
1:F:161:ARG:HB3	1:F:232:PRO:HD2	1.93	0.49
1:Q:34:ARG:O	1:Q:37:GLU:N	2.44	0.49
1:Q:303:PRO:HB2	1:Q:306:TYR:OH	2.12	0.49
2:R:158:THR:HB	2:R:160:HIS:CE1	2.47	0.49
2:R:257:ASP:OD1	2:R:257:ASP:N	2.44	0.49
3:S:605:ASP:OD1	3:S:605:ASP:N	2.36	0.49
1:A:148:GLU:HG3	1:A:656:LYS:HE2	1.94	0.49
3:C:627:ILE:H	3:C:631:GLN:NE2	2.10	0.49
1:F:319:PRO:HB2	1:F:321:GLY:HA3	1.94	0.49
1:Q:139:LEU:CG	1:Q:140:ASP:HA	2.41	0.49
1:Q:730:GLN:CG	1:Q:731:ALA:N	2.74	0.49
1:A:226:ALA:O	1:A:229:SER:OG	2.27	0.49
1:F:427:PRO:HA	1:F:464:ARG:HH22	1.77	0.49
5:J:6:ARG:HH11	5:J:10:GLN:NE2	2.10	0.49
2:L:121:VAL:HG21	2:L:165:VAL:HG11	1.94	0.49
2:L:256:MET:O	2:L:258:HIS:HD2	1.95	0.49
2:B:358:TYR:CE1	2:B:361:CYS:HB3	2.47	0.49
3:C:597:ILE:HG23	3:C:615:LYS:HD2	1.95	0.49
1:K:729:SER:H	1:K:730:GLN:HB2	1.71	0.49
1:Q:689:HIS:HD2	1:Q:726:TYR:H	1.60	0.49
1:A:135:GLY:O	1:A:139:LEU:N	2.45	0.49
2:G:355:ARG:O	2:G:397:HIS:HB2	2.11	0.49
2:L:199:HIS:HB3	2:L:202:ASP:O	2.13	0.49
1:A:528:GLN:HG3	1:K:81:ARG:HE	1.77	0.49
2:B:326:ASN:HA	2:B:358:TYR:CE1	2.47	0.49
1:F:137:GLU:N	1:F:138:VAL:HA	2.27	0.49
1:F:318:LYS:CG	1:F:319:PRO:HA	2.42	0.49
1:F:446:THR:HG23	1:F:447:TYR:CD1	2.47	0.49
2:R:120:ARG:HB3	2:R:139:VAL:HG22	1.95	0.49
2:R:329:VAL:HG11	2:R:352:ILE:HD12	1.95	0.49
3:S:569:ASP:N	3:S:569:ASP:OD1	2.44	0.49
1:A:677:ALA:O	1:A:685:ARG:NH2	2.42	0.49
1:F:224:PHE:CE1	1:F:241:LYS:HA	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:397:HIS:CD2	2:G:398:LYS:HG2	2.47	0.49
3:H:671:ILE:HA	3:H:674:ILE:HD12	1.95	0.49
1:K:634:LYS:HG2	1:K:635:ASN:ND2	2.27	0.49
2:L:395:ASP:HB3	2:L:396:PRO:C	2.37	0.49
1:Q:74:VAL:N	1:Q:75:SER:HA	2.28	0.49
1:A:67:PRO:HG3	2:B:105:SER:HA	1.95	0.49
1:A:125:GLU:OE1	2:B:236:ARG:NH2	2.46	0.49
1:A:730:GLN:HG3	1:A:732:ASP:N	2.28	0.49
1:A:733:ALA:H	1:A:734:LEU:HD13	1.76	0.49
2:B:186:TYR:HE2	2:B:220:ILE:HG22	1.76	0.49
2:B:386:LEU:HD21	2:B:416:THR:HG21	1.95	0.49
1:F:30:LYS:HE3	1:F:173:GLU:OE1	2.12	0.49
2:G:310:ASP:OD2	2:G:322:LYS:NZ	2.36	0.49
1:K:136:ASP:N	1:K:136:ASP:OD1	2.41	0.49
1:Q:234:LYS:HD2	1:Q:234:LYS:N	2.28	0.49
3:M:586:GLU:HB2	3:M:587:LYS:CB	2.41	0.48
1:Q:224:PHE:CZ	1:Q:244:TYR:HB3	2.49	0.48
1:A:133:TYR:CE1	1:A:136:ASP:HB2	2.48	0.48
1:F:594:TRP:HZ2	3:H:630:ASN:HD21	1.60	0.48
1:F:661:TYR:O	1:F:662:MET:HB2	2.13	0.48
1:K:236:THR:HG22	1:K:237:ALA:N	2.28	0.48
1:K:627:PHE:CE2	1:K:721:GLU:HB2	2.47	0.48
1:Q:117:GLN:HA	1:Q:117:GLN:OE1	2.13	0.48
1:A:427:PRO:HA	1:A:464:ARG:HH22	1.79	0.48
1:K:317:ASN:HD21	1:K:332:LYS:HD2	1.78	0.48
1:A:322:PRO:HG3	1:F:59:GLU:HG2	1.95	0.48
2:G:332:LYS:NZ	2:G:338:ASP:O	2.26	0.48
1:Q:432:TRP:CE3	1:Q:432:TRP:CA	2.90	0.48
1:A:45:ASN:O	1:A:49:ILE:HG13	2.14	0.48
1:A:67:PRO:O	1:A:68:VAL:HG12	2.14	0.48
1:F:613:HIS:NE2	3:H:581:VAL:HB	2.29	0.48
1:K:451:PHE:CE2	1:K:467:TYR:HD1	2.28	0.48
3:M:664:HIS:HB2	3:M:674:ILE:HD11	1.94	0.48
1:Q:123:GLU:OE1	1:Q:123:GLU:N	2.32	0.48
2:B:282:PRO:HB3	3:C:575:ARG:NH1	2.23	0.48
2:G:241:SER:HB3	2:G:254:CYS:SG	2.54	0.48
2:G:319:ILE:O	2:G:330:CYS:HA	2.14	0.48
2:B:400:LYS:HE3	2:B:401:CYS:O	2.14	0.48
1:F:141:GLN:H	1:F:141:GLN:CD	2.21	0.48
2:G:180:MET:HG3	2:G:180:MET:O	2.13	0.48
3:M:575:ARG:O	3:M:578:GLU:HG2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:364:TRP:HD1	5:U:5:GLN:HB3	1.78	0.48
1:F:302:THR:OG1	1:F:305:THR:N	2.39	0.48
2:B:322:LYS:HE2	2:B:358:TYR:OH	2.13	0.48
1:F:83:CYS:HB2	1:F:98:LEU:HD21	1.95	0.48
1:K:71:LEU:HB2	2:L:180:MET:SD	2.54	0.48
1:K:236:THR:HG22	1:K:238:GLU:H	1.78	0.48
2:L:323:SER:C	2:L:325:GLU:H	2.21	0.48
2:B:418:PHE:CE1	2:B:425:LEU:HD13	2.49	0.48
1:F:244:TYR:CD1	1:F:244:TYR:C	2.92	0.48
1:F:689:HIS:HD2	1:F:726:TYR:H	1.61	0.48
1:K:91:PHE:HE2	2:L:131:GLU:HB2	1.78	0.48
1:K:606:ILE:CG2	1:K:707:ARG:HD2	2.43	0.48
2:L:122:THR:HG1	2:L:137:SER:HG	1.61	0.48
1:A:165:PHE:HE1	1:A:170:ILE:HD13	1.79	0.47
1:F:272:VAL:CG1	1:F:276:GLN:HB2	2.44	0.47
1:F:446:THR:HG23	1:F:447:TYR:HD1	1.79	0.47
1:Q:96:ILE:HG13	2:R:134:LEU:HG	1.95	0.47
1:A:330:GLY:H	1:A:333:GLU:HB2	1.78	0.47
1:A:594:TRP:O	1:A:597:LYS:HG2	2.14	0.47
1:K:10:LYS:HB3	1:K:12:PRO:HD2	1.96	0.47
1:Q:534:CYS:HB3	1:Q:537:VAL:HG22	1.96	0.47
2:R:95:PRO:HB3	2:R:430:ASP:HA	1.96	0.47
2:B:288:PRO:HB3	3:C:578:GLU:OE2	2.14	0.47
1:F:730:GLN:HG3	1:F:732:ASP:N	2.30	0.47
2:R:170:GLY:HA2	2:R:193:ILE:HG13	1.95	0.47
3:S:645:GLN:O	3:S:649:LYS:HD3	2.14	0.47
1:A:70:ILE:CD1	2:B:135:LEU:HD22	2.44	0.47
1:A:89:LEU:O	1:A:90:ASP:HB3	2.14	0.47
1:F:243:LYS:O	1:F:247:LEU:HG	2.14	0.47
1:F:619:SER:HB2	1:F:625:GLY:CA	2.45	0.47
2:G:148:TYR:CZ	5:J:7:M3L:HM11	2.49	0.47
3:H:597:ILE:HG23	3:H:615:LYS:HD2	1.96	0.47
3:H:606:VAL:O	3:H:611:LYS:HE3	2.14	0.47
2:L:189:HIS:NE2	2:L:208:SER:OG	2.38	0.47
2:R:210:SER:OG	2:R:211:LYS:N	2.47	0.47
2:B:397:HIS:HA	2:B:398:LYS:C	2.39	0.47
1:F:99:LYS:NZ	2:G:180:MET:O	2.47	0.47
1:F:619:SER:HB2	1:F:625:GLY:HA3	1.96	0.47
1:K:106:SER:HB2	2:L:169:ARG:NH1	2.30	0.47
1:K:263:ASN:HA	3:M:607:ASN:HD21	1.76	0.47
3:M:633:ASN:ND2	3:M:673:SER:OG	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:440:PHE:CD2	1:Q:469:PHE:HE2	2.33	0.47
2:R:211:LYS:HG3	2:R:238:GLU:CD	2.39	0.47
1:A:302:THR:HG23	1:A:304:ASN:N	2.30	0.47
2:B:191:ASN:HD21	2:B:211:LYS:HE2	1.79	0.47
1:F:139:LEU:HB3	1:F:141:GLN:HA	1.97	0.47
2:G:161:PRO:O	2:G:177:PRO:HD2	2.14	0.47
2:G:232:VAL:HG11	3:H:591:TRP:CZ3	2.49	0.47
1:Q:456:ARG:NE	3:S:675:ASP:OD1	2.32	0.47
2:R:79:LYS:HE3	2:R:390:ASP:OD2	2.15	0.47
2:R:356:PHE:CZ	2:R:397:HIS:HB3	2.50	0.47
1:A:19:VAL:HG22	1:A:178:LEU:HD21	1.97	0.47
1:A:129:HIS:HB3	2:B:302:ARG:HH21	1.78	0.47
1:F:121:MET:SD	1:F:645:ILE:HD11	2.54	0.47
1:K:19:VAL:HG22	1:K:178:LEU:HD22	1.97	0.47
1:K:22:GLU:OE2	1:K:181:TYR:CZ	2.67	0.47
2:L:101:PHE:CD1	2:L:113:PHE:HB3	2.49	0.47
2:L:201:ARG:NH1	2:L:247:LEU:HD22	2.30	0.47
2:L:286:ASN:O	3:M:578:GLU:HB3	2.14	0.47
1:Q:68:VAL:HG11	2:R:123:LEU:HD23	1.96	0.47
3:S:606:VAL:O	3:S:611:LYS:HE3	2.15	0.47
1:A:322:PRO:HG3	1:F:59:GLU:CG	2.44	0.47
3:C:650:LYS:HB2	3:C:652:LEU:HG	1.96	0.47
1:K:162:GLU:OE1	1:K:162:GLU:N	2.48	0.47
1:Q:30:LYS:CE	1:Q:34:ARG:HH21	2.28	0.47
1:A:70:ILE:HD11	2:B:135:LEU:HD13	1.95	0.47
1:A:70:ILE:HD11	2:B:135:LEU:HD22	1.95	0.47
2:B:399:ALA:HA	2:B:400:LYS:HA	1.71	0.47
1:F:447:TYR:CB	1:F:454:ILE:HD11	2.45	0.47
1:F:730:GLN:HG3	1:F:732:ASP:H	1.80	0.47
3:H:581:VAL:HG12	3:H:582:ASP:OD1	2.15	0.47
1:K:324:CYS:HA	1:K:463:CYS:HB3	1.96	0.47
2:R:331:TRP:HB3	2:R:352:ILE:HD13	1.96	0.47
1:F:583:ASP:OD1	3:H:629:ASP:HB2	2.15	0.46
2:G:209:VAL:HG13	2:G:239:VAL:HB	1.97	0.46
1:K:150:ILE:CG2	1:K:155:GLY:HA2	2.45	0.46
1:Q:274:ARG:HG3	1:Q:442:VAL:HA	1.96	0.46
3:S:682:ARG:HA	3:S:685:GLN:HG3	1.97	0.46
1:A:145:PHE:CE2	1:A:660:LYS:HG2	2.51	0.46
2:B:180:MET:HE2	2:B:180:MET:HB3	1.75	0.46
1:F:96:ILE:HG22	1:F:97:PRO:HD2	1.95	0.46
3:H:569:ASP:OD1	3:H:569:ASP:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:65:ILE:O	1:K:66:GLN:HB3	2.15	0.46
2:B:189:HIS:HE1	2:B:208:SER:OG	1.98	0.46
1:F:439:MET:HE1	3:H:657:MET:SD	2.55	0.46
3:H:587:LYS:HE2	3:H:593:ARG:NH1	2.28	0.46
1:K:265:ASP:HB3	3:M:651:ASN:O	2.15	0.46
1:F:129:HIS:H	1:F:129:HIS:CD2	2.34	0.46
1:F:291:LYS:HG2	3:H:621:VAL:HG21	1.98	0.46
3:H:648:ILE:HD13	3:H:685:GLN:HG2	1.97	0.46
2:G:86:ASN:ND2	2:G:87:SER:H	2.13	0.46
1:Q:528:GLN:CG	1:Q:529:PRO:HD2	2.45	0.46
1:A:566:CYS:HB2	1:A:571:CYS:HB2	1.96	0.46
2:B:396:PRO:C	2:B:398:LYS:HB2	2.40	0.46
1:F:539:ALA:O	1:F:540:GLN:HB2	2.15	0.46
3:H:664:HIS:HB2	3:H:674:ILE:HD11	1.98	0.46
1:A:734:LEU:HD13	1:A:734:LEU:N	2.31	0.46
1:F:308:ARG:HG3	3:H:667:ASN:OD1	2.15	0.46
2:G:323:SER:C	2:G:325:GLU:H	2.23	0.46
1:Q:104:VAL:HG12	2:R:185:HIS:CG	2.50	0.46
1:Q:161:ARG:HD3	1:Q:233:ASP:OD2	2.16	0.46
1:Q:234:LYS:HD2	1:Q:234:LYS:H	1.81	0.46
1:Q:666:LEU:O	4:T:27:MET:HG3	2.14	0.46
2:R:256:MET:O	2:R:258:HIS:CD2	2.63	0.46
2:B:91:ASP:OD1	2:B:91:ASP:N	2.35	0.46
3:C:565:TYR:HB2	3:C:574:LEU:HD23	1.98	0.46
3:C:589:PRO:HG2	3:C:592:LEU:HB2	1.97	0.46
1:F:45:ASN:ND2	2:G:317:ASP:H	1.88	0.46
1:F:65:ILE:HG22	2:G:161:PRO:HG3	1.97	0.46
1:F:234:LYS:CB	1:F:240:LEU:HD21	2.42	0.46
1:F:440:PHE:O	1:F:444:ILE:HG23	2.15	0.46
1:K:180:GLN:HG2	1:K:181:TYR:HD2	1.80	0.46
2:L:171:ILE:HG23	2:L:187:VAL:HG22	1.98	0.46
3:M:608:GLU:HG3	3:M:609:GLY:N	2.31	0.46
1:Q:98:LEU:HD13	2:R:139:VAL:HG21	1.98	0.46
1:Q:168:ASP:O	1:Q:172:VAL:HG23	2.16	0.46
2:R:99:VAL:HG23	2:R:115:THR:HG22	1.97	0.46
1:A:64:ARG:O	2:B:159:SER:HB3	2.16	0.46
1:A:137:GLU:N	1:A:137:GLU:OE1	2.49	0.46
1:A:734:LEU:HD12	7:A:1009:SAH:C4	2.46	0.46
2:B:189:HIS:CD2	2:B:210:SER:CB	2.99	0.46
1:F:98:LEU:HB3	2:G:139:VAL:HG23	1.98	0.46
2:G:215:LEU:HB2	2:G:229:PHE:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:580:GLU:HB3	3:H:581:VAL:CA	2.35	0.46
3:M:585:ASP:CG	3:M:586:GLU:HB3	2.41	0.46
2:B:176:ASN:HD22	2:B:177:PRO:HD2	1.81	0.46
2:B:229:PHE:HD2	2:B:263:TRP:CE3	2.34	0.46
2:B:260:LEU:HD13	2:B:331:TRP:CZ2	2.51	0.46
1:F:648:GLN:HE22	1:F:668:ASN:HD21	1.64	0.46
3:H:665:ASP:O	3:H:667:ASN:N	2.49	0.46
1:K:303:PRO:HB2	1:K:306:TYR:OH	2.16	0.46
2:L:91:ASP:CG	2:L:120:ARG:HH12	2.24	0.46
2:R:392:GLU:HB3	2:R:393:VAL:HG22	1.97	0.46
1:A:531:ASP:OD1	1:K:81:ARG:NH2	2.48	0.45
3:H:579:MET:HA	3:H:580:GLU:HB2	1.97	0.45
1:K:263:ASN:N	3:M:607:ASN:HD21	2.14	0.45
3:M:641:GLU:OE2	3:M:680:LYS:NZ	2.49	0.45
1:Q:460:THR:C	1:Q:461:LYS:HG2	2.41	0.45
2:R:358:TYR:CE1	2:R:361:CYS:HB3	2.51	0.45
3:S:607:ASN:O	3:S:611:LYS:HG3	2.16	0.45
1:A:158:HIS:HA	1:A:159:GLY:HA2	1.56	0.45
2:B:128:SER:HA	2:B:129:GLN:HA	1.63	0.45
1:F:138:VAL:O	1:F:139:LEU:HB2	2.16	0.45
1:K:41:MET:HG3	2:L:336:MET:CE	2.46	0.45
5:E:3:GLN:HG2	5:E:4:ALA:H	1.82	0.45
1:F:70:ILE:HD13	1:F:70:ILE:HG21	1.74	0.45
1:K:34:ARG:O	1:K:37:GLU:N	2.49	0.45
1:Q:134:MET:CG	1:Q:661:TYR:HE1	2.29	0.45
1:Q:528:GLN:HG3	1:Q:529:PRO:HD2	1.98	0.45
1:A:531:ASP:OD2	1:K:81:ARG:NH2	2.49	0.45
1:F:439:MET:HE1	3:H:657:MET:HB3	1.98	0.45
1:Q:109:ILE:HA	2:R:190:GLY:O	2.16	0.45
2:R:315:LEU:HD22	2:R:320:LEU:HD11	1.99	0.45
1:A:160:ASP:O	1:A:232:PRO:HD2	2.16	0.45
1:A:439:MET:HE3	1:A:443:LEU:HG	1.97	0.45
1:F:96:ILE:CG2	1:F:97:PRO:HD2	2.47	0.45
1:F:96:ILE:HD11	2:G:134:LEU:HG	1.98	0.45
1:F:104:VAL:HG21	2:G:171:ILE:HG21	1.99	0.45
2:G:170:GLY:HA2	2:G:193:ILE:HD12	1.99	0.45
1:K:235:GLY:O	1:K:239:GLU:HB2	2.16	0.45
3:M:597:ILE:HG23	3:M:615:LYS:HD2	1.97	0.45
2:R:326:ASN:HA	2:R:358:TYR:CE1	2.51	0.45
2:R:436:ARG:NE	2:R:438:ASP:OD1	2.48	0.45
3:S:647:ILE:HG23	3:S:652:LEU:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:GLU:O	1:A:63:ARG:HG3	2.17	0.45
1:K:531:ASP:O	1:K:537:VAL:HG21	2.16	0.45
2:L:288:PRO:HG3	3:M:567:HIS:CE1	2.51	0.45
1:Q:238:GLU:H	1:Q:238:GLU:HG3	1.31	0.45
1:Q:294:CYS:SG	1:Q:297:HIS:HB2	2.56	0.45
1:A:138:VAL:HG12	1:A:141:GLN:H	1.81	0.45
1:A:447:TYR:HB2	1:A:454:ILE:HD11	1.98	0.45
2:B:274:ILE:O	2:B:277:SER:OG	2.20	0.45
1:F:619:SER:HB3	1:F:622:ALA:O	2.17	0.45
1:Q:175:VAL:HG21	1:Q:244:TYR:HE1	1.78	0.45
1:Q:334:PHE:CD2	1:Q:467:TYR:OH	2.60	0.45
1:A:128:LEU:HB3	1:A:153:TYR:CE2	2.52	0.45
1:K:87:SER:HG	2:L:86:ASN:HD21	1.64	0.45
1:K:698:LYS:HB2	1:K:711:PHE:HE2	1.81	0.45
2:L:150:CYS:HA	2:L:164:ALA:O	2.16	0.45
1:Q:104:VAL:O	1:Q:104:VAL:HG23	2.16	0.45
1:Q:440:PHE:CD2	1:Q:440:PHE:C	2.95	0.45
2:B:184:LYS:NZ	2:B:220:ILE:O	2.36	0.45
2:B:306:ARG:N	2:B:325:GLU:OE2	2.48	0.45
1:F:98:LEU:HD21	2:G:137:SER:HB3	1.97	0.45
1:F:154:ASP:CB	1:F:156:LYS:HE2	2.46	0.45
1:K:57:ASN:HA	2:L:420:ARG:HH22	1.82	0.45
2:L:238:GLU:HB2	2:L:256:MET:HG3	1.98	0.45
2:L:315:LEU:HD22	2:L:320:LEU:HD11	1.99	0.45
1:A:245:LYS:O	1:A:248:THR:HG22	2.17	0.45
1:F:89:LEU:O	1:F:90:ASP:HB3	2.17	0.45
1:F:264:ILE:HG12	1:F:265:ASP:OD1	2.17	0.45
1:F:667:PHE:O	1:F:674:VAL:HG13	2.17	0.45
1:K:14:CYS:SG	1:K:15:TRP:HD1	2.40	0.45
1:Q:583:ASP:OD1	3:S:629:ASP:HB2	2.18	0.45
2:R:274:ILE:O	2:R:277:SER:OG	2.25	0.45
1:A:182:ASN:O	1:A:182:ASN:ND2	2.51	0.44
1:A:230:MET:HB2	1:A:231:PHE:HD1	1.82	0.44
3:M:648:ILE:CD1	3:M:685:GLN:HG2	2.46	0.44
1:Q:264:ILE:N	1:Q:265:ASP:HB2	2.31	0.44
1:Q:302:THR:N	1:Q:303:PRO:HA	2.32	0.44
2:R:232:VAL:HG22	2:R:295:HIS:HB3	1.99	0.44
2:B:211:LYS:HG3	2:B:238:GLU:CG	2.47	0.44
3:C:567:HIS:HB2	3:C:570:THR:O	2.17	0.44
1:K:19:VAL:HG11	1:K:227:ILE:HG22	2.00	0.44
3:M:596:THR:O	3:M:600:ILE:HG12	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:610:GLU:HA	3:M:613:VAL:HG12	2.00	0.44
1:Q:70:ILE:HG13	1:Q:70:ILE:O	2.16	0.44
2:R:131:GLU:OE1	2:R:133:ARG:NH2	2.39	0.44
2:R:418:PHE:CE1	2:R:425:LEU:HD13	2.52	0.44
1:A:330:GLY:CA	1:A:334:PHE:H	2.20	0.44
1:A:560:CYS:HB2	1:A:572:PRO:HD2	2.00	0.44
3:C:616:LEU:HD22	3:C:643:TYR:CD2	2.49	0.44
1:F:148:GLU:HA	1:F:151:LYS:HD2	1.97	0.44
1:K:23:TYR:OH	1:K:165:PHE:O	2.28	0.44
1:Q:13:VAL:HA	1:Q:16:ARG:HG2	1.99	0.44
1:Q:15:TRP:O	1:Q:19:VAL:HG23	2.18	0.44
2:R:293:LYS:HG3	2:R:295:HIS:NE2	2.32	0.44
1:A:89:LEU:HD23	1:A:89:LEU:HA	1.78	0.44
1:A:220:SER:O	1:A:223:ILE:HG13	2.17	0.44
1:A:668:ASN:HA	1:A:674:VAL:HG13	1.98	0.44
2:B:189:HIS:CD2	2:B:210:SER:HB2	2.53	0.44
2:B:396:PRO:HA	2:B:397:HIS:ND1	2.32	0.44
1:K:65:ILE:HG22	2:L:161:PRO:HG3	1.98	0.44
1:K:70:ILE:HD13	1:K:70:ILE:HG21	1.74	0.44
1:K:528:GLN:H	1:K:528:GLN:CD	2.13	0.44
2:L:199:HIS:HB2	2:L:205:LEU:HB2	1.99	0.44
1:Q:138:VAL:HB	1:Q:140:ASP:C	2.43	0.44
1:Q:302:THR:HG1	1:Q:305:THR:H	1.66	0.44
3:S:645:GLN:HG3	3:S:649:LYS:HE2	1.99	0.44
1:A:41:MET:HE3	1:A:41:MET:HB3	1.87	0.44
1:A:68:VAL:HG11	2:B:110:PRO:CG	2.48	0.44
1:F:99:LYS:O	2:G:138:TYR:HA	2.17	0.44
3:H:632:MET:SD	3:H:663:MET:HE1	2.58	0.44
1:K:730:GLN:HG3	1:K:731:ALA:N	2.33	0.44
2:L:254:CYS:HB2	2:L:309:VAL:HB	1.99	0.44
1:Q:144:THR:O	1:Q:148:GLU:HG3	2.16	0.44
1:Q:439:MET:HE1	3:S:657:MET:HB3	1.99	0.44
1:Q:697:ALA:O	4:T:30:PRO:HD2	2.17	0.44
1:Q:728:TYR:CD2	1:Q:734:LEU:HD21	2.51	0.44
2:R:441:ARG:CZ	2:R:441:ARG:HB2	2.46	0.44
1:A:158:HIS:O	2:B:258:HIS:CE1	2.70	0.44
2:B:325:GLU:O	2:B:326:ASN:HB2	2.18	0.44
3:C:639:PHE:CE2	3:C:647:ILE:HD11	2.52	0.44
1:K:129:HIS:H	1:K:129:HIS:HD2	1.66	0.44
1:Q:457:LEU:HD12	1:Q:458:ILE:H	1.78	0.44
3:S:596:THR:CG2	3:S:622:MET:HE1	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:CYS:HB2	1:A:98:LEU:HD13	2.00	0.44
1:A:161:ARG:HE	1:A:163:CYS:C	2.26	0.44
1:A:231:PHE:CD1	1:A:231:PHE:N	2.85	0.44
1:A:316:ASP:CG	1:A:332:LYS:HE2	2.43	0.44
1:A:443:LEU:HB3	1:A:454:ILE:HG13	2.00	0.44
2:B:227:ALA:HA	2:B:292:GLN:O	2.17	0.44
1:F:110:MET:O	2:G:190:GLY:HA3	2.18	0.44
1:F:161:ARG:NH2	1:F:233:ASP:CG	2.75	0.44
1:F:437:ALA:O	1:F:441:ARG:HG3	2.18	0.44
1:K:11:GLY:N	1:K:12:PRO:CD	2.80	0.44
2:L:210:SER:HB3	2:L:212:ASP:OD1	2.16	0.44
2:L:392:GLU:HA	2:L:393:VAL:HA	1.70	0.44
3:M:662:SER:O	3:M:666:PHE:HD1	2.01	0.44
