



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:05 PM UTC

PDB ID : 7F4T / pdb_00007f4t
Title : Crystal structure of SAM-bound TthMTA1-Ptep2 complex
Authors : Chen, J.; Liu, L.
Deposited on : 2021-06-21
Resolution : 3.68 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

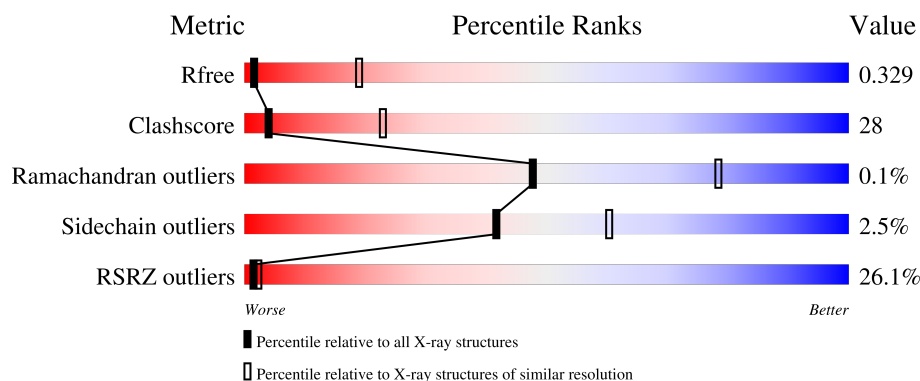
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.68 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	1263 (3.80-3.56)
Clashscore	190562	1305 (3.80-3.56)
Ramachandran outliers	187476	1259 (3.80-3.56)
Sidechain outliers	187428	1256 (3.80-3.56)
RSRZ outliers	180081	1262 (3.80-3.56)

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	247	10% 58% 29% 12%
1	E	247	14% 60% 28% 12%
1	H	247	11% 58% 30% 12%
1	K	247	16% 62% 26% 12%
2	B	128	22% 55% 38% 5%

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Mol	Chain	Length	Quality of chain
2	D	128	
2	G	128	
2	J	128	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SAM	E	401	-	-	X	-
3	SAM	H	401	-	-	X	-
3	SAM	K	401	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10725 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.

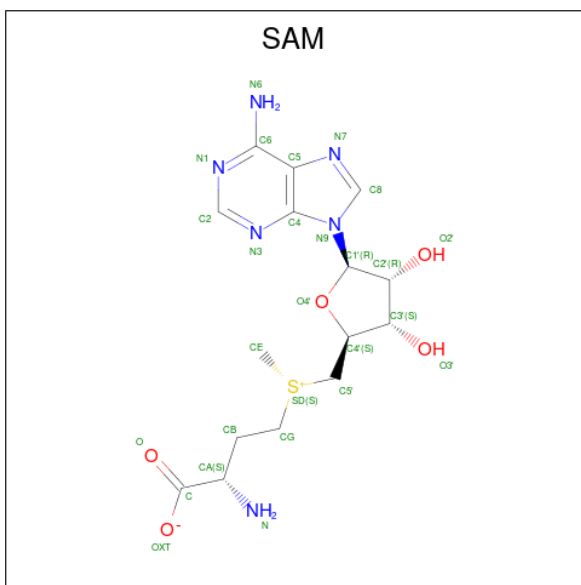
- Molecule 1 is a protein called MT-a70 family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	0	0
			1743	1107	305	321	10			
1	E	218	Total	C	N	O	S	0	0	0
			1743	1107	305	321	10			
1	H	218	Total	C	N	O	S	0	0	0
			1737	1104	302	321	10			
1	K	218	Total	C	N	O	S	0	0	0
			1743	1107	305	321	10			

- Molecule 2 is a protein called Ptep2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	125	Total	C	N	O	S	0	0	0
			968	622	162	179	5			
2	D	125	Total	C	N	O	S	0	0	0
			907	584	154	166	3			
2	G	124	Total	C	N	O	S	0	0	0
			908	584	157	163	4			
2	J	124	Total	C	N	O	S	0	0	0
			856	551	146	156	3			

- Molecule 3 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: $C_{15}H_{22}N_6O_5S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 27	C 15	N 6	O 5	S 1	0	0
3	E	1	Total 27	C 15	N 6	O 5	S 1	0	0
3	H	1	Total 27	C 15	N 6	O 5	S 1	0	0
3	K	1	Total 27	C 15	N 6	O 5	S 1	0	0

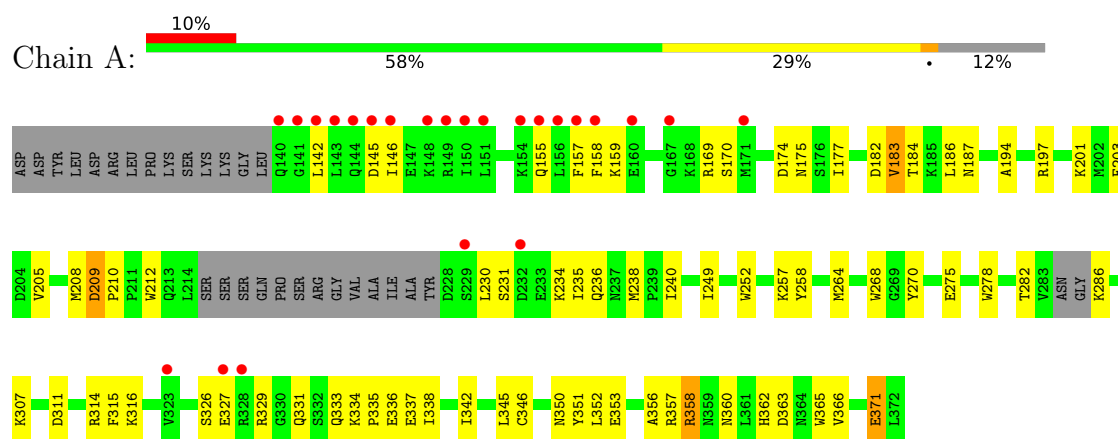
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total O 1 1	0	0
4	K	1	Total O 1 1	0	0
4	B	3	Total O 3 3	0	0
4	D	5	Total O 5 5	0	0
4	G	2	Total O 2 2	0	0

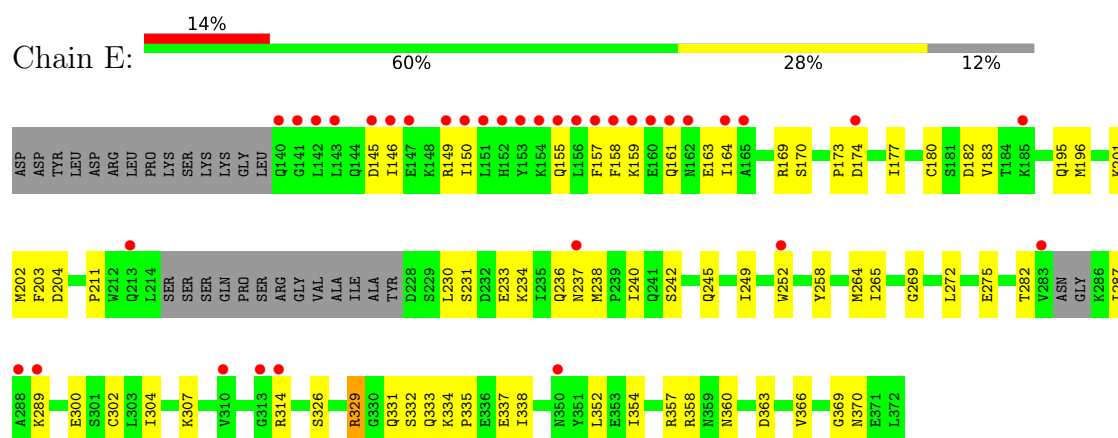
3 Residue-property plots [i](#)