1:Q:264:ILE:HB	1:Q:265:ASP:HB2	1.99	0.44
1:Q:443:LEU:HD13	1:Q:457:LEU:HD11	2.00	0.44
2:R:194:ASN:ND2	2:R:240:LEU:HD23	2.31	0.44
1:A:223:ILE:O	1:A:226:ALA:N	2.51	0.44
1:A:244:TYR:CD1	1:A:244:TYR:C	2.96	0.44
1:A:583:ASP:OD1	3:C:629:ASP:HB2	2.18	0.44
1:F:98:LEU:CD2	2:G:137:SER:HB3	2.48	0.44
2:L:145:GLU:OE1	2:L:169:ARG:HB2	2.18	0.44
1:Q:436:GLU:OE2	1:Q:461:LYS:NZ	2.51	0.44
1:A:10:LYS:HE3	1:A:222:LYS:HE3	2.00	0.44
1:A:303:PRO:HB2	1:A:306:TYR:OH	2.18	0.44
2:B:253:SER:O	2:B:260:LEU:HA	2.18	0.44
2:B:361:CYS:SG	2:B:366:MET:HG3	2.58	0.44
1:Q:89:LEU:O	1:Q:90:ASP:HB3	2.17	0.44
1:Q:168:ASP:N	1:Q:168:ASP:OD1	2.51	0.44
2:R:395:ASP:N	2:R:396:PRO:HA	2.32	0.44
1:A:263:ASN:HD22	1:A:265:ASP:H	1.66	0.43
2:B:294:ILE:HD12	2:B:294:ILE:N	2.32	0.43
3:C:581:VAL:HA	3:C:582:ASP:HA	1.60	0.43
1:F:125:GLU:O	1:F:125:GLU:HG3	2.18	0.43
1:F:172:VAL:O	1:F:175:VAL:HG22	2.17	0.43
1:K:515:ASN:OD1	1:K:515:ASN:N	2.49	0.43
2:L:227:ALA:HA	2:L:292:GLN:O	2.17	0.43
1:Q:171:PHE:CZ	1:Q:224:PHE:HE2	2.35	0.43
1:Q:607:GLN:HG2	1:Q:702:VAL:CG1	2.48	0.43
2:R:323:SER:HB3	2:R:325:GLU:HG3	1.99	0.43
3:C:561:HIS:N	3:C:562:ASN:HB3	2.33	0.43
1:F:98:LEU:HD23	1:F:98:LEU:HA	1.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:175:VAL:HG23	1:F:176:ASN:N	2.32	0.43
1:F:223:ILE:HG13	1:F:224:PHE:N	2.34	0.43
1:F:650:GLU:HA	1:F:653:ARG:NH1	2.33	0.43
2:L:86:ASN:HD22	2:L:87:SER:N	2.16	0.43
1:A:67:PRO:HG3	2:B:105:SER:HB3	1.97	0.43
1:A:330:GLY:O	1:A:467:TYR:OH	2.31	0.43
1:F:660:LYS:HD2	1:F:660:LYS:HA	1.83	0.43
1:K:19:VAL:HG22	1:K:178:LEU:CD2	2.48	0.43
1:K:20:LYS:HB2	1:K:230:MET:HE2	1.99	0.43
2:L:210:SER:OG	2:L:211:LYS:N	2.50	0.43
1:A:566:CYS:HB2	1:A:571:CYS:CB	2.49	0.43
2:G:378:ALA:HA	2:G:387:TYR:O	2.18	0.43
1:K:72:THR:HG22	1:K:74:VAL:N	2.34	0.43
1:Q:169:GLU:O	1:Q:173:GLU:HG2	2.18	0.43
1:Q:654:ARG:O	1:Q:657:VAL:HG12	2.19	0.43
1:A:128:LEU:CD2	1:A:157:VAL:HG22	2.47	0.43
1:A:141:GLN:HA	1:A:142:ASP:HA	1.67	0.43
1:A:428:GLU:OE2	1:F:51:GLU:OE2	2.35	0.43
2:G:160:HIS:HB3	2:G:176:ASN:HD21	1.83	0.43
1:Q:129:HIS:HA	1:Q:158:HIS:HB2	2.00	0.43
2:R:258:HIS:CE1	2:R:307:ASN:HA	2.53	0.43
3:S:664:HIS:HB2	3:S:674:ILE:HD11	2.01	0.43
1:K:22:GLU:OE1	1:K:178:LEU:HD23	2.18	0.43
1:K:244:TYR:CD1	1:K:244:TYR:C	2.97	0.43
1:K:304:ASN:HA	1:K:307:LYS:HD3	2.00	0.43
1:K:326:GLN:HB2	1:K:327:HIS:HB2	2.00	0.43
1:K:425:GLU:OE2	1:K:426:PRO:HD2	2.19	0.43
1:K:472:LYS:O	1:K:476:ILE:HG12	2.18	0.43
2:L:315:LEU:HD13	2:L:370:MET:HE1	1.99	0.43
1:Q:139:LEU:HD12	1:Q:140:ASP:HA	2.00	0.43
1:Q:440:PHE:CD2	1:Q:469:PHE:CE2	3.07	0.43
1:A:257:PRO:N	1:A:258:PRO:HD3	2.34	0.43
1:A:337:ALA:O	1:A:341:GLU:HG3	2.19	0.43
1:Q:96:ILE:HG22	1:Q:97:PRO:O	2.18	0.43
1:Q:557:PHE:CG	1:Q:558:PRO:HD2	2.54	0.43
1:Q:563:LYS:CB	1:Q:587:THR:HG22	2.45	0.43
2:R:414:ARG:HA	2:R:414:ARG:HD3	1.81	0.43
2:B:101:PHE:CD1	2:B:113:PHE:HB3	2.54	0.43
1:F:168:ASP:O	1:F:172:VAL:HG23	2.19	0.43
1:F:261:THR:HG22	1:F:262:PRO:O	2.19	0.43
1:F:263:ASN:N	3:H:607:ASN:OD1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:427:PRO:C	1:F:464:ARG:HH22	2.27	0.43
1:F:644:GLU:O	1:F:675:VAL:HA	2.18	0.43
2:G:268:LYS:C	2:G:272:ASN:HD22	2.25	0.43
2:G:322:LYS:HB3	2:G:322:LYS:HE3	1.42	0.43
1:K:224:PHE:CE1	1:K:241:LYS:HA	2.54	0.43
1:K:714:ARG:HG3	1:K:715:ALA:O	2.19	0.43
2:R:414:ARG:NH1	5:U:8:PHE:HD1	2.17	0.43
2:B:186:TYR:CE2	2:B:220:ILE:HG22	2.53	0.43
2:B:199:HIS:HB3	2:B:202:ASP:O	2.19	0.43
2:B:204:ASN:O	2:B:220:ILE:HG12	2.19	0.43
1:F:131:ILE:HD13	1:F:131:ILE:HG21	1.80	0.43
1:F:272:VAL:HG12	1:F:276:GLN:HB2	1.99	0.43
2:G:397:HIS:NE2	2:G:398:LYS:HG2	2.34	0.43
3:H:610:GLU:HA	3:H:613:VAL:HG12	2.01	0.43
3:M:666:PHE:O	3:M:667:ASN:HB2	2.19	0.43
1:Q:263:ASN:OD1	3:S:609:GLY:HA3	2.19	0.43
1:Q:270:LYS:HE3	1:Q:270:LYS:HB3	1.75	0.43
1:Q:461:LYS:HA	1:Q:461:LYS:HD3	1.69	0.43
1:Q:665:PHE:CD2	1:Q:678:THR:HG22	2.49	0.43
1:A:245:LYS:HA	1:A:248:THR:HG22	2.00	0.42
1:A:438:SER:O	1:A:442:VAL:HG23	2.18	0.42
1:A:516:HIS:HB3	1:A:671:ASN:ND2	2.34	0.42
2:B:241:SER:HB3	2:B:254:CYS:SG	2.59	0.42
1:F:22:GLU:O	1:F:26:LEU:HD12	2.18	0.42
1:F:612:LYS:HA	1:F:612:LYS:HD3	1.84	0.42
1:K:243:LYS:HE3	1:K:243:LYS:HA	2.01	0.42
1:K:591:ALA:O	1:K:594:TRP:CZ2	2.72	0.42
1:Q:460:THR:O	1:Q:461:LYS:CE	2.61	0.42
3:S:633:ASN:ND2	3:S:673:SER:OG	2.51	0.42
1:A:533:SER:HB3	1:K:81:ARG:HB3	2.00	0.42
2:B:136:GLN:HE21	2:B:180:MET:HE2	1.84	0.42
1:F:45:ASN:HD21	2:G:317:ASP:N	1.88	0.42
1:F:141:GLN:H	1:F:141:GLN:NE2	2.16	0.42
2:G:197:LYS:O	2:G:206:LEU:HD12	2.18	0.42
1:K:238:GLU:H	1:K:238:GLU:HG3	1.63	0.42
1:K:242:GLU:O	1:K:246:GLU:HG3	2.19	0.42
2:L:88:LEU:HD11	2:L:132:ILE:HG21	2.01	0.42
2:L:161:PRO:O	2:L:177:PRO:HD2	2.19	0.42
1:Q:138:VAL:HB	1:Q:139:LEU:HA	2.01	0.42
1:A:68:VAL:O	1:A:68:VAL:HG13	2.19	0.42
1:A:68:VAL:CG2	2:B:110:PRO:HG2	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:254:CYS:HB3	2:B:260:LEU:CD2	2.47	0.42
3:C:632:MET:SD	3:C:663:MET:HE1	2.59	0.42
1:F:96:ILE:CD1	2:G:134:LEU:HG	2.48	0.42
1:F:634:LYS:HG3	1:F:713:LYS:O	2.19	0.42
2:G:307:ASN:OD1	5:J:5:GLN:HG3	2.18	0.42
1:K:110:MET:HE3	1:K:624:TRP:NE1	2.34	0.42
1:K:451:PHE:HE2	1:K:467:TYR:CD1	2.29	0.42
3:M:579:MET:O	3:M:581:VAL:N	2.53	0.42
1:Q:457:LEU:HD12	1:Q:457:LEU:C	2.44	0.42
1:Q:582:PRO:HB2	3:S:628:ALA:HB2	2.00	0.42
2:R:294:ILE:N	2:R:294:ILE:HD12	2.34	0.42
2:R:375:LYS:HG2	2:R:392:GLU:OE1	2.19	0.42
1:A:516:HIS:HB3	1:A:671:ASN:HD21	1.84	0.42
2:G:399:ALA:HB1	2:G:400:LYS:HB2	2.01	0.42
1:K:168:ASP:OD2	2:L:348:SER:HB3	2.20	0.42
1:Q:168:ASP:O	1:Q:171:PHE:HB3	2.20	0.42
2:R:308:TYR:CE2	5:U:5:GLN:HB2	2.54	0.42
1:A:66:GLN:O	1:A:66:GLN:HG3	2.20	0.42
1:A:67:PRO:HG3	2:B:105:SER:CA	2.49	0.42
1:A:129:HIS:CE1	2:B:236:ARG:HG3	2.54	0.42
1:A:241:LYS:HG2	1:A:245:LYS:HE3	2.00	0.42
3:C:570:THR:O	3:C:572:LEU:N	2.53	0.42
1:F:431:GLU:H	1:F:431:GLU:HG3	1.64	0.42
2:G:191:ASN:HD22	2:G:211:LYS:HG2	1.84	0.42
1:Q:701:MET:HE2	1:Q:701:MET:HB2	1.91	0.42
1:A:159:GLY:HA2	1:A:233:ASP:OD2	2.19	0.42
1:F:328:LEU:C	1:F:328:LEU:HD12	2.45	0.42
2:G:248:GLY:O	2:G:265:ILE:HD11	2.20	0.42
1:K:145:PHE:CE1	1:K:660:LYS:HD3	2.55	0.42
1:K:726:TYR:O	1:K:727:ARG:HB2	2.20	0.42
1:Q:128:LEU:HD22	1:Q:153:TYR:CG	2.54	0.42
1:A:129:HIS:CB	2:B:302:ARG:HH21	2.33	0.42
1:A:737:VAL:HA	1:A:738:GLY:HA2	1.58	0.42
2:L:155:ASP:O	2:L:159:SER:N	2.49	0.42
2:L:399:ALA:HA	2:L:400:LYS:HA	1.77	0.42
1:Q:328:LEU:CG	1:Q:425:GLU:HG2	2.44	0.42
1:Q:638:ILE:HD13	1:Q:638:ILE:HG21	1.84	0.42
3:S:587:LYS:HB2	3:S:588:ASP:HA	2.02	0.42
1:A:557:PHE:CD2	1:A:558:PRO:O	2.72	0.42
1:A:599:VAL:HG22	1:A:600:SER:N	2.35	0.42
2:B:210:SER:OG	2:B:211:LYS:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:129:HIS:HE1	2:G:236:ARG:HG3	1.84	0.42
1:K:158:HIS:O	2:L:258:HIS:CE1	2.72	0.42
1:K:263:ASN:HB3	3:M:607:ASN:ND2	2.34	0.42
1:Q:727:ARG:NH2	4:T:30:PRO:HG3	2.22	0.42
1:A:169:GLU:O	1:A:173:GLU:HG3	2.20	0.42
1:A:599:VAL:HG22	1:A:600:SER:H	1.85	0.42
1:A:731:ALA:O	1:A:733:ALA:HA	2.20	0.42
2:G:95:PRO:HB3	2:G:430:ASP:HA	2.01	0.42
1:K:302:THR:HB	1:K:524:ASP:OD2	2.19	0.42
2:L:183:ILE:HG13	2:L:184:LYS:HG3	2.02	0.42
2:R:187:VAL:HG12	2:R:187:VAL:O	2.19	0.42
2:R:395:ASP:OD1	2:R:395:ASP:C	2.62	0.42
1:A:726:TYR:O	1:A:727:ARG:HB2	2.20	0.42
2:B:385:LYS:HG3	2:B:405:THR:HG22	2.01	0.42
1:F:121:MET:HB2	1:F:295:PHE:O	2.20	0.42
1:F:571:CYS:SG	1:F:573:CYS:HB2	2.59	0.42
2:G:319:ILE:HG23	2:G:319:ILE:HD12	1.78	0.42
2:L:118:SER:OG	2:L:119:ASN:N	2.53	0.42
1:Q:714:ARG:HG3	1:Q:715:ALA:O	2.20	0.42
2:R:392:GLU:HB3	2:R:393:VAL:CG2	2.50	0.42
1:F:18:ARG:NH1	1:F:18:ARG:HG3	2.35	0.41
1:F:227:ILE:CD1	1:F:240:LEU:HD13	2.50	0.41
3:H:597:ILE:HA	3:H:615:LYS:HD2	2.02	0.41
1:K:308:ARG:HG2	1:K:309:LYS:N	2.31	0.41
2:L:429:CYS:HB2	2:L:433:SER:OG	2.20	0.41
1:Q:31:ARG:HE	1:Q:31:ARG:HB2	1.67	0.41
1:Q:311:THR:OG1	1:Q:313:THR:HG23	2.20	0.41
1:Q:582:PRO:HB2	1:Q:594:TRP:HH2	1.84	0.41
1:A:70:ILE:HG12	2:B:135:LEU:HD22	2.01	0.41
1:A:134:MET:HE3	1:A:134:MET:HB2	1.76	0.41
2:B:254:CYS:HB2	2:B:309:VAL:HB	2.02	0.41
2:B:404:LEU:HD22	2:B:437:TRP:CE3	2.55	0.41
3:C:610:GLU:O	3:C:614:MET:HG3	2.20	0.41
1:F:73:SER:O	2:G:180:MET:HE1	2.19	0.41
1:F:99:LYS:NZ	2:G:180:MET:HG3	2.35	0.41
1:F:443:LEU:HA	1:F:446:THR:HG22	2.01	0.41
3:H:609:GLY:O	3:H:613:VAL:HG12	2.19	0.41
2:R:86:ASN:ND2	2:R:87:SER:H	2.15	0.41
1:A:320:CYS:HB2	1:A:324:CYS:SG	2.60	0.41
2:B:336:MET:HE1	2:B:353:LEU:HD21	2.02	0.41
1:F:13:VAL:O	1:F:17:LYS:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:302:THR:HB	1:F:524:ASP:OD2	2.20	0.41
2:G:298:ASP:HA	2:G:345:PRO:HG3	2.03	0.41
1:K:180:GLN:CG	1:K:181:TYR:HD2	2.34	0.41
2:L:195:GLU:HG3	2:L:196:LEU:N	2.36	0.41
3:S:662:SER:O	3:S:666:PHE:HD2	2.03	0.41
1:A:38:VAL:HG12	2:B:353:LEU:HD22	2.02	0.41
1:A:340:ALA:O	1:A:344:LYS:HG3	2.21	0.41
1:A:613:HIS:CE1	3:C:582:ASP:HB3	2.56	0.41
2:B:235:HIS:CD2	2:B:239:VAL:HG22	2.55	0.41
3:C:606:VAL:HG12	3:C:611:LYS:HG3	2.01	0.41
2:G:258:HIS:CE1	2:G:307:ASN:HA	2.55	0.41
2:L:132:ILE:HD11	2:L:436:ARG:HB2	2.02	0.41
3:M:657:MET:HE3	3:M:657:MET:HB2	1.98	0.41
1:Q:271:SER:C	1:Q:272:VAL:CG2	2.93	0.41
1:Q:341:GLU:O	1:Q:344:LYS:HB2	2.20	0.41
2:R:378:ALA:HA	2:R:387:TYR:O	2.20	0.41
1:A:117:GLN:OE1	1:A:117:GLN:HA	2.20	0.41
1:A:258:PRO:HA	1:A:259:GLU:HA	1.79	0.41
3:C:579:MET:HG3	3:C:581:VAL:CG1	2.48	0.41
1:K:180:GLN:HG2	1:K:181:TYR:CD2	2.56	0.41
1:K:270:LYS:HE3	1:K:270:LYS:HB3	1.88	0.41
2:R:258:HIS:CD2	2:R:258:HIS:N	2.89	0.41
4:T:25:ALA:C	4:T:26:ARG:HG3	2.46	0.41
2:B:376:MET:HG3	2:B:418:PHE:CZ	2.54	0.41
3:C:593:ARG:HD2	3:C:619:LEU:CD2	2.50	0.41
1:K:30:LYS:HA	1:K:30:LYS:HD2	1.85	0.41
1:K:515:ASN:CA	1:K:671:ASN:HD21	2.31	0.41
2:L:196:LEU:HD22	2:L:206:LEU:HD11	2.01	0.41
2:L:285:THR:OG1	2:L:287:ARG:HG2	2.21	0.41
3:S:607:ASN:OD1	3:S:610:GLU:N	2.40	0.41
1:A:98:LEU:HD12	2:B:137:SER:O	2.20	0.41
1:A:730:GLN:HG3	1:A:731:ALA:N	2.36	0.41
3:C:671:ILE:HA	3:C:674:ILE:HD12	2.01	0.41
1:F:265:ASP:HA	3:H:654:ARG:NH1	2.36	0.41
1:F:582:PRO:HB2	1:F:594:TRP:HH2	1.85	0.41
2:L:221:GLN:CD	2:R:284:LYS:HD3	2.45	0.41
2:L:294:ILE:N	2:L:294:ILE:HD12	2.36	0.41
1:Q:161:ARG:HE	2:R:306:ARG:HD2	1.85	0.41
1:A:166:ILE:HG21	1:A:234:LYS:HE3	2.01	0.41
1:A:691:VAL:O	1:A:693:PRO:HD3	2.21	0.41
2:B:422:SER:HB2	2:B:439:ARG:NH1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:344:LYS:O	1:F:345:THR:HB	2.21	0.41
2:G:202:ASP:OD2	2:G:278:TYR:OH	2.32	0.41
1:K:68:VAL:CG1	1:K:69:HIS:N	2.83	0.41
1:K:71:LEU:HD11	1:K:97:PRO:CG	2.47	0.41
1:K:605:SER:HB3	1:K:637:PHE:CD2	2.56	0.41
1:Q:263:ASN:HB3	1:Q:265:ASP:C	2.46	0.41
2:R:82:PHE:CE2	2:R:439:ARG:HB2	2.56	0.41
2:R:377:LEU:O	2:R:388:VAL:HA	2.21	0.41
1:A:320:CYS:CB	1:A:324:CYS:HB2	2.50	0.41
1:A:475:SER:O	2:R:201:ARG:NH2	2.53	0.41
2:B:85:VAL:CG2	2:B:130:GLY:HA2	2.51	0.41
2:B:395:ASP:O	2:B:397:HIS:ND1	2.53	0.41
1:F:132:PRO:HB2	1:F:134:MET:CE	2.51	0.41
1:F:454:ILE:HD12	1:F:454:ILE:N	2.36	0.41
1:F:545:LYS:NZ	1:F:583:ASP:OD2	2.50	0.41
1:F:594:TRP:CH2	3:H:628:ALA:HB2	2.55	0.41
1:F:621:VAL:HG13	1:F:736:TYR:HB3	2.02	0.41
2:G:148:TYR:CE2	5:J:7:M3L:HM11	2.55	0.41
2:L:86:ASN:ND2	2:L:87:SER:H	2.16	0.41
2:L:136:GLN:HE22	2:L:180:MET:HG2	1.86	0.41
1:Q:12:PRO:HD2	1:Q:15:TRP:HD1	1.85	0.41
1:Q:30:LYS:HE2	1:Q:34:ARG:NE	2.30	0.41
1:Q:227:ILE:HG13	1:Q:240:LEU:HD13	2.02	0.41
1:Q:455:ALA:HB2	1:Q:466:VAL:HG21	2.02	0.41
1:Q:618:PRO:HD3	3:S:566:PHE:CE1	2.56	0.41
1:Q:732:ASP:HA	1:Q:733:ALA:HA	1.53	0.41
3:S:592:LEU:HD12	3:S:592:LEU:HA	1.89	0.41
3:S:607:ASN:OD1	3:S:607:ASN:C	2.64	0.41
1:A:265:ASP:OD1	3:C:654:ARG:HB2	2.21	0.41
2:B:245:ASP:OD1	2:B:249:GLU:N	2.54	0.41
1:F:442:VAL:O	1:F:446:THR:HG22	2.21	0.41
2:L:237:ASP:O	2:L:238:GLU:C	2.64	0.41
1:Q:91:PHE:O	1:Q:92:PRO:C	2.63	0.41
1:A:110:MET:HE3	1:A:624:TRP:NE1	2.35	0.40
1:A:161:ARG:NH1	1:A:164:GLY:N	2.61	0.40
1:A:565:GLN:H	1:A:565:GLN:HG2	1.38	0.40
1:A:689:HIS:CD2	1:A:726:TYR:H	2.37	0.40
1:A:714:ARG:HG2	1:A:715:ALA:O	2.21	0.40
2:G:211:LYS:HG3	2:G:238:GLU:CG	2.50	0.40
2:L:395:ASP:OD1	2:L:395:ASP:C	2.65	0.40
3:M:586:GLU:CB	3:M:587:LYS:HB3	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:133:TYR:CE2	1:Q:136:ASP:HB2	2.55	0.40
1:Q:691:VAL:C	1:Q:693:PRO:HD3	2.46	0.40
2:R:368:PHE:HB3	2:R:379:LEU:HB2	2.03	0.40
1:A:89:LEU:HD21	2:B:85:VAL:O	2.21	0.40
1:A:129:HIS:HE1	2:B:236:ARG:HG3	1.86	0.40
1:A:168:ASP:HB2	2:B:349:ASN:ND2	2.36	0.40
1:A:224:PHE:HB3	1:A:237:ALA:HB1	2.02	0.40
1:A:436:GLU:OE2	1:A:460:THR:HG23	2.21	0.40
2:B:397:HIS:O	2:B:397:HIS:CD2	2.74	0.40
7:F:1009:SAH:O4'	7:F:1009:SAH:HA	2.21	0.40
2:G:147:PHE:HA	2:G:167:GLY:HA3	2.04	0.40
1:Q:432:TRP:CD1	1:Q:469:PHE:CE1	2.99	0.40
1:Q:447:TYR:HB3	1:Q:454:ILE:HD11	2.03	0.40
3:S:610:GLU:HA	3:S:613:VAL:HG12	2.02	0.40
1:A:302:THR:HG22	1:A:305:THR:CG2	2.46	0.40
1:A:302:THR:N	1:A:303:PRO:HA	2.36	0.40
1:A:531:ASP:CG	1:K:81:ARG:NH2	2.80	0.40
3:C:607:ASN:HB3	3:C:610:GLU:H	1.86	0.40
3:C:648:ILE:HD13	3:C:685:GLN:HG2	2.03	0.40
1:F:56:LEU:HD11	2:G:246:LEU:O	2.22	0.40
1:F:89:LEU:C	1:F:89:LEU:HD12	2.46	0.40
1:F:134:MET:HB3	1:F:134:MET:HE2	1.50	0.40
1:F:235:GLY:HA2	1:F:236:THR:C	2.46	0.40
1:F:314:ALA:N	1:F:315:LEU:HD12	2.36	0.40
1:F:454:ILE:HD12	1:F:454:ILE:H	1.87	0.40
1:F:644:GLU:HG3	1:F:680:LYS:HG2	2.03	0.40
4:I:22:THR:HA	4:I:23:LYS:HA	1.65	0.40
1:K:110:MET:O	2:L:190:GLY:HA3	2.20	0.40
2:L:286:ASN:ND2	3:M:577:GLN:HB2	2.36	0.40
2:L:424:ILE:HD13	2:L:424:ILE:HG21	1.91	0.40
1:Q:578:ARG:HE	1:Q:578:ARG:HB3	1.55	0.40
1:Q:605:SER:HB3	1:Q:637:PHE:CD2	2.56	0.40
1:A:15:TRP:O	1:A:19:VAL:HG23	2.21	0.40
1:A:270:LYS:O	1:A:272:VAL:HG23	2.20	0.40
1:A:734:LEU:HB3	7:A:1009:SAH:C6	2.51	0.40
7:A:1009:SAH:H5'2	7:A:1009:SAH:H8	2.03	0.40
2:B:213:HIS:CD2	2:B:237:ASP:C	3.00	0.40
2:B:282:PRO:CB	3:C:575:ARG:HH12	2.26	0.40
2:B:387:TYR:HD2	2:B:401:CYS:SG	2.45	0.40
1:F:22:GLU:OE2	1:F:177:ALA:CB	2.68	0.40
1:F:119:ASN:HB3	1:F:645:ILE:HG23	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:285:THR:HG21	2:G:287:ARG:HE	1.86	0.40
1:K:427:PRO:HB3	1:K:468:GLU:HG3	2.03	0.40
1:K:606:ILE:HG21	1:K:707:ARG:HD2	2.04	0.40
2:L:318:LEU:HD13	2:L:353:LEU:HD12	2.03	0.40
1:Q:426:PRO:HA	1:Q:427:PRO:HD3	1.97	0.40
1:Q:677:ALA:HA	1:Q:680:LYS:O	2.21	0.40
3:S:666:PHE:O	3:S:667:ASN:HB2	2.21	0.40
1:A:145:PHE:CZ	1:A:660:LYS:HG2	2.56	0.40
1:F:162:GLU:H	1:F:162:GLU:CD	2.23	0.40
1:F:302:THR:HB	1:F:524:ASP:CG	2.47	0.40
2:L:172:ILE:O	2:L:185:HIS:HA	2.22	0.40
2:L:211:LYS:HG3	2:L:238:GLU:CD	2.46	0.40
1:Q:224:PHE:HZ	1:Q:244:TYR:CG	2.40	0.40
1:Q:606:ILE:HG22	1:Q:707:ARG:HD2	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:568:THR:OG1	1:Q:561:ARG:NH1[3_644]	2.11	0.09
1:F:561:ARG:NH1	1:K:568:THR:OG1[2_545]	2.16	0.04