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

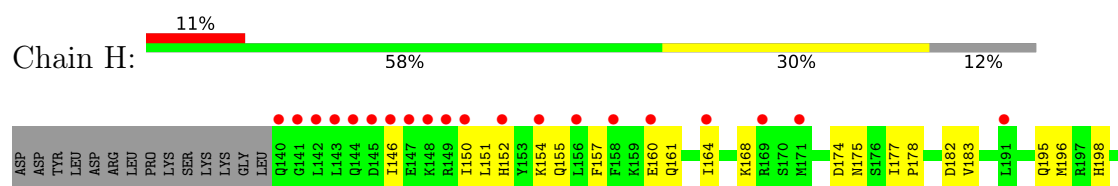
- Molecule 1: MT-a70 family protein

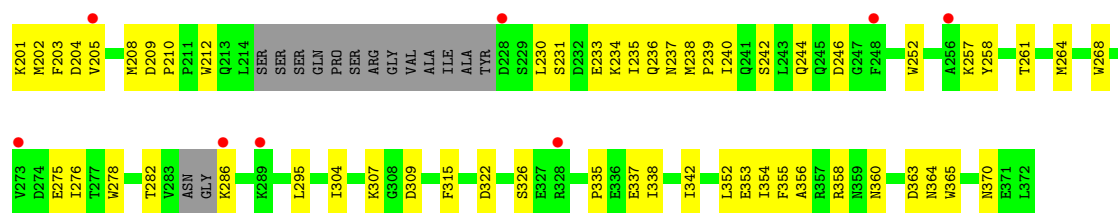


- Molecule 1: MT-a70 family protein

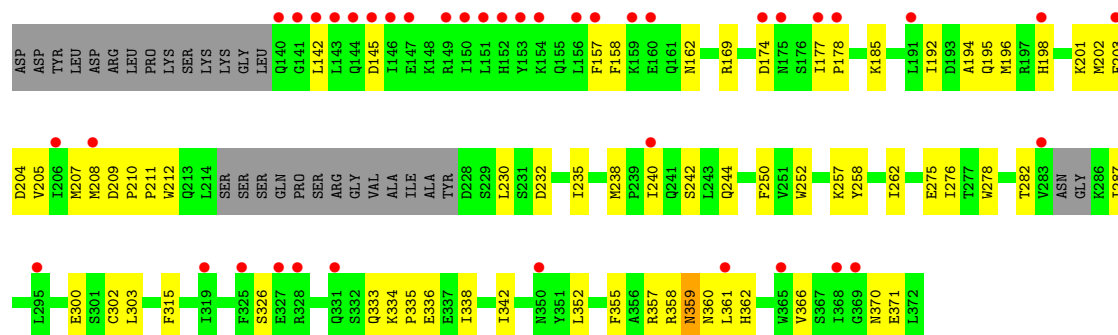


- Molecule 1: MT-a70 family protein

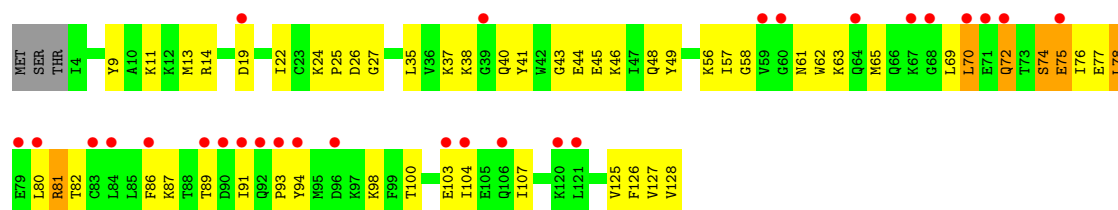




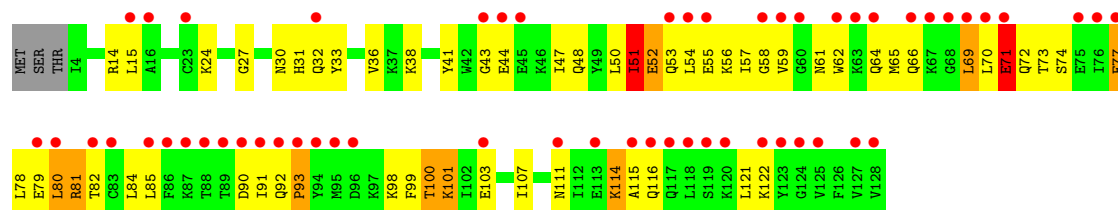
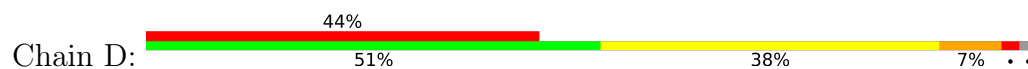
• Molecule 1: MT-a70 family protein



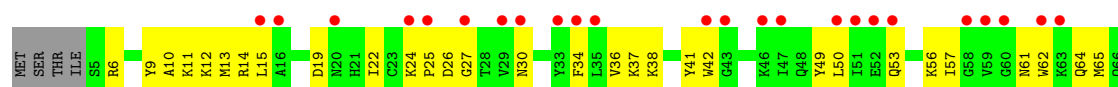
• Molecule 2: Ptep2

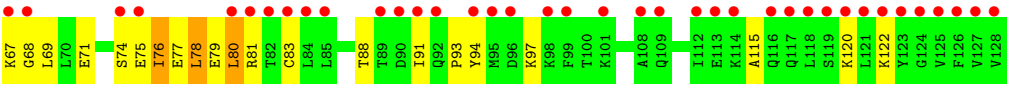


• Molecule 2: Ptep2

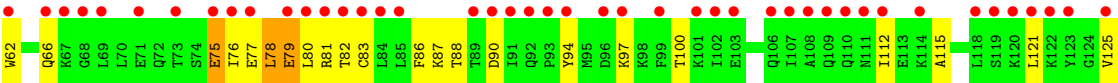
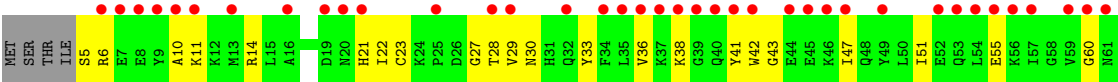


• Molecule 2: Ptep2





● Molecule 2: Ptep2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	98.13Å 110.19Å 102.64Å 90.00° 91.64° 90.00°	Depositor
Resolution (Å)	49.04 – 3.68 49.04 – 3.68	Depositor EDS
% Data completeness (in resolution range)	76.0 (49.04-3.68) 76.0 (49.04-3.68)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 3.67Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660, PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.283 , 0.329 0.283 , 0.329	Depositor DCC
R_{free} test set	915 reflections (3.84%)	wwPDB-VP
Wilson B-factor (Å ²)	15.0	Xtriage
Anisotropy	0.742	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 35.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.047 for l,k,-h 0.065 for h,-k,-l 0.059 for l,-k,h	Xtriage
F_o, F_c correlation	0.75	EDS
Total number of atoms	10725	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.38	2/1778 (0.1%)	0.54	4/2397 (0.2%)
1	E	0.19	0/1778	0.37	0/2397
1	H	0.16	0/1772	0.37	0/2390
1	K	0.15	0/1778	0.36	0/2397
2	B	0.29	0/981	0.64	1/1315 (0.1%)
2	D	0.35	0/920	0.94	9/1238 (0.7%)
2	G	0.25	0/920	0.73	2/1235 (0.2%)
2	J	0.22	0/865	0.58	1/1163 (0.1%)
All	All	0.26	2/10792 (0.0%)	0.55	17/14532 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	209	ASP	C-N	5.90	1.40	1.33
1	A	210	PRO	N-CD	5.01	1.54	1.47

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	68	GLY	N-CA-C	15.84	131.66	112.49
2	D	52	GLU	N-CA-C	9.59	121.33	111.07
2	G	38	LYS	CB-CA-C	-8.56	106.70	116.63
2	D	114	LYS	N-CA-C	8.48	120.52	111.28
2	J	75	GLU	N-CA-C	-7.57	100.54	110.53
2	D	115	ALA	N-CA-C	7.51	119.46	111.28
1	A	209	ASP	CA-C-N	-6.82	113.36	120.38
1	A	209	ASP	C-N-CA	-6.82	113.36	120.38
2	D	116	GLN	N-CA-C	6.51	118.38	111.28
2	D	84	LEU	N-CA-C	-6.40	104.30	111.28
2	D	93	PRO	N-CA-CB	6.29	109.85	103.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	51	ILE	N-CA-C	5.74	116.48	110.62
2	D	69	LEU	CA-CB-CG	-5.55	96.88	116.30
2	D	71	GLU	N-CA-C	-5.50	104.64	111.90
1	A	210	PRO	CA-C-N	-5.39	113.10	119.84
1	A	210	PRO	C-N-CA	-5.39	113.10	119.84
2	B	72	GLN	N-CA-C	-5.11	104.12	110.41

There are no chirality outliers.

There are no planarity outliers.

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	1743	0	1684	91	1
1	E	1743	0	1684	63	0
1	H	1737	0	1673	87	1
1	K	1743	0	1684	73	0
2	B	968	0	946	83	0
2	D	907	0	796	126	4
2	G	908	0	827	79	0
2	J	856	0	715	58	4
3	A	27	0	22	5	0
3	E	27	0	20	9	0
3	H	27	0	22	15	0
3	K	27	0	21	26	0
4	B	3	0	0	1	0
4	D	5	0	0	1	0
4	E	1	0	0	0	0
4	G	2	0	0	0	0
4	K	1	0	0	0	0
All	All	10725	0	10094	583	5

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 28.

All (583) 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)
2:D:57:ILE:CG1	2:D:65:MET:HB3	1.06	1.54
1:K:157:PHE:CD1	2:J:80:LEU:HD21	1.45	1.49
1:H:152:HIS:CB	2:B:76:ILE:HD12	1.40	1.49
1:A:142:LEU:CD1	2:G:75:GLU:HB2	1.40	1.49
2:D:57:ILE:CG1	2:D:65:MET:CB	1.92	1.47
1:K:157:PHE:CE1	2:J:80:LEU:CD2	2.00	1.42
1:K:157:PHE:CE1	2:J:80:LEU:HD22	1.51	1.41
2:G:49:TYR:HB3	2:G:69:LEU:CG	1.48	1.41
2:D:55:GLU:CB	2:D:100:THR:HA	1.55	1.35
1:H:152:HIS:CA	2:B:76:ILE:HD12	1.58	1.34
2:B:49:TYR:HD1	2:B:69:LEU:CG	1.41	1.33
1:K:157:PHE:CD1	2:J:80:LEU:CD2	2.09	1.32
2:D:79:GLU:OE2	2:D:91:ILE:HD13	1.19	1.32
1:A:142:LEU:HD13	2:G:75:GLU:CB	1.57	1.31
1:K:209:ASP:OD2	3:K:401:SAM:N	1.61	1.30
2:G:75:GLU:O	2:G:78:LEU:HD23	1.22	1.29
2:B:74:SER:OG	2:B:78:LEU:HD21	1.30	1.28
1:H:152:HIS:CA	2:B:76:ILE:CD1	2.10	1.28
1:H:152:HIS:HA	2:B:76:ILE:CD1	1.63	1.27
1:E:182:ASP:OD1	3:E:401:SAM:N6	1.69	1.26
2:D:82:THR:O	2:D:85:LEU:HB2	1.18	1.26
1:A:142:LEU:HD23	1:A:142:LEU:O	1.33	1.24
1:A:142:LEU:HG	1:A:145:ASP:CB	1.67	1.23
2:B:49:TYR:CD1	2:B:69:LEU:CG	2.20	1.23
2:D:82:THR:HA	2:D:85:LEU:CD1	1.68	1.22
2:G:75:GLU:O	2:G:78:LEU:CD2	1.87	1.21
1:A:209:ASP:OD2	1:A:334:LYS:HE3	1.40	1.19
2:D:82:THR:CA	2:D:85:LEU:HD12	1.73	1.18
1:A:209:ASP:OD2	1:A:334:LYS:CE	1.91	1.18
2:D:55:GLU:CB	2:D:100:THR:CA	2.22	1.18
2:D:70:LEU:O	2:D:71:GLU:HG2	1.41	1.17
1:A:142:LEU:CD1	2:G:75:GLU:CB	2.18	1.14
1:K:142:LEU:HG	1:K:145:ASP:CB	1.77	1.14
2:G:49:TYR:CB	2:G:69:LEU:CG	2.26	1.14
1:H:152:HIS:HA	2:B:76:ILE:HD13	1.18	1.13
1:K:142:LEU:HD23	1:K:142:LEU:O	1.46	1.13
2:D:82:THR:O	2:D:85:LEU:CB	1.97	1.11
2:B:74:SER:OG	2:B:78:LEU:CD2	1.99	1.10
2:D:55:GLU:CA	2:D:100:THR:HA	1.82	1.09
2:D:62:TRP:CH2	2:D:79:GLU:CD	2.31	1.09
2:G:49:TYR:C	2:G:69:LEU:CG	2.27	1.08
2:D:62:TRP:CZ2	2:D:79:GLU:OE1	2.08	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:152:HIS:HB3	2:B:76:ILE:HD12	1.07	1.06
2:D:48:GLN:HA	2:D:51:ILE:HD11	1.11	1.05
1:A:142:LEU:CG	1:A:145:ASP:HB2	1.86	1.05
1:H:209:ASP:OD2	3:H:401:SAM:N	1.89	1.04
2:D:62:TRP:CH2	2:D:79:GLU:CG	2.41	1.03
1:A:208:MET:HE1	1:A:268:TRP:CZ3	1.92	1.03
2:J:78:LEU:HD12	2:J:78:LEU:H	1.19	1.03
1:A:208:MET:HE1	1:A:268:TRP:HZ3	1.21	1.00
1:H:182:ASP:OD1	3:H:401:SAM:N6	1.95	1.00
1:K:157:PHE:CZ	2:J:80:LEU:HD22	1.95	1.00
2:D:48:GLN:CA	2:D:51:ILE:HD11	1.91	0.99
2:D:57:ILE:O	2:D:61:ASN:HB2	1.62	0.99
1:K:142:LEU:HG	1:K:145:ASP:HB2	0.99	0.99
1:H:152:HIS:HB3	2:B:76:ILE:CD1	1.93	0.98
1:E:360:ASN:ND2	3:E:401:SAM:OXT	1.98	0.97
2:D:62:TRP:CZ2	2:D:79:GLU:CD	2.43	0.97
2:D:48:GLN:O	2:D:51:ILE:HG12	1.65	0.96
2:D:47:ILE:O	2:D:51:ILE:HD13	1.64	0.96
2:D:52:GLU:O	2:D:101:LYS:HD2	1.65	0.96
1:H:152:HIS:CB	2:B:76:ILE:CD1	2.36	0.95
2:D:79:GLU:OE2	2:D:91:ILE:CD1	2.14	0.94
1:A:282:THR:HG1	1:A:286:LYS:N	1.65	0.94
2:B:70:LEU:CD1	2:B:74:SER:HB3	1.97	0.94
2:B:70:LEU:HD11	2:B:74:SER:N	1.80	0.94
2:D:57:ILE:CG1	2:D:65:MET:CA	2.45	0.94
1:K:142:LEU:CG	1:K:145:ASP:HB2	1.96	0.94
1:H:152:HIS:O	2:B:76:ILE:HD11	1.67	0.93
1:K:211:PRO:HG3	3:K:401:SAM:N7	1.82	0.92
2:D:55:GLU:HA	2:D:100:THR:HA	1.48	0.92
2:B:70:LEU:HD11	2:B:74:SER:H	1.34	0.91
2:D:55:GLU:CB	2:D:100:THR:CB	2.48	0.90
1:A:142:LEU:O	1:A:142:LEU:CD2	2.20	0.90
1:A:142:LEU:HG	1:A:145:ASP:HB2	0.91	0.90
2:D:48:GLN:HA	2:D:51:ILE:CD1	2.00	0.90
1:A:142:LEU:HD12	2:G:75:GLU:HB2	1.54	0.88
1:H:152:HIS:C	2:B:76:ILE:CD1	2.46	0.88
2:B:40:GLN:OE1	2:B:75:GLU:OE2	1.91	0.88
2:D:62:TRP:CH2	2:D:79:GLU:HG3	2.08	0.88