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	569/746 (76%)	534 (94%)	34 (6%)	1 (0%)	43 66
1	F	558/746 (75%)	526 (94%)	31 (6%)	1 (0%)	43 66
1	K	552/746 (74%)	527 (96%)	23 (4%)	2 (0%)	30 53
1	Q	555/746 (74%)	527 (95%)	27 (5%)	1 (0%)	43 66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	363/367 (99%)	348 (96%)	15 (4%)	0	100	100
2	G	363/367 (99%)	355 (98%)	8 (2%)	0	100	100
2	L	363/367 (99%)	354 (98%)	9 (2%)	0	100	100
2	R	363/367 (99%)	352 (97%)	11 (3%)	0	100	100
3	C	123/129 (95%)	120 (98%)	3 (2%)	0	100	100
3	H	122/129 (95%)	119 (98%)	2 (2%)	1 (1%)	16	37
3	M	123/129 (95%)	118 (96%)	4 (3%)	1 (1%)	16	37
3	S	123/129 (95%)	121 (98%)	2 (2%)	0	100	100
4	D	7/13 (54%)	7 (100%)	0	0	100	100
4	I	7/13 (54%)	7 (100%)	0	0	100	100
4	O	7/13 (54%)	7 (100%)	0	0	100	100
4	T	7/13 (54%)	7 (100%)	0	0	100	100
5	E	8/12 (67%)	8 (100%)	0	0	100	100
5	J	7/12 (58%)	7 (100%)	0	0	100	100
5	P	6/12 (50%)	6 (100%)	0	0	100	100
5	U	7/12 (58%)	6 (86%)	1 (14%)	0	100	100
All	All	4233/5068 (84%)	4056 (96%)	170 (4%)	7 (0%)	43	66