1:H:152:HIS:O	2:B:76:ILE:CD1	2.21	0.87
1:A:360:ASN:ND2	3:A:401:SAM:OXT	2.08	0.87
2:D:82:THR:HA	2:D:85:LEU:HD12	0.91	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:126:PHE:CG	4:B:201:HOH:O	2.28	0.86
2:G:49:TYR:CA	2:G:69:LEU:CG	2.51	0.86
2:B:74:SER:HG	2:B:78:LEU:HD21	1.34	0.85
1:A:209:ASP:OD2	1:A:334:LYS:HE2	1.75	0.85
1:A:142:LEU:HB3	2:G:76:ILE:HG12	1.58	0.85
2:D:55:GLU:HA	2:D:99:PHE:O	1.77	0.85
2:B:62:TRP:HA	2:B:65:MET:HB2	1.59	0.84
1:A:142:LEU:HB3	2:G:76:ILE:CD1	2.06	0.84
2:B:70:LEU:HD12	2:B:74:SER:HB3	1.55	0.84
1:A:201:LYS:HZ1	1:A:314:ARG:HD3	1.40	0.84
2:G:50:LEU:HD12	2:G:65:MET:HE3	1.59	0.84
2:D:90:ASP:OD1	4:D:201:HOH:O	1.96	0.83
2:D:55:GLU:CB	2:D:101:LYS:H	1.91	0.83
1:K:371:GLU:OE2	3:K:401:SAM:O3'	1.96	0.83
1:K:201:LYS:NZ	1:K:204:ASP:OD1	2.11	0.82
1:H:152:HIS:ND1	2:B:76:ILE:HB	1.95	0.82
3:H:401:SAM:O3'	3:H:401:SAM:SD	2.31	0.81
1:A:282:THR:OG1	1:A:286:LYS:N	2.13	0.81
2:B:49:TYR:HB3	2:B:69:LEU:CG	2.10	0.81
1:H:360:ASN:ND2	3:H:401:SAM:OXT	2.13	0.81
2:J:76:ILE:HA	2:J:78:LEU:CD1	2.10	0.81
2:G:79:GLU:HG2	2:G:80:LEU:HD13	1.64	0.80
1:K:157:PHE:CG	2:J:80:LEU:HD21	2.15	0.79
1:K:142:LEU:O	1:K:142:LEU:CD2	2.29	0.79
1:A:142:LEU:C	2:G:76:ILE:HD11	2.06	0.79
2:D:47:ILE:O	2:D:51:ILE:CD1	2.31	0.78
1:E:183:VAL:HG13	3:E:401:SAM:H2	1.66	0.78
1:A:142:LEU:HD13	2:G:75:GLU:CG	2.14	0.77
1:A:208:MET:CE	1:A:268:TRP:HZ3	1.97	0.77
2:D:62:TRP:HH2	2:D:79:GLU:CD	1.92	0.77
1:A:142:LEU:HB3	2:G:76:ILE:CG1	2.14	0.77
2:D:53:GLN:O	2:D:56:LYS:HB3	1.84	0.77
2:B:77:GLU:O	2:B:80:LEU:N	2.17	0.76
1:A:311:ASP:HB3	1:K:185:LYS:HE2	1.67	0.76
1:E:177:ILE:HD12	1:E:366:VAL:HG22	1.68	0.76
1:H:282:THR:HG1	1:H:286:LYS:N	1.85	0.75
1:K:355:PHE:O	3:K:401:SAM:HE3	1.86	0.75
1:A:142:LEU:HD13	2:G:75:GLU:HB2	0.76	0.75
2:D:81:ARG:O	2:D:81:ARG:NE	2.20	0.74
1:E:195:GLN:NE2	1:E:201:LYS:O	2.20	0.74
2:B:70:LEU:C	2:B:70:LEU:HD22	2.13	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:54:LEU:C	2:D:56:LYS:H	1.93	0.74
2:D:52:GLU:O	2:D:101:LYS:CD	2.35	0.74
1:A:157:PHE:HZ	2:B:81:ARG:NH2	1.86	0.73
1:A:142:LEU:HD22	2:G:76:ILE:HG13	1.70	0.73
1:E:326:SER:OG	1:E:337:GLU:OE1	2.07	0.73
2:B:24:LYS:HG2	2:B:25:PRO:HD2	1.69	0.72
2:D:57:ILE:O	2:D:61:ASN:CB	2.38	0.72
2:D:62:TRP:HZ2	2:D:79:GLU:OE1	1.68	0.72
1:A:157:PHE:HZ	2:B:81:ARG:HH21	1.34	0.72
1:A:142:LEU:HD22	2:G:76:ILE:CG1	2.19	0.72
2:D:80:LEU:HD13	2:D:80:LEU:C	2.15	0.72
2:J:75:GLU:CG	2:J:77:GLU:HB2	2.20	0.72
2:D:55:GLU:CB	2:D:101:LYS:N	2.53	0.71
2:D:70:LEU:HB3	2:D:74:SER:CB	2.20	0.71
2:J:42:TRP:CD1	2:J:81:ARG:HD2	2.26	0.71
1:H:201:LYS:NZ	1:H:204:ASP:OD1	2.22	0.71
2:B:75:GLU:HA	2:G:122:LYS:HD3	1.73	0.71
2:B:80:LEU:C	2:B:80:LEU:HD23	2.15	0.70
1:A:194:ALA:HB2	1:E:237:ASN:HD21	1.56	0.70
1:A:177:ILE:HD12	1:A:366:VAL:HG22	1.74	0.70
1:E:201:LYS:NZ	1:E:204:ASP:OD1	2.25	0.69
2:G:57:ILE:HG22	2:G:61:ASN:HB3	1.74	0.69
3:K:401:SAM:H5'2	3:K:401:SAM:H8	1.72	0.69
2:D:50:LEU:HA	2:D:69:LEU:HB3	1.74	0.68
1:H:161:GLN:OE1	2:G:81:ARG:NH1	2.26	0.68
1:E:158:PHE:HE1	2:D:80:LEU:CD2	2.06	0.68
1:E:170:SER:H	2:D:31:HIS:HD2	1.42	0.68
2:D:82:THR:C	2:D:85:LEU:HB2	2.15	0.68
1:H:238:MET:HE2	1:H:240:ILE:HD11	1.76	0.68
1:H:258:TYR:OH	1:H:275:GLU:OE1	2.11	0.68
2:G:75:GLU:O	2:G:78:LEU:HD21	1.91	0.68
1:H:233:GLU:O	1:H:237:ASN:ND2	2.27	0.68
1:K:196:MET:HE2	1:K:202:MET:HE2	1.74	0.68
2:B:75:GLU:C	2:B:77:GLU:H	2.01	0.68
2:B:80:LEU:HD23	2:B:80:LEU:O	1.94	0.68
2:D:66:GLN:O	2:D:72:GLN:N	2.28	0.67
1:K:333:GLN:HA	3:K:401:SAM:OXT	1.94	0.67
1:E:158:PHE:HE1	2:D:80:LEU:HD23	1.59	0.67
1:H:155:GLN:HE22	2:G:122:LYS:HB3	1.59	0.67
2:D:82:THR:O	2:D:85:LEU:N	2.28	0.67
2:B:87:LYS:HA	2:B:125:VAL:HG23	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:70:LEU:HD13	2:B:70:LEU:O	1.95	0.66
1:K:252:TRP:HZ2	1:K:338:ILE:HG13	1.60	0.66
1:K:360:ASN:OD1	3:K:401:SAM:O	2.13	0.66
2:D:61:ASN:HB3	2:D:64:GLN:HB3	1.76	0.66
1:H:276:ILE:HD13	1:H:322:ASP:HA	1.78	0.66
1:K:157:PHE:CE1	2:J:80:LEU:HD23	2.24	0.66