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	68	VAL
1	K	66	GLN
1	F	139	LEU
3	M	582	ASP
1	K	265	ASP
1	Q	104	VAL
3	H	609	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	520/667 (78%)	494 (95%)	26 (5%)	22	47
1	F	507/667 (76%)	491 (97%)	16 (3%)	34	59
1	K	503/667 (75%)	484 (96%)	19 (4%)	29	55
1	Q	505/667 (76%)	489 (97%)	16 (3%)	34	59
2	B	328/329 (100%)	323 (98%)	5 (2%)	57	76
2	G	328/329 (100%)	321 (98%)	7 (2%)	47	69
2	L	328/329 (100%)	327 (100%)	1 (0%)	86	92
2	R	328/329 (100%)	326 (99%)	2 (1%)	78	89
3	C	119/121 (98%)	118 (99%)	1 (1%)	73	85
3	H	118/121 (98%)	115 (98%)	3 (2%)	42	66
3	M	119/121 (98%)	118 (99%)	1 (1%)	73	85
3	S	119/121 (98%)	118 (99%)	1 (1%)	73	85
4	D	6/7 (86%)	6 (100%)	0	100	100
4	I	6/7 (86%)	6 (100%)	0	100	100
4	O	6/7 (86%)	6 (100%)	0	100	100
4	T	6/7 (86%)	6 (100%)	0	100	100
5	E	8/9 (89%)	6 (75%)	2 (25%)	0	1
5	J	7/9 (78%)	7 (100%)	0	100	100
5	P	6/9 (67%)	6 (100%)	0	100	100
5	U	7/9 (78%)	7 (100%)	0	100	100
All	All	3874/4532 (86%)	3774 (97%)	100 (3%)	40	65