2:D:70:LEU:C	2:D:71:GLU:HG2	2.17	0.66
1:A:358:ARG:HH11	1:A:358:ARG:CG	2.09	0.66
1:K:230:LEU:HD23	1:K:235:ILE:HG12	1.77	0.66
2:D:111:ASN:O	2:D:114:LYS:HG2	1.95	0.66
2:D:57:ILE:CG1	2:D:65:MET:N	2.58	0.66
2:D:82:THR:CB	2:D:85:LEU:HD12	2.26	0.66
2:J:47:ILE:O	2:J:51:ILE:N	2.26	0.66
1:K:360:ASN:ND2	3:K:401:SAM:O	2.29	0.66
2:J:83:CYS:O	2:J:87:LYS:N	2.27	0.66
1:E:157:PHE:CE1	1:E:161:GLN:HG3	2.31	0.65
1:A:142:LEU:HD12	2:G:75:GLU:CB	2.18	0.65
1:K:209:ASP:HB3	3:K:401:SAM:HE2	1.76	0.65
1:H:155:GLN:NE2	2:G:122:LYS:O	2.28	0.65
2:B:49:TYR:CB	2:B:69:LEU:CG	2.75	0.65
2:D:70:LEU:O	2:D:73:THR:N	2.28	0.65
2:J:94:TYR:HA	2:J:97:LYS:HD2	1.78	0.65
2:J:5:SER:OG	2:J:6:ARG:N	2.23	0.65
2:G:53:GLN:O	2:G:57:ILE:HG12	1.97	0.65
2:D:62:TRP:HH2	2:D:79:GLU:HG3	1.59	0.65
2:D:82:THR:O	2:D:85:LEU:CA	2.45	0.65
1:H:152:HIS:CA	2:B:76:ILE:HD13	1.95	0.64
1:H:160:GLU:OE2	1:H:168:LYS:NZ	2.30	0.64
1:H:195:GLN:NE2	1:H:201:LYS:O	2.31	0.64
1:E:182:ASP:OD1	3:E:401:SAM:C6	2.45	0.64
1:K:169:ARG:NH2	1:K:174:ASP:OD2	2.30	0.64
1:E:258:TYR:OH	1:E:275:GLU:OE1	2.15	0.64
1:A:231:SER:HB3	1:A:234:LYS:HD3	1.78	0.64
1:H:353:GLU:HG2	1:H:356:ALA:HB2	1.79	0.64
2:B:61:ASN:O	2:B:65:MET:N	2.29	0.63
2:D:78:LEU:C	2:D:78:LEU:HD12	2.23	0.63
2:G:24:LYS:HG3	2:G:30:ASN:HB3	1.80	0.63
1:E:158:PHE:CE1	2:D:80:LEU:HD23	2.32	0.63
2:J:21:HIS:O	2:J:30:ASN:ND2	2.27	0.63
1:A:169:ARG:NH2	1:A:174:ASP:OD2	2.31	0.63
1:A:371:GLU:OE2	3:A:401:SAM:O3'	2.16	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:49:TYR:CG	2:B:69:LEU:CG	2.81	0.63
1:H:177:ILE:HD13	2:G:13:MET:HB2	1.80	0.62
2:D:82:THR:HA	2:D:85:LEU:CG	2.28	0.62
1:A:142:LEU:HB3	2:G:76:ILE:HD11	1.80	0.62
1:H:174:ASP:O	2:G:14:ARG:NH2	2.30	0.62
2:B:86:PHE:CE1	2:B:104:ILE:HG22	2.35	0.61
1:K:177:ILE:HD12	1:K:366:VAL:HG22	1.82	0.61
1:K:195:GLN:NE2	1:K:201:LYS:O	2.34	0.61
1:K:211:PRO:CG	3:K:401:SAM:N7	2.60	0.61
2:J:41:TYR:CE2	2:J:43:GLY:HA2	2.35	0.61
2:B:78:LEU:O	2:B:82:THR:OG1	2.14	0.61
2:J:78:LEU:H	2:J:78:LEU:CD1	1.93	0.61
2:D:43:GLY:O	2:D:47:ILE:N	2.33	0.61
1:K:238:MET:HE2	1:K:240:ILE:HD11	1.83	0.61
2:B:77:GLU:O	2:B:81:ARG:N	2.30	0.60
1:H:252:TRP:HZ2	1:H:338:ILE:HG13	1.66	0.60
1:K:282:THR:HG23	1:K:287:ILE:O	2.01	0.60
2:J:62:TRP:CE3	2:J:78:LEU:HB2	2.36	0.60
2:G:11:LYS:HG2	2:G:14:ARG:HH12	1.65	0.60
2:D:62:TRP:CH2	2:D:79:GLU:CB	2.84	0.60
1:H:152:HIS:CG	2:B:76:ILE:HD12	2.31	0.60
1:E:169:ARG:NH2	1:E:174:ASP:OD2	2.35	0.60
2:B:70:LEU:HD22	2:B:72:GLN:N	2.17	0.60
2:D:62:TRP:CH2	2:D:79:GLU:HB2	2.37	0.59
2:B:11:LYS:HA	2:B:14:ARG:HH12	1.66	0.59
1:A:142:LEU:CD1	2:G:75:GLU:CG	2.77	0.59
1:E:329:ARG:HG2	1:E:329:ARG:O	2.03	0.59
1:A:205:VAL:HG11	1:A:342:ILE:HD13	1.84	0.59
1:H:182:ASP:OD1	3:H:401:SAM:C6	2.51	0.59
1:H:282:THR:OG1	1:H:286:LYS:N	2.35	0.59
2:J:62:TRP:CZ3	2:J:78:LEU:HB2	2.38	0.59
2:J:77:GLU:N	2:J:78:LEU:HD12	2.17	0.59
1:K:178:PRO:HG2	2:J:22:ILE:HG21	1.84	0.59
2:G:79:GLU:HG2	2:G:80:LEU:CD1	2.33	0.59
1:E:370:ASN:OD1	3:E:401:SAM:C4	2.51	0.58
2:D:44:GLU:HA	2:D:47:ILE:HD12	1.84	0.58
2:G:75:GLU:CG	2:G:77:GLU:CB	2.82	0.58
1:A:182:ASP:OD1	3:A:401:SAM:N1	2.37	0.58
2:D:77:GLU:C	2:D:79:GLU:H	2.10	0.58
1:H:209:ASP:OD2	3:H:401:SAM:CG	2.52	0.58
1:H:209:ASP:OD2	3:H:401:SAM:HG1	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:MET:HE3	1:A:240:ILE:HD11	1.85	0.57
1:K:360:ASN:CG	3:K:401:SAM:O	2.47	0.57
2:J:76:ILE:HA	2:J:78:LEU:HD11	1.85	0.57
1:A:208:MET:HE1	1:A:268:TRP:CH2	2.39	0.57
2:J:76:ILE:C	2:J:78:LEU:HD12	2.28	0.57
1:A:212:TRP:CG	1:A:257:LYS:HG3	2.40	0.56
2:J:62:TRP:CZ2	2:J:79:GLU:HB3	2.40	0.56
1:E:170:SER:N	2:D:31:HIS:HD2	2.02	0.56
1:A:358:ARG:HH11	1:A:358:ARG:HG2	1.70	0.56
2:J:76:ILE:O	2:J:76:ILE:HG22	2.05	0.56
1:K:336:GLU:OE2	1:K:362:HIS:NE2	2.38	0.56
2:J:78:LEU:O	2:J:82:THR:OG1	2.22	0.56
1:A:252:TRP:HZ2	1:A:338:ILE:HG13	1.70	0.56
1:K:209:ASP:O	3:K:401:SAM:HE1	2.06	0.56
2:D:79:GLU:OE2	2:D:91:ILE:HG21	2.06	0.56
2:J:36:VAL:HG11	2:J:41:TYR:HA	1.89	0.55
2:G:49:TYR:O	2:G:69:LEU:CG	2.54	0.55