All (100) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	GLU
1	A	68	VAL
1	A	77	LEU
1	A	98	LEU
1	A	127	VAL
1	A	134	MET
1	A	137	GLU
1	A	161	ARG
1	A	231	PHE
1	A	233	ASP
1	A	284	LEU

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Mol	Chain	Res	Type
1	A	311	THR
1	A	312	GLU
1	A	424	ILE
1	A	527	ARG
1	A	538	ILE
1	A	565	GLN
1	A	587	THR
1	A	593	HIS
1	A	597	LYS
1	A	626	ILE
1	A	663	CYS
1	A	708	ILE
1	A	714	ARG
1	A	734	LEU
1	A	737	VAL
2	B	79	LYS
2	B	189	HIS
2	B	209	VAL
2	B	386	LEU
2	B	404	LEU
3	C	592	LEU
5	E	6	ARG
5	E	11	SER
1	F	68	VAL
1	F	71	LEU
1	F	89	LEU
1	F	96	ILE
1	F	134	MET
1	F	141	GLN
1	F	169	GLU
1	F	233	ASP
1	F	260	CYS
1	F	264	ILE
1	F	270	LYS
1	F	339	THR
1	F	439	MET
1	F	460	THR
1	F	528	GLN
1	F	663	CYS
2	G	78	CYS
2	G	88	LEU
2	G	189	HIS

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Mol	Chain	Res	Type
2	G	359	SER
2	G	386	LEU
2	G	395	ASP
2	G	397	HIS
3	H	572	LEU
3	H	605	ASP
3	H	607	ASN
1	K	72	THR
1	K	77	LEU
1	K	117	GLN
1	K	118	GLN
1	K	139	LEU
1	K	149	LEU
1	K	157	VAL
1	K	227	ILE
1	K	233	ASP
1	K	240	LEU
1	K	243	LYS
1	K	247	LEU
1	K	311	THR
1	K	328	LEU
1	K	329	GLU
1	K	515	ASN
1	K	565	GLN
1	K	645	ILE
1	K	718	THR
2	L	195	GLU
3	M	596	THR
1	Q	66	GLN
1	Q	75	SER
1	Q	126	THR
1	Q	234	LYS
1	Q	238	GLU
1	Q	239	GLU
1	Q	242	GLU
1	Q	429	ASN
1	Q	432	TRP
1	Q	439	MET
1	Q	458	ILE
1	Q	563	LYS
1	Q	565	GLN
1	Q	732	ASP

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Mol	Chain	Res	Type
1	Q	734	LEU
1	Q	735	LYS
2	R	324	CYS
2	R	395	ASP
3	S	605	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (113) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	A	69	HIS
1	A	158	HIS
1	A	182	ASN
1	A	263	ASN
1	A	282	HIS
1	A	326	GLN
1	A	429	ASN
1	A	555	ASN
1	A	689	HIS
2	B	94	GLN
2	B	136	GLN
2	B	185	HIS
2	B	189	HIS
2	B	221	GLN
2	B	258	HIS
2	B	286	ASN
2	B	349	ASN
2	B	360	GLN
3	C	562	ASN
3	C	599	GLN
3	C	607	ASN
3	C	631	GLN
3	C	633	ASN
3	C	642	ASN
3	C	655	ASN
1	F	45	ASN
1	F	69	HIS
1	F	117	GLN
1	F	129	HIS
1	F	141	GLN
1	F	176	ASN
1	F	180	GLN

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Mol	Chain	Res	Type
1	F	297	HIS
1	F	326	GLN
1	F	429	ASN
1	F	519	ASN
1	F	570	GLN
1	F	598	ASN
1	F	607	GLN
1	F	668	ASN
1	F	730	GLN
2	G	86	ASN
2	G	136	GLN
2	G	160	HIS
2	G	176	ASN
2	G	191	ASN
2	G	194	ASN
2	G	258	HIS
2	G	286	ASN
2	G	349	ASN
2	G	360	GLN
2	G	374	GLN
3	H	642	ASN
3	H	651	ASN
5	J	5	GLN
5	J	10	GLN
1	K	45	ASN
1	K	117	GLN
1	K	129	HIS
1	K	180	GLN
1	K	273	GLN
1	K	304	ASN
1	K	317	ASN
1	K	326	GLN
1	K	429	ASN
1	K	515	ASN
1	K	613	HIS
1	K	648	GLN
1	K	668	ASN
1	K	671	ASN
1	K	689	HIS
1	K	730	GLN
2	L	86	ASN
2	L	100	GLN

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Mol	Chain	Res	Type
2	L	213	HIS
2	L	258	HIS
2	L	286	ASN
2	L	349	ASN
2	L	397	HIS
3	M	567	HIS
3	M	599	GLN
3	M	633	ASN
3	M	645	GLN
3	M	655	ASN
3	M	667	ASN
5	P	5	GLN
1	Q	129	HIS
1	Q	141	GLN
1	Q	152	ASN
1	Q	158	HIS
1	Q	268	ASN
1	Q	317	ASN
1	Q	525	HIS
1	Q	671	ASN
1	Q	689	HIS
1	Q	692	ASN
1	Q	706	HIS
2	R	86	ASN
2	R	136	GLN
2	R	185	HIS
2	R	258	HIS
2	R	286	ASN
2	R	307	ASN
2	R	349	ASN
2	R	360	GLN
3	S	624	HIS
3	S	631	GLN
3	S	633	ASN
3	S	642	ASN
3	S	645	GLN
3	S	685	GLN
5	U	10	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	M3L	U	7	5	10,11,12	0.60	0	9,14,16	1.69	2 (22%)
5	M3L	P	7	5	10,11,12	0.51	0	9,14,16	0.94	0
5	M3L	J	7	5	10,11,12	0.56	0	9,14,16	1.33	1 (11%)
5	M3L	E	7	5	10,11,12	0.51	0	9,14,16	1.47	1 (11%)