1:H:152:HIS:CG	2:B:76:ILE:HB	2.41	0.55
2:G:75:GLU:CG	2:G:77:GLU:H	2.20	0.55
1:E:158:PHE:CE1	2:D:80:LEU:CD2	2.88	0.55
2:D:80:LEU:HD22	2:D:80:LEU:O	2.06	0.55
2:D:54:LEU:C	2:D:56:LYS:N	2.65	0.55
2:D:52:GLU:HG3	2:D:53:GLN:N	2.22	0.54
2:G:79:GLU:CG	2:G:80:LEU:CD1	2.86	0.54
2:J:41:TYR:HE2	2:J:43:GLY:HA2	1.72	0.54
2:D:70:LEU:O	2:D:71:GLU:CG	2.34	0.54
2:G:26:ASP:N	2:G:26:ASP:OD1	2.38	0.54
1:A:278:TRP:CD1	1:A:335:PRO:HG3	2.43	0.54
2:G:57:ILE:HG22	2:G:61:ASN:CB	2.38	0.54
1:H:155:GLN:NE2	2:G:122:LYS:HB3	2.22	0.54
1:H:230:LEU:HD23	1:H:235:ILE:HG12	1.90	0.54
2:B:11:LYS:HA	2:B:14:ARG:NH1	2.22	0.54
1:H:246:ASP:OD1	1:H:309:ASP:N	2.41	0.54
1:H:360:ASN:CG	3:H:401:SAM:OXT	2.50	0.53
2:J:75:GLU:O	2:J:77:GLU:N	2.37	0.53
1:A:278:TRP:HE1	1:A:326:SER:HB2	1.73	0.53
2:D:41:TYR:CE2	2:D:43:GLY:HA2	2.43	0.53
1:E:370:ASN:OD1	3:E:401:SAM:N9	2.42	0.53
1:A:158:PHE:HE2	2:B:89:THR:HG22	1.73	0.53
1:E:203:PHE:CD2	1:E:352:LEU:HD12	2.44	0.53
1:H:177:ILE:HD11	2:G:10:ALA:HA	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:371:GLU:CD	3:K:401:SAM:O2'	2.52	0.53
3:K:401:SAM:HE3	3:K:401:SAM:O4'	2.09	0.53
2:D:78:LEU:HD12	2:D:79:GLU:N	2.23	0.53
1:E:252:TRP:HZ2	1:E:338:ILE:HG13	1.74	0.53
2:B:44:GLU:O	2:B:48:GLN:HG2	2.09	0.53
2:D:57:ILE:O	2:D:61:ASN:ND2	2.40	0.53
2:G:19:ASP:H	2:G:22:ILE:HD12	1.74	0.53
1:H:238:MET:HE1	1:H:354:ILE:HG21	1.89	0.53
2:D:70:LEU:O	2:D:71:GLU:C	2.52	0.53
1:H:278:TRP:CD1	1:H:335:PRO:HG3	2.43	0.53
2:B:57:ILE:O	2:B:61:ASN:ND2	2.42	0.53
2:D:62:TRP:HH2	2:D:79:GLU:CG	2.04	0.53
2:G:79:GLU:CG	2:G:80:LEU:HD13	2.39	0.52
1:H:183:VAL:HG22	3:H:401:SAM:N1	2.23	0.52
1:K:211:PRO:HB3	3:K:401:SAM:C8	2.38	0.52
2:D:55:GLU:CB	2:D:100:THR:C	2.82	0.52
2:D:66:GLN:O	2:D:72:GLN:HA	2.09	0.52
2:G:22:ILE:O	2:G:30:ASN:ND2	2.43	0.52
1:A:142:LEU:CG	1:A:145:ASP:CB	2.63	0.52
2:J:62:TRP:CH2	2:J:79:GLU:HA	2.44	0.52
3:K:401:SAM:C8	3:K:401:SAM:C3'	2.85	0.52
1:E:173:PRO:HB2	1:E:363:ASP:OD2	2.10	0.52
1:E:146:ILE:O	1:E:150:ILE:HG13	2.10	0.52
1:H:151:LEU:HA	1:H:154:LYS:HD3	1.92	0.52
1:H:236:GLN:HG2	1:H:264:MET:HG3	1.91	0.51
1:K:158:PHE:CD2	2:J:125:VAL:HG21	2.45	0.51
2:J:76:ILE:CA	2:J:78:LEU:CD1	2.86	0.51
2:J:112:ILE:HG23	2:J:121:LEU:HD21	1.93	0.51
1:A:157:PHE:CD1	2:B:80:LEU:HD21	2.45	0.51
1:H:360:ASN:OD1	3:H:401:SAM:OXT	2.29	0.51
2:J:88:THR:C	2:J:90:ASP:H	2.19	0.51
1:H:322:ASP:OD1	1:H:322:ASP:N	2.41	0.51
2:J:23:CYS:HA	2:J:29:VAL:HA	1.93	0.51
1:A:142:LEU:HG	1:A:145:ASP:HB3	1.83	0.51
1:A:183:VAL:HG13	3:A:401:SAM:H2	1.93	0.51
1:E:265:ILE:HD11	1:E:272:LEU:HD13	1.93	0.51
2:B:56:LYS:HG3	2:B:57:ILE:HG12	1.92	0.51
2:J:115:ALA:HB2	2:J:126:PHE:CG	2.45	0.51
2:B:19:ASP:HB2	2:B:22:ILE:HG13	1.93	0.51
2:D:66:GLN:O	2:D:72:GLN:CA	2.59	0.51
2:G:24:LYS:HB3	2:G:25:PRO:HD2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:ARG:HH22	1:E:237:ASN:HA	1.76	0.51
1:E:164:ILE:HG23	2:D:32:GLN:HG2	1.93	0.51
1:K:142:LEU:CG	1:K:145:ASP:CB	2.71	0.51
2:D:62:TRP:CZ3	2:D:79:GLU:HB2	2.46	0.51
1:E:211:PRO:HG2	1:E:230:LEU:HB2	1.93	0.50
1:A:258:TYR:OH	1:A:275:GLU:OE1	2.17	0.50
1:H:204:ASP:O	1:H:244:GLN:NE2	2.45	0.50
1:E:329:ARG:H	1:E:329:ARG:HD2	1.76	0.50
1:H:355:PHE:HB3	3:H:401:SAM:H5'2	1.94	0.50
3:E:401:SAM:O3'	3:E:401:SAM:SD	2.63	0.50
1:A:331:GLN:HA	1:A:333:GLN:H	1.77	0.50
1:H:178:PRO:HG2	2:G:22:ILE:HG21	1.94	0.50
1:K:201:LYS:NZ	1:K:201:LYS:HB3	2.27	0.50
1:K:208:MET:HE2	1:K:210:PRO:HG3	1.93	0.50
1:K:232:ASP:OD2	1:K:257:LYS:NZ	2.35	0.49
1:H:338:ILE:O	1:H:342:ILE:HG13	2.12	0.49
1:E:370:ASN:OD1	3:E:401:SAM:C8	2.60	0.49
1:H:264:MET:HE3	1:H:268:TRP:CH2	2.46	0.49
1:A:142:LEU:CB	2:G:76:ILE:HD11	2.43	0.49
1:A:236:GLN:OE1	1:A:264:MET:HA	2.13	0.49
1:K:358:ARG:HH12	2:J:38:LYS:H	1.60	0.49
2:D:33:TYR:HA	2:D:41:TYR:CD1	2.48	0.49
2:D:52:GLU:O	2:D:101:LYS:CE	2.61	0.49
2:D:78:LEU:C	2:D:78:LEU:CD1	2.85	0.49
1:E:180:CYS:HA	1:E:369:GLY:O	2.13	0.49
1:K:203:PHE:O	1:K:244:GLN:HG3	2.13	0.49
2:J:86:PHE:CG	2:J:88:THR:HG22	2.48	0.49
1:E:238:MET:HE2	1:E:240:ILE:HD11	1.94	0.49
1:H:210:PRO:HB3	1:H:235:ILE:HD13	1.94	0.49
1:H:212:TRP:CG	1:H:257:LYS:HG3	2.47	0.49
2:D:57:ILE:C	2:D:61:ASN:HB2	2.34	0.49
2:D:82:THR:HG22	2:D:85:LEU:HD12	1.95	0.49
1:H:231:SER:HB3	1:H:234:LYS:HD3	1.95	0.49
1:K:371:GLU:CD	3:K:401:SAM:HO2'	2.20	0.49
2:B:80:LEU:C	2:B:80:LEU:CD2	2.86	0.49
2:G:74:SER:CB	2:G:78:LEU:HD22	2.43	0.49
2:J:10:ALA:O	2:J:14:ARG:HG3	2.13	0.49
3:K:401:SAM:C8	3:K:401:SAM:H3'	2.43	0.48
2:B:75:GLU:C	2:B:77:GLU:N	2.68	0.48
1:A:353:GLU:HG2	1:A:356:ALA:HB2	1.94	0.48
1:H:155:GLN:OE1	2:G:122:LYS:HD2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:355:PHE:HB3	3:H:401:SAM:C5'	2.43	0.48
2:B:75:GLU:HG3	2:G:122:LYS:HD3	1.95	0.48
1:K:211:PRO:HB3	3:K:401:SAM:H8	1.94	0.48
1:H:203:PHE:CD1	1:H:352:LEU:HB2	2.49	0.48
1:K:205:VAL:HG11	1:K:342:ILE:HD13	1.96	0.48
2:D:82:THR:CG2	2:D:85:LEU:HD12	2.43	0.48
2:D:103:GLU:O	2:D:107:ILE:HG12	2.13	0.48
1:E:358:ARG:HH12	2:D:38:LYS:H	1.61	0.48
2:B:89:THR:HG21	2:B:127:VAL:HG13	1.95	0.48
2:J:115:ALA:HB3	2:J:121:LEU:HD13	1.96	0.48
1:A:201:LYS:HE2	1:A:201:LYS:HB3	1.59	0.48
1:A:208:MET:HE2	1:A:249:ILE:HD11	1.95	0.48
1:K:209:ASP:HB3	3:K:401:SAM:CE	2.43	0.48
2:D:14:ARG:NH1	2:D:27:GLY:O	2.47	0.48
1:A:315:PHE:CD1	1:A:346:CYS:HB2	2.49	0.48
2:B:63:LYS:HB3	2:B:63:LYS:HE2	1.67	0.48
2:D:80:LEU:C	2:D:80:LEU:CD1	2.85	0.48
1:K:158:PHE:O	1:K:162:ASN:HB2	2.13	0.47
2:G:57:ILE:CG2	2:G:64:GLN:HB3	2.44	0.47
1:A:186:LEU:HD12	1:A:187:ASN:H	1.79	0.47
2:G:88:THR:HG21	2:G:94:TYR:HE1	1.78	0.47
1:A:201:LYS:HB2	1:A:350:ASN:ND2	2.28	0.47
2:D:53:GLN:O	2:D:56:LYS:CB	2.60	0.47
2:J:75:GLU:C	2:J:77:GLU:H	2.23	0.47
1:K:300:GLU:OE2	1:K:334:LYS:NZ	2.36	0.47
1:H:196:MET:HE1	1:H:202:MET:HG2	1.97	0.47
1:H:276:ILE:HG12	1:H:304:ILE:HD11	1.96	0.47
1:K:209:ASP:CG	3:K:401:SAM:N	2.62	0.47
2:J:11:LYS:HD3	2:J:28:THR:HG23	1.95	0.47
1:E:300:GLU:OE2	1:E:334:LYS:NZ	2.48	0.47
2:D:81:ARG:C	2:D:81:ARG:CD	2.86	0.47
2:G:57:ILE:CG2	2:G:61:ASN:HB3	2.42	0.47
1:E:331:GLN:HA	1:E:333:GLN:N	2.30	0.47
1:E:155:GLN:HB3	2:D:122:LYS:CE	2.45	0.47
2:D:58:GLY:HA2	2:D:98:LYS:HA	1.97	0.47
1:E:170:SER:H	2:D:31:HIS:CD2	2.29	0.46
1:H:205:VAL:HG11	1:H:342:ILE:HG21	1.96	0.46
1:E:252:TRP:CE3	1:E:302:CYS:HB2	2.50	0.46
1:H:364:ASN:HB3	2:G:6:ARG:NH2	2.30	0.46
2:B:56:LYS:HG3	2:B:57:ILE:N	2.29	0.46
1:E:331:GLN:CB	1:E:332:SER:HA	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:204:ASP:HB3	1:H:315:PHE:CZ	2.50	0.46
1:E:231:SER:HB3	1:E:234:LYS:HD3	1.96	0.46
1:H:307:LYS:O	1:H:307:LYS:HG3	2.14	0.46
2:G:15:LEU:HD21	2:G:27:GLY:HA2	1.97	0.46
1:K:192:ILE:HG23	1:K:202:MET:HE1	1.98	0.46
1:K:192:ILE:HD11	1:K:242:SER:HB2	1.98	0.46
1:E:242:SER:O	1:E:245:GLN:NE2	2.48	0.46
1:H:239:PRO:O	1:H:242:SER:OG	2.34	0.46
2:D:53:GLN:C	2:D:55:GLU:N	2.72	0.46
1:E:238:MET:O	1:E:240:ILE:HG12	2.15	0.46
1:H:353:GLU:HB2	1:H:365:TRP:CZ3	2.51	0.46
2:B:24:LYS:CG	2:B:25:PRO:HD2	2.41	0.46
2:D:53:GLN:O	2:D:55:GLU:N	2.48	0.46
2:G:36:VAL:HG11	2:G:41:TYR:HA	1.97	0.46
2:D:15:LEU:HD23	2:D:15:LEU:H	1.79	0.46
3:K:401:SAM:H8	3:K:401:SAM:C5'	2.43	0.46
2:J:75:GLU:C	2:J:77:GLU:N	2.73	0.45
1:A:329:ARG:O	1:A:333:GLN:HB3	2.16	0.45
2:D:70:LEU:CB	2:D:74:SER:CB	2.91	0.45
1:E:252:TRP:CD2	1:E:302:CYS:HB2	2.51	0.45
1:K:370:ASN:H	3:K:401:SAM:C2	2.29	0.45
2:D:70:LEU:C	2:D:72:GLN:N	2.69	0.45
2:J:22:ILE:HG12	2:J:33:TYR:CE1	2.51	0.45
1:K:211:PRO:CB	3:K:401:SAM:N7	2.79	0.45
2:B:41:TYR:CE2	2:B:43:GLY:HA2	2.52	0.45
2:B:77:GLU:C	2:B:80:LEU:H	2.25	0.45
1:K:278:TRP:CD1	1:K:335:PRO:HG3	2.52	0.45
2:G:94:TYR:HA	2:G:97:LYS:HD2	1.99	0.45
1:H:198:HIS:CE1	2:G:12:LYS:HB3	2.52	0.45
1:H:203:PHE:CE2	1:H:352:LEU:HD12	2.52	0.45
1:K:338:ILE:O	1:K:342:ILE:HG13	2.17	0.45
2:B:46:LYS:HD3	2:B:46:LYS:HA	1.60	0.45
1:H:326:SER:OG	1:H:337:GLU:OE1	2.34	0.45
2:D:52:GLU:CG	2:D:69:LEU:CG	2.94	0.45
1:H:370:ASN:OD1	3:H:401:SAM:N9	2.50	0.45
1:H:210:PRO:HB2	1:H:212:TRP:CE2	2.52	0.44
2:B:26:ASP:OD1	2:B:27:GLY:N	2.50	0.44
2:D:57:ILE:CG1	2:D:61:ASN:O	2.66	0.44
2:D:82:THR:HG22	2:D:85:LEU:CD1	2.47	0.44
2:J:66:GLN:CG	2:J:78:LEU:HD21	2.47	0.44
1:A:230:LEU:HD23	1:A:235:ILE:HG12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:86:PHE:HE1	2:B:104:ILE:HG22	1.82	0.44
2:D:70:LEU:CG	2:D:74:SER:CB	2.96	0.44
1:K:359:ASN:HD22	1:K:360:ASN:ND2	2.16	0.44
2:B:70:LEU:CG	2:B:74:SER:HB3	2.47	0.44
2:D:52:GLU:HG2	2:D:69:LEU:CG	2.47	0.44
2:J:76:ILE:HG23	2:J:78:LEU:HD13	2.00	0.44
1:K:178:PRO:HB3	1:K:361:LEU:HD21	1.99	0.44
1:K:357:ARG:NH1	3:K:401:SAM:HG2	2.32	0.44
2:D:81:ARG:NE	2:D:81:ARG:C	2.76	0.44
1:E:201:LYS:HE3	1:E:314:ARG:CZ	2.48	0.44
2:J:112:ILE:HG12	2:J:121:LEU:HD11	2.00	0.44
1:A:157:PHE:CE1	2:B:80:LEU:CD2	3.01	0.44
1:A:270:TYR:CE2	1:A:307:LYS:HG2	2.52	0.44
1:E:174:ASP:O	2:D:14:ARG:NH2	2.51	0.44
1:K:207:MET:HE1	1:K:252:TRP:HE1	1.83	0.44
2:D:24:LYS:CG	2:D:30:ASN:HB2	2.48	0.44
2:J:79:GLU:H	2:J:79:GLU:HG3	1.55	0.44
1:A:155:GLN:O	1:A:159:LYS:N	2.45	0.44
1:E:357:ARG:N	1:E:360:ASN:OD1	2.45	0.44
2:D:53:GLN:O	2:D:56:LYS:N	2.51	0.44
1:A:238:MET:O	1:A:240:ILE:HG12	2.17	0.43
1:E:326:SER:HB2	1:E:335:PRO:HB3	2.00	0.43
1:A:142:LEU:O	1:A:142:LEU:CG	2.66	0.43
1:E:282:THR:HG23	1:E:287:ILE:O	2.17	0.43
1:E:329:ARG:NH1	1:E:329:ARG:HG3	2.34	0.43
1:H:157:PHE:HZ	2:G:81:ARG:CZ	2.31	0.43
2:D:77:GLU:C	2:D:79:GLU:N	2.76	0.43
1:A:170:SER:HB2	2:B:35:LEU:HG	2.00	0.43
2:J:78:LEU:CD1	2:J:78:LEU:N	2.73	0.43
1:E:183:VAL:HG13	3:E:401:SAM:C2	2.45	0.43
1:E:236:GLN:HG2	1:E:264:MET:HG2	2.00	0.43
1:K:142:LEU:O	1:K:142:LEU:CG	2.66	0.43
1:E:159:LYS:NZ	1:E:163:GLU:OE2	2.52	0.43
1:E:249:ILE:O	1:E:304:ILE:HA	2.19	0.43
1:A:142:LEU:HD22	2:G:76:ILE:HG12	1.99	0.43
1:A:326:SER:OG	1:A:337:GLU:OE1	2.33	0.43
1:H:183:VAL:HG13	3:H:401:SAM:H2	2.01	0.43
1:K:258:TYR:OH	1:K:275:GLU:OE1	2.32	0.43
2:J:11:LYS:HD2	2:J:27:GLY:HA3	2.00	0.43
1:A:331:GLN:HA	1:A:333:GLN:N	2.33	0.43
1:H:358:ARG:HH12	2:G:37:LYS:HA	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:194:ALA:O	1:K:198:HIS:ND1	2.52	0.43
1:E:352:LEU:HD22	1:E:354:ILE:HG12	2.00	0.43
1:K:326:SER:HB2	1:K:335:PRO:HB3	2.01	0.43
1:A:158:PHE:CE2	2:B:89:THR:HG22	2.54	0.42
1:A:203:PHE:CD2	1:A:352:LEU:HD12	2.54	0.42
1:E:155:GLN:HB3	2:D:122:LYS:HE3	2.01	0.42
2:G:67:LYS:O	2:G:71:GLU:HA	2.19	0.42
1:E:269:GLY:O	1:E:307:LYS:HE2	2.19	0.42
2:B:70:LEU:C	2:B:70:LEU:CD2	2.85	0.42
2:G:57:ILE:HG23	2:G:64:GLN:HB3	2.01	0.42
2:G:83:CYS:SG	2:G:91:ILE:HB	2.59	0.42
1:A:316:LYS:N	1:A:345:LEU:O	2.49	0.42
1:H:208:MET:HE2	1:H:210:PRO:HG3	2.01	0.42
1:H:370:ASN:OD1	3:H:401:SAM:C8	2.67	0.42
1:K:203:PHE:CD2	1:K:352:LEU:HD12	2.53	0.42
2:D:30:ASN:HD21	2:D:32:GLN:HB2	1.83	0.42
2:J:55:GLU:HB2	2:J:100:THR:HA	2.01	0.42
1:K:204:ASP:HB3	1:K:315:PHE:CE1	2.55	0.42
1:H:178:PRO:HG3	2:G:34:PHE:HZ	1.85	0.42
1:H:352:LEU:HD22	1:H:354:ILE:HG13	2.02	0.42
2:G:62:TRP:O	2:G:65:MET:HG3	2.20	0.42
2:J:76:ILE:CA	2:J:78:LEU:HD12	2.50	0.42
1:H:146:ILE:O	1:H:150:ILE:HG13	2.19	0.42
2:B:37:LYS:HD3	2:B:38:LYS:CB	2.50	0.42
2:B:70:LEU:HD22	2:B:72:GLN:H	1.83	0.42
2:D:80:LEU:HD13	2:D:81:ARG:N	2.35	0.42
2:G:80:LEU:CD1	2:G:80:LEU:N	2.83	0.42
2:G:115:ALA:O	2:G:120:LYS:N	2.53	0.42
1:H:175:ASN:HB2	1:H:363:ASP:OD2	2.20	0.42
2:B:65:MET:HE3	2:B:65:MET:HB3	1.79	0.42
2:J:14:ARG:NH1	2:J:28:THR:HA	2.35	0.42
2:J:88:THR:HG21	2:J:94:TYR:HE1	1.83	0.42
2:D:62:TRP:CZ3	2:D:79:GLU:HG3	2.54	0.42
2:D:66:GLN:CG	2:D:72:GLN:HA	2.50	0.42
2:J:78:LEU:HD12	2:J:78:LEU:N	2.05	0.42
1:A:357:ARG:N	1:A:360:ASN:OD1	2.33	0.41
1:H:178:PRO:HG3	2:G:34:PHE:CZ	2.55	0.41
1:H:257:LYS:O	1:H:261:THR:OG1	2.36	0.41
1:K:210:PRO:HB2	1:K:212:TRP:CE2	2.55	0.41
2:B:13:MET:HE3	2:B:13:MET:HB3	1.87	0.41
1:E:145:ASP:O	1:E:149:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:142:LEU:HD23	1:K:142:LEU:C	2.34	0.41
2:D:54:LEU:O	2:D:56:LYS:N	2.53	0.41
2:B:9:TYR:CE2	2:B:13:MET:HG3	2.55	0.41
2:D:58:GLY:O	2:D:59:VAL:C	2.62	0.41
1:A:182:ASP:OD1	3:A:401:SAM:C6	2.69	0.41
1:H:164:ILE:HA	1:H:168