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
5	M3L	U	7	5	-	4/9/10/12	-
5	M3L	P	7	5	-	3/9/10/12	-
5	M3L	J	7	5	-	2/9/10/12	-
5	M3L	E	7	5	-	4/9/10/12	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	U	7	M3L	CM3-NZ-CM1	-3.31	100.27	108.98
5	E	7	M3L	CM3-NZ-CM1	-3.23	100.49	108.98
5	J	7	M3L	CM2-NZ-CM1	-3.20	100.56	108.98
5	U	7	M3L	CD-CE-NZ	2.03	123.42	115.97

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	7	M3L	N-CA-CB-CG
5	E	7	M3L	CD-CE-NZ-CM2
5	U	7	M3L	CD-CE-NZ-CM2
5	E	7	M3L	CD-CE-NZ-CM3
5	P	7	M3L	CD-CE-NZ-CM2
5	U	7	M3L	CD-CE-NZ-CM3
5	E	7	M3L	CD-CE-NZ-CM1
5	U	7	M3L	CD-CE-NZ-CM1
5	J	7	M3L	N-CA-CB-CG
5	P	7	M3L	N-CA-CB-CG
5	U	7	M3L	N-CA-CB-CG
5	P	7	M3L	CD-CE-NZ-CM3
5	J	7	M3L	CD-CE-NZ-CM1

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	U	7	M3L	1	0
5	J	7	M3L	2	0
5	E	7	M3L	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 36 ligands modelled in this entry, 32 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	SAH	Q	1009	-	27,28,28	1.07	4 (14%)	36,40,40	1.92	10 (27%)
7	SAH	A	1009	-	27,28,28	1.12	5 (18%)	36,40,40	1.85	10 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	SAH	K	1009	-	27,28,28	1.08	4 (14%)	36,40,40	2.15	10 (27%)
7	SAH	F	1009	-	27,28,28	1.18	4 (14%)	36,40,40	1.87	10 (27%)

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
7	SAH	Q	1009	-	-	8/15/31/31	0/3/3/3
7	SAH	A	1009	-	-	4/15/31/31	0/3/3/3
7	SAH	K	1009	-	-	5/15/31/31	0/3/3/3
7	SAH	F	1009	-	-	4/15/31/31	0/3/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	F	1009	SAH	C5-N7	-2.92	1.33	1.39
7	F	1009	SAH	C2-N1	2.87	1.39	1.33
7	K	1009	SAH	C2-N3	2.79	1.38	1.33
7	A	1009	SAH	OXT-C	-2.51	1.22	1.30
7	K	1009	SAH	C2-N1	2.39	1.38	1.33
7	Q	1009	SAH	C2-N1	2.32	1.38	1.33
7	Q	1009	SAH	C2-N3	2.30	1.38	1.33
7	A	1009	SAH	C2-N1	2.26	1.38	1.33
7	A	1009	SAH	C8-N7	2.26	1.36	1.31
7	A	1009	SAH	C5-N7	-2.25	1.35	1.39
7	K	1009	SAH	C8-N7	2.24	1.36	1.31
7	F	1009	SAH	C2-N3	2.21	1.37	1.33
7	A	1009	SAH	C2-N3	2.20	1.37	1.33
7	Q	1009	SAH	C5-N7	-2.18	1.35	1.39
7	K	1009	SAH	OXT-C	-2.10	1.24	1.30
7	F	1009	SAH	C8-N7	2.07	1.35	1.31
7	Q	1009	SAH	C8-N7	2.02	1.35	1.31

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	K	1009	SAH	C5'-SD-CG	-5.68	85.42	102.26
7	A	1009	SAH	N3-C2-N1	-5.30	120.56	128.58
7	K	1009	SAH	N3-C2-N1	-5.29	120.57	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	Q	1009	SAH	C5'-SD-CG	-5.15	86.98	102.26
7	F	1009	SAH	C5'-SD-CG	-5.01	87.40	102.26
7	K	1009	SAH	C5-C4-N3	-4.87	120.00	126.72
7	Q	1009	SAH	N3-C2-N1	-4.76	121.38	128.58
7	F	1009	SAH	N3-C2-N1	-4.56	121.67	128.58
7	Q	1009	SAH	C5-C4-N3	-3.94	121.29	126.72
7	A	1009	SAH	C5-C4-N3	-3.90	121.35	126.72
7	K	1009	SAH	C2-N3-C4	3.67	120.79	111.83
7	F	1009	SAH	C2'-C1'-N9	-3.51	104.59	113.30
7	K	1009	SAH	N9-C8-N7	-3.49	108.98	113.94
7	F	1009	SAH	C5-C4-N3	-3.31	122.16	126.72
7	K	1009	SAH	C5-N7-C8	3.29	108.62	103.45
7	Q	1009	SAH	C2'-C1'-N9	-3.09	105.64	113.30
7	A	1009	SAH	C2-N3-C4	3.04	119.25	111.83
7	A	1009	SAH	N9-C8-N7	-2.98	109.71	113.94
7	A	1009	SAH	C2'-C1'-N9	-2.89	106.13	113.30
7	Q	1009	SAH	C2-N3-C4	2.83	118.74	111.83
7	K	1009	SAH	N3-C4-N9	2.78	131.89	127.17
7	K	1009	SAH	C4-C5-N7	-2.77	107.41	110.58
7	F	1009	SAH	C6-C5-C4	2.75	120.94	117.18
7	Q	1009	SAH	N9-C8-N7	-2.70	110.11	113.94
7	A	1009	SAH	C5-N7-C8	2.62	107.56	103.45
7	A	1009	SAH	C5'-SD-CG	-2.54	94.73	102.26
7	Q	1009	SAH	OXT-C-O	-2.42	118.58	124.08
7	A	1009	SAH	N3-C4-N9	2.37	131.20	127.17
7	Q	1009	SAH	C5-N7-C8	2.37	107.17	103.45
7	F	1009	SAH	N9-C8-N7	-2.33	110.64	113.94
7	A	1009	SAH	OXT-C-O	-2.25	118.96	124.08
7	Q	1009	SAH	N3-C4-N9	2.23	130.97	127.17
7	F	1009	SAH	C5-N7-C8	2.23	106.96	103.45
7	A	1009	SAH	C3'-C2'-C1'	2.18	105.59	101.46
7	F	1009	SAH	C2-N3-C4	2.16	117.10	111.83
7	K	1009	SAH	C2'-C1'-N9	-2.15	107.97	113.30
7	F	1009	SAH	OXT-C-O	-2.13	119.24	124.08
7	Q	1009	SAH	CB-CA-C	2.12	116.07	110.45
7	K	1009	SAH	C5-C4-N9	2.10	108.11	105.81
7	F	1009	SAH	N6-C6-N1	2.08	123.02	118.38

There are no chirality outliers.

All (21) torsion outliers are listed below:

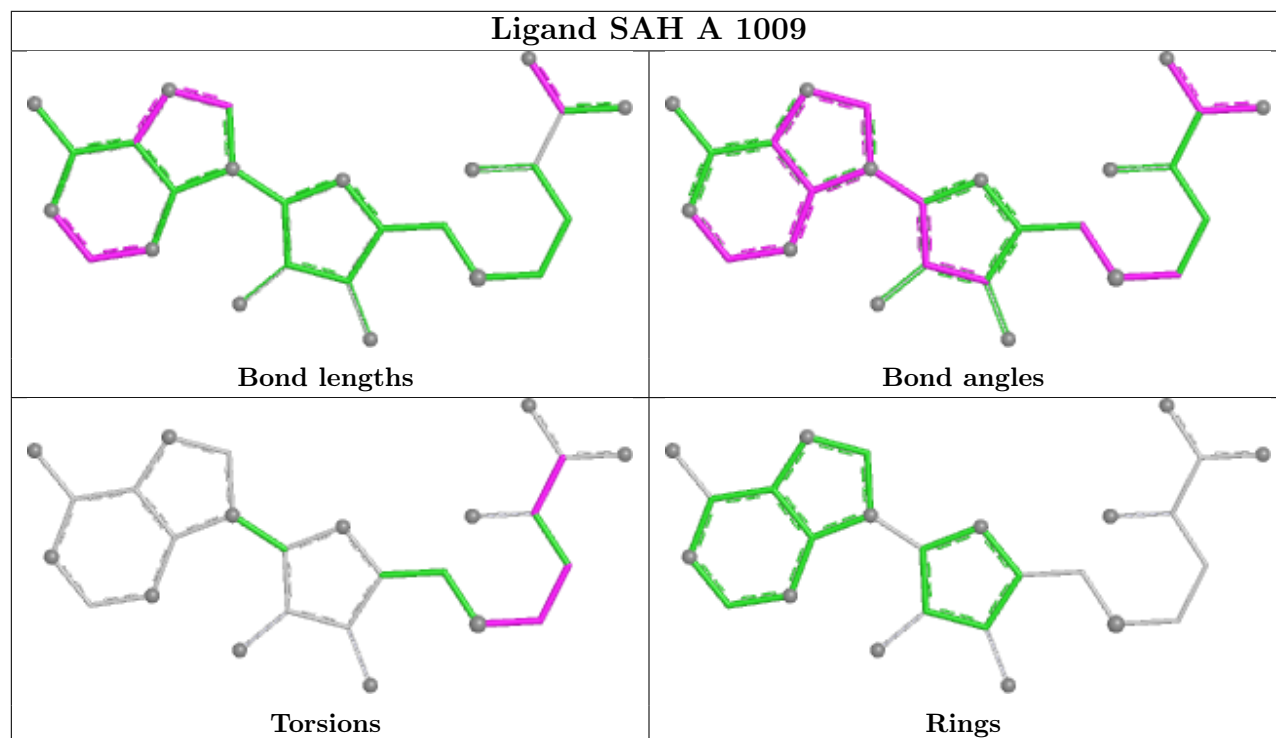
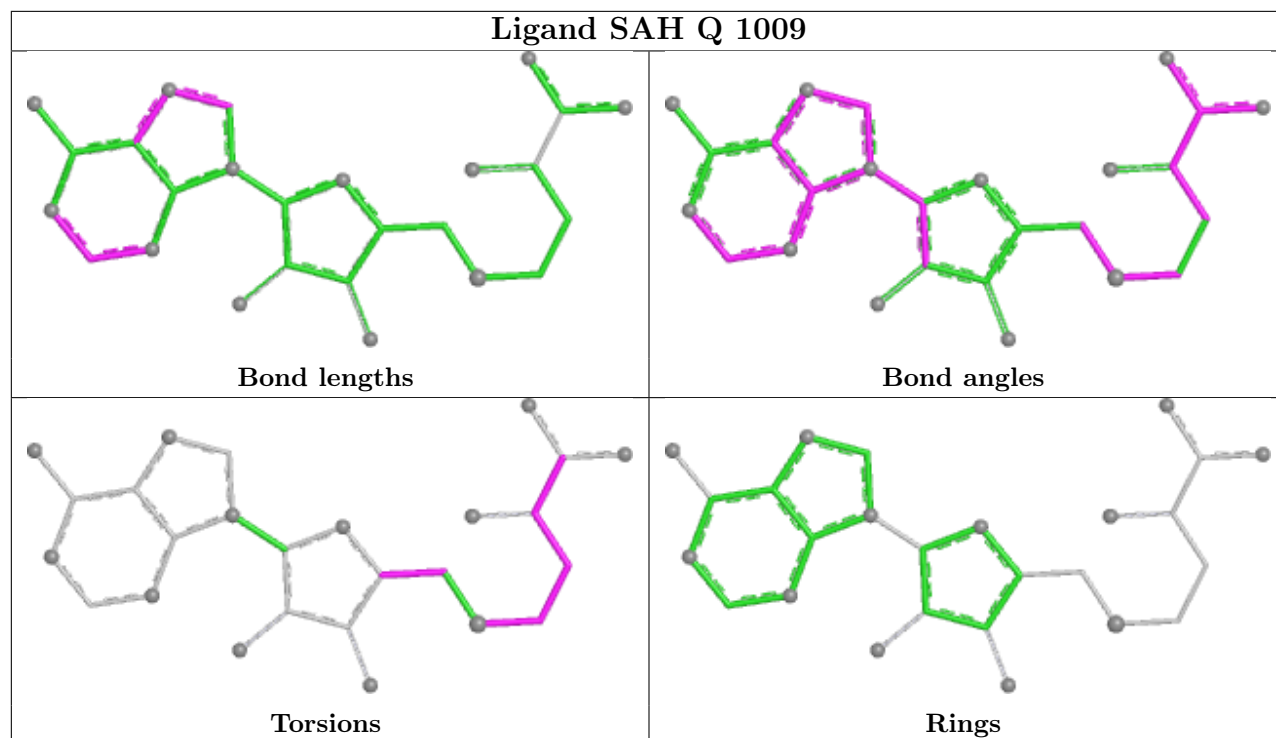
Mol	Chain	Res	Type	Atoms
7	K	1009	SAH	O4'-C4'-C5'-SD
7	K	1009	SAH	C3'-C4'-C5'-SD
7	Q	1009	SAH	O-C-CA-N
7	Q	1009	SAH	CA-CB-CG-SD
7	Q	1009	SAH	OXT-C-CA-N
7	F	1009	SAH	CA-CB-CG-SD
7	A	1009	SAH	CA-CB-CG-SD
7	K	1009	SAH	CB-CG-SD-C5'
7	Q	1009	SAH	C3'-C4'-C5'-SD
7	Q	1009	SAH	C-CA-CB-CG
7	F	1009	SAH	OXT-C-CA-CB
7	Q	1009	SAH	CB-CG-SD-C5'
7	A	1009	SAH	O-C-CA-N
7	F	1009	SAH	CB-CG-SD-C5'
7	F	1009	SAH	O-C-CA-CB
7	A	1009	SAH	CB-CG-SD-C5'
7	K	1009	SAH	OXT-C-CA-CB
7	Q	1009	SAH	O-C-CA-CB
7	K	1009	SAH	O-C-CA-CB
7	A	1009	SAH	O-C-CA-CB
7	Q	1009	SAH	OXT-C-CA-CB

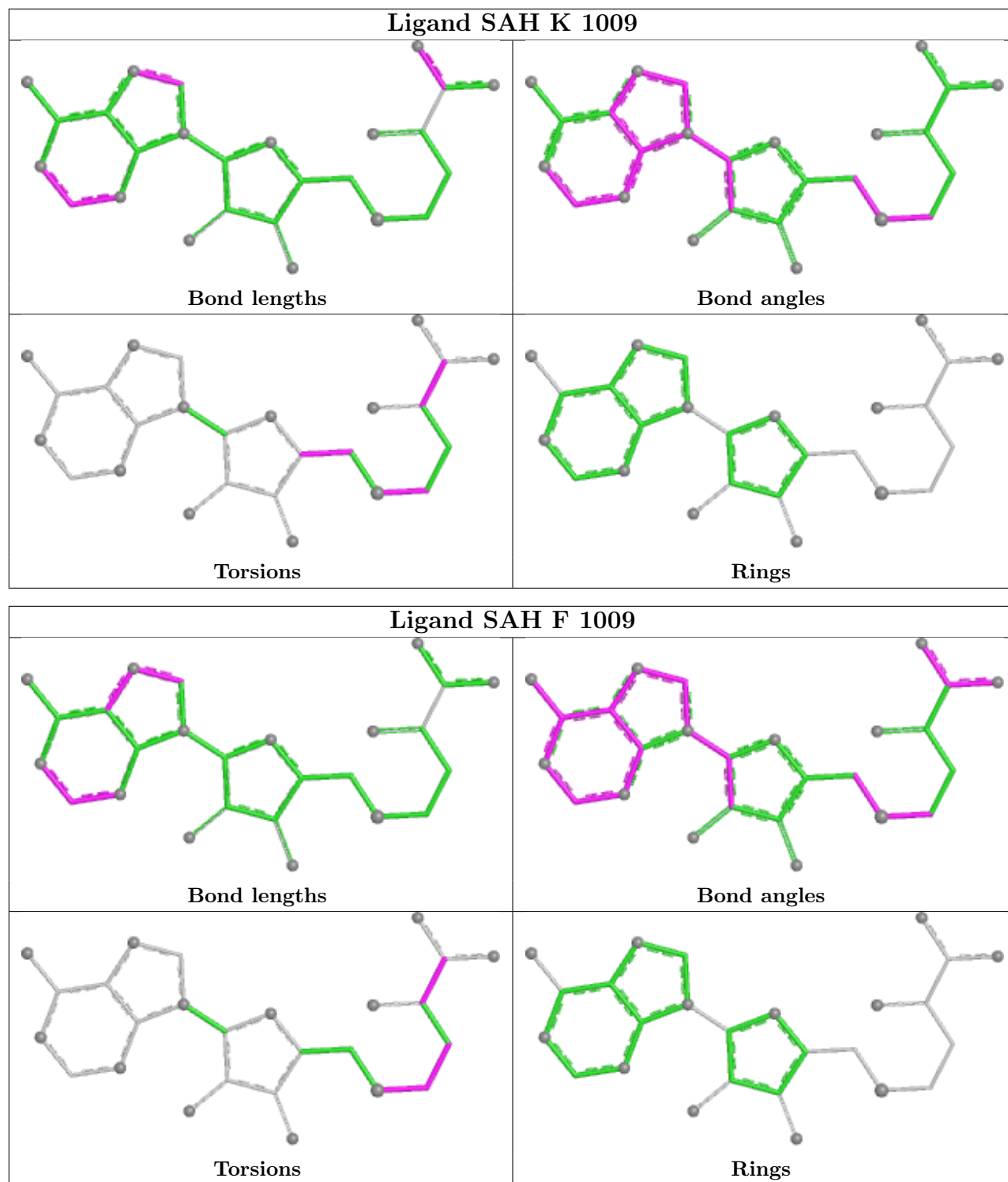
There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	Q	1009	SAH	1	0
7	A	1009	SAH	6	0
7	K	1009	SAH	1	0
7	F	1009	SAH	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

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	581/746 (77%)	0.35	27 (4%) 37 31	38, 84, 159, 196	0
1	F	568/746 (76%)	0.42	28 (4%) 35 29	40, 92, 162, 224	0
1	K	562/746 (75%)	0.38	24 (4%) 40 32	43, 92, 165, 189	0
1	Q	565/746 (75%)	0.49	36 (6%) 25 21	45, 86, 165, 202	0
2	B	365/367 (99%)	0.17	6 (1%) 70 63	51, 79, 121, 171	0
2	G	365/367 (99%)	0.10	6 (1%) 70 63	49, 75, 115, 177	0
2	L	365/367 (99%)	-0.01	4 (1%) 78 73	40, 65, 103, 140	0
2	R	365/367 (99%)	-0.06	3 (0%) 82 78	35, 61, 92, 147	0
3	C	125/129 (96%)	0.10	3 (2%) 59 51	47, 72, 148, 172	0
3	H	124/129 (96%)	0.35	3 (2%) 59 51	58, 89, 143, 187	0
3	M	125/129 (96%)	0.36	2 (1%) 70 63	56, 92, 135, 158	0
3	S	125/129 (96%)	0.09	1 (0%) 82 78	54, 89, 139, 159	0
4	D	9/13 (69%)	0.35	0 100 100	67, 86, 111, 118	0
4	I	9/13 (69%)	0.84	0 100 100	60, 81, 103, 113	0
4	O	9/13 (69%)	2.16	4 (44%) 0 0	47, 55, 59, 73	9 (100%)
4	T	9/13 (69%)	2.09	5 (55%) 0 0	48, 53, 61, 63	9 (100%)
5	E	10/12 (83%)	0.83	0 100 100	67, 89, 139, 140	0
5	J	9/12 (75%)	0.78	1 (11%) 10 9	62, 82, 127, 133	0
5	P	8/12 (66%)	0.50	0 100 100	69, 84, 117, 140	0
5	U	9/12 (75%)	1.34	1 (11%) 10 9	71, 95, 133, 134	0
All	All	4307/5068 (84%)	0.28	154 (3%) 46 38	35, 79, 155, 224	18 (0%)

All (154) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	O	25	ALA	5.3
1	Q	739	ILE	4.4
1	F	138	VAL	4.4
3	H	581	VAL	4.4
1	Q	737	VAL	4.3
1	K	446	THR	4.3
5	U	2	LEU	4.3
1	A	330	GLY	4.2
1	Q	736	TYR	4.1
1	F	424	ILE	4.1
2	G	393	VAL	4.0
1	Q	235	GLY	3.9
2	G	396	PRO	3.8
1	Q	732	ASP	3.7
1	K	219	PRO	3.7
1	K	311	THR	3.5
1	K	73	SER	3.4
1	Q	264	ILE	3.4
1	F	74	VAL	3.4
1	Q	314	ALA	3.4
1	F	235	GLY	3.3
1	K	78	ARG	3.3
4	T	25	ALA	3.3
1	Q	72	THR	3.3
1	K	77	LEU	3.3
1	F	739	ILE	3.3
1	A	103	ALA	3.2
1	K	72	THR	3.2
4	T	22	THR	3.2
1	Q	430	VAL	3.2
1	A	74	VAL	3.2
2	L	393	VAL	3.1
1	Q	733	ALA	3.1
2	L	130	GLY	3.1
1	F	736	TYR	3.0
1	A	46	ARG	3.0
1	A	734	LEU	3.0
1	Q	313	THR	3.0
1	A	77	LEU	3.0
1	Q	234	LYS	2.9
1	F	23	TYR	2.9
1	F	731	ALA	2.9
1	A	91	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
1	Q	134	MET	2.8
1	K	731	ALA	2.8
1	K	305	THR	2.8
1	Q	477	ILE	2.8
1	K	138	VAL	2.8
1	F	477	ILE	2.8
1	F	322	PRO	2.8
1	Q	661	TYR	2.8
1	Q	261	THR	2.8
3	H	588	ASP	2.8
1	A	67	PRO	2.8
1	A	139	LEU	2.7
4	T	23	LYS	2.7
4	O	30	PRO	2.7
1	Q	734	LEU	2.7
2	B	396	PRO	2.7
1	K	91	PHE	2.6
1	Q	232	PRO	2.6
1	A	71	LEU	2.6
1	K	74	VAL	2.6
1	F	733	ALA	2.6
2	B	398	LYS	2.6
1	A	138	VAL	2.6
2	B	440	LEU	2.6
2	R	393	VAL	2.6
1	A	331	ALA	2.6
1	Q	135	GLY	2.6
1	F	178	LEU	2.6
1	A	737	VAL	2.6
1	F	458	ILE	2.6
1	F	516	HIS	2.5
1	A	15	TRP	2.5
1	F	427	PRO	2.5
1	F	328	LEU	2.5
1	Q	138	VAL	2.5
2	B	399	ALA	2.5
1	Q	735	LYS	2.5
1	Q	77	LEU	2.5
2	G	187	VAL	2.5
1	K	66	GLN	2.5
1	Q	564	ALA	2.5
1	K	139	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	Q	328	LEU	2.5
1	F	330	GLY	2.5
2	G	399	ALA	2.5
1	A	101	LEU	2.5
1	Q	649	ASP	2.4
3	C	637	MET	2.4
1	A	257	PRO	2.4
1	A	79	GLY	2.4
2	R	78	CYS	2.4
2	R	316	GLY	2.4
1	Q	731	ALA	2.4
1	A	733	ALA	2.4
4	T	24	ALA	2.3
3	M	637	MET	2.3
1	F	91	PHE	2.3
1	K	732	ASP	2.3
3	M	580	GLU	2.3
3	C	581	VAL	2.3
3	H	627	ILE	2.3
1	A	72	THR	2.3
4	T	30	PRO	2.3
1	Q	231	PHE	2.3
5	J	2	LEU	2.2
1	A	126	THR	2.2
1	A	731	ALA	2.2
1	F	318	LYS	2.2
1	A	140	ASP	2.2
1	F	15	TRP	2.2
1	F	73	SER	2.2
1	Q	277	SER	2.2
1	Q	729	SER	2.2
1	A	328	LEU	2.2
1	F	77	LEU	2.2
4	O	29	ALA	2.2
1	A	317	ASN	2.2
1	Q	136	ASP	2.2
1	A	736	TYR	2.2
1	A	231	PHE	2.2
1	F	139	LEU	2.2
1	F	734	LEU	2.2
1	K	478	ALA	2.2
4	O	24	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	327	HIS	2.2
1	F	19	VAL	2.1
2	L	396	PRO	2.1
1	K	278	LEU	2.1
1	K	328	LEU	2.1
2	B	397	HIS	2.1
1	K	479	PRO	2.1
1	F	597	LYS	2.1
1	Q	17	LYS	2.1
3	C	587	LYS	2.1
3	S	672	MET	2.1
1	K	67	PRO	2.1
1	K	239	GLU	2.1
1	Q	82	GLU	2.1
1	K	664	SER	2.1
1	F	309	LYS	2.1
2	B	393	VAL	2.1
1	K	65	ILE	2.1
1	F	339	THR	2.0
1	Q	223	ILE	2.0
1	Q	728	TYR	2.0
2	G	397	HIS	2.0
1	K	526	PRO	2.0
1	Q	738	GLY	2.0
2	G	108	GLY	2.0
2	L	316	GLY	2.0
1	Q	325	TYR	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	M3L	J	7	12/13	0.95	0.09	41,52,63,65	0
5	M3L	E	7	12/13	0.96	0.13	40,58,78,90	0
5	M3L	P	7	12/13	0.96	0.11	39,57,65,71	0
5	M3L	U	7	12/13	0.97	0.09	34,59,68,68	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	SAH	K	1009	26/26	0.89	0.14	60,74,184,324	0
7	SAH	Q	1009	26/26	0.89	0.15	55,77,177,321	0
7	SAH	F	1009	26/26	0.90	0.11	40,75,86,146	0
7	SAH	A	1009	26/26	0.93	0.08	58,77,90,93	0
6	ZN	K	1002	1/1	0.97	0.05	122,122,122,122	0
6	ZN	F	1003	1/1	0.99	0.03	65,65,65,65	0
6	ZN	F	1004	1/1	0.99	0.03	65,65,65,65	0
6	ZN	F	1008	1/1	0.99	0.03	54,54,54,54	0
6	ZN	K	1001	1/1	0.99	0.05	69,69,69,69	0
6	ZN	A	1002	1/1	0.99	0.03	64,64,64,64	0
6	ZN	K	1004	1/1	0.99	0.04	70,70,70,70	0
6	ZN	K	1007	1/1	0.99	0.03	54,54,54,54	0
6	ZN	Q	1001	1/1	0.99	0.04	60,60,60,60	0
6	ZN	Q	1002	1/1	0.99	0.04	128,128,128,128	0
6	ZN	Q	1003	1/1	0.99	0.02	69,69,69,69	0
6	ZN	Q	1004	1/1	0.99	0.03	77,77,77,77	0
6	ZN	Q	1006	1/1	0.99	0.04	66,66,66,66	0
6	ZN	Q	1007	1/1	0.99	0.05	54,54,54,54	0
6	ZN	A	1003	1/1	0.99	0.04	51,51,51,51	0
6	ZN	A	1004	1/1	0.99	0.06	63,63,63,63	0
6	ZN	A	1005	1/1	0.99	0.02	56,56,56,56	0
6	ZN	F	1002	1/1	0.99	0.03	110,110,110,110	0
6	ZN	A	1007	1/1	1.00	0.04	52,52,52,52	0
6	ZN	K	1008	1/1	1.00	0.04	59,59,59,59	0
6	ZN	F	1005	1/1	1.00	0.02	67,67,67,67	0
6	ZN	F	1006	1/1	1.00	0.04	60,60,60,60	0
6	ZN	F	1007	1/1	1.00	0.03	54,54,54,54	0
6	ZN	A	1008	1/1	1.00	0.03	58,58,58,58	0
6	ZN	Q	1005	1/1	1.00	0.02	72,72,72,72	0
6	ZN	F	1001	1/1	1.00	0.02	63,63,63,63	0
6	ZN	A	1001	1/1	1.00	0.02	54,54,54,54	0
6	ZN	Q	1008	1/1	1.00	0.03	50,50,50,50	0

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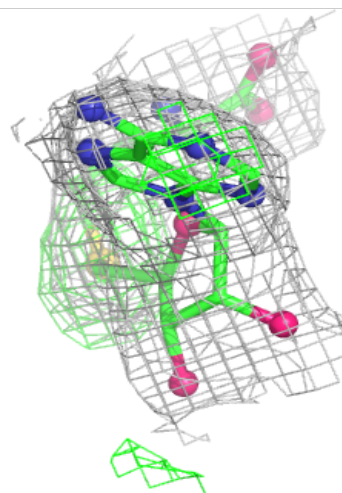
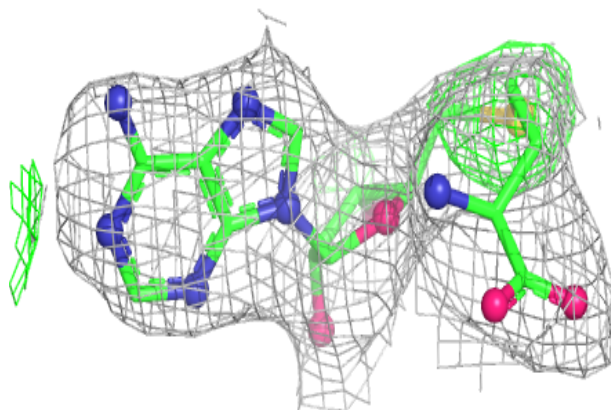
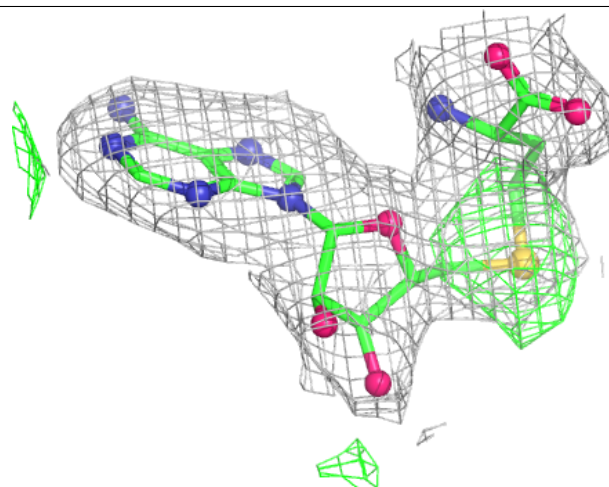
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	ZN	K	1003	1/1	1.00	0.02	66,66,66,66	0
6	ZN	A	1006	1/1	1.00	0.03	58,58,58,58	0
6	ZN	K	1005	1/1	1.00	0.02	74,74,74,74	0
6	ZN	K	1006	1/1	1.00	0.03	63,63,63,63	0

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.

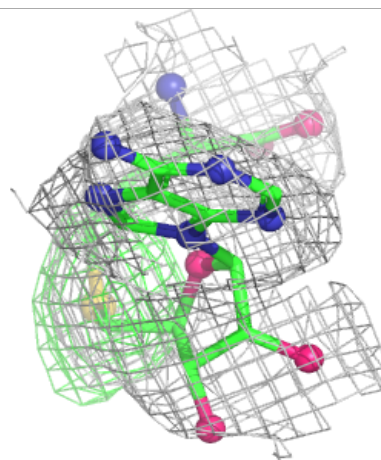
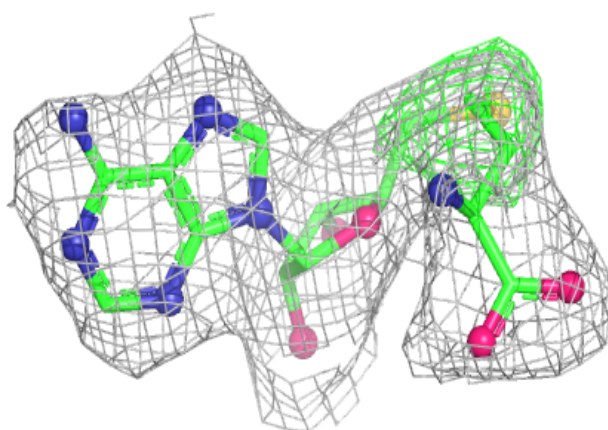
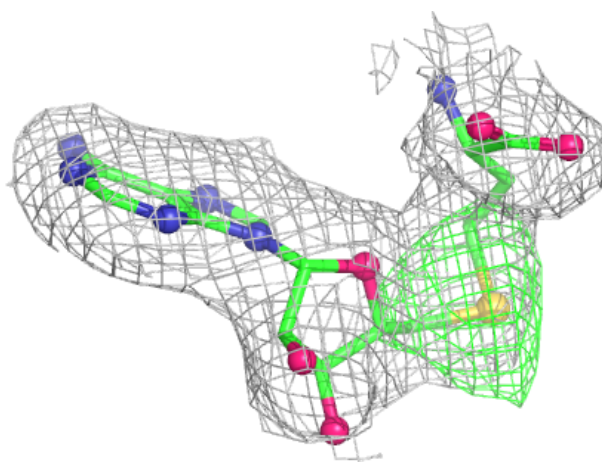
Electron density around SAH K 1009:

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



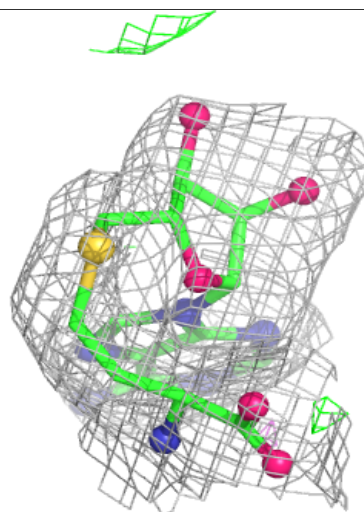
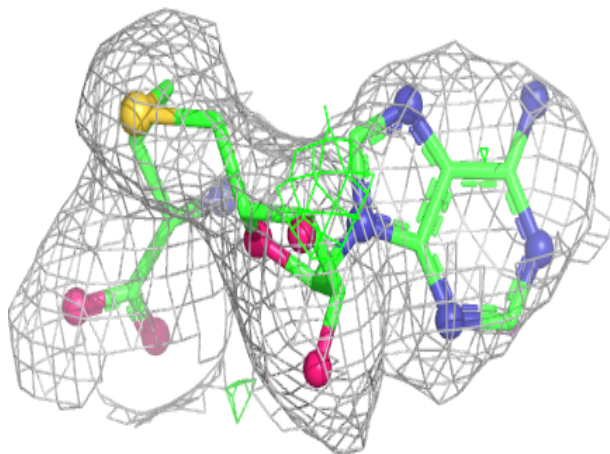
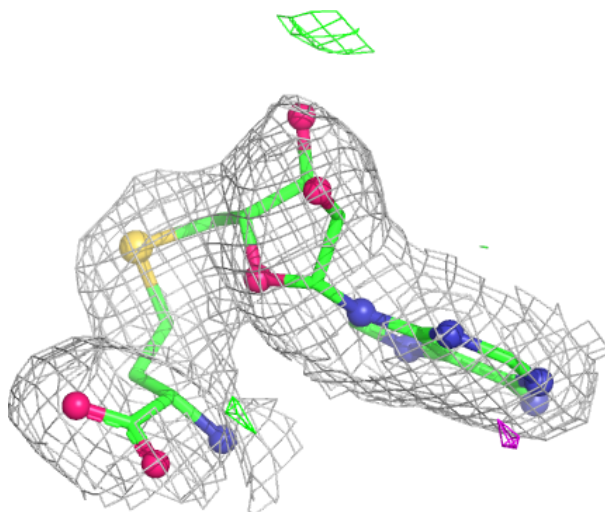
Electron density around SAH Q 1009:

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



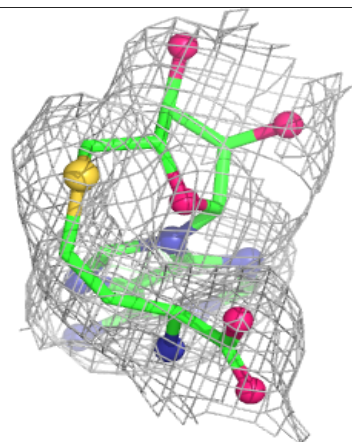
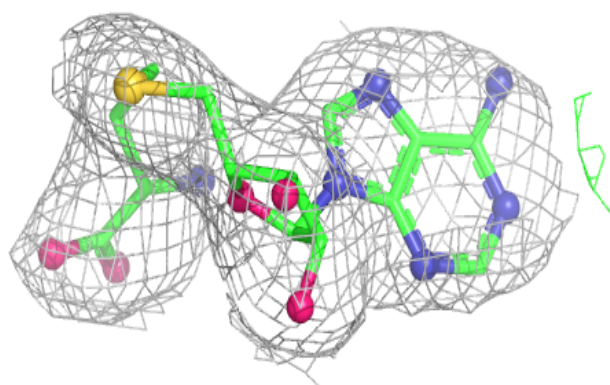
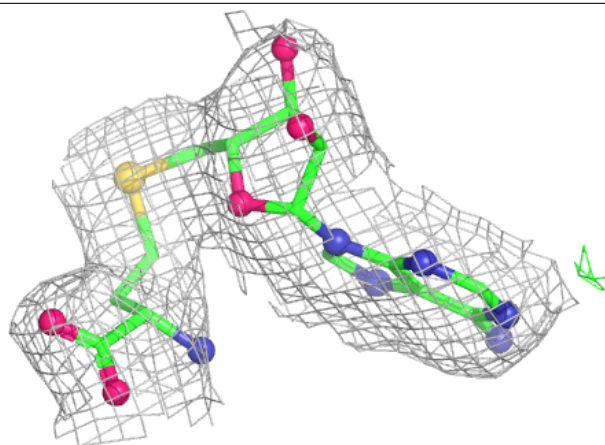
Electron density around SAH F 1009:

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



Electron density around SAH A 1009:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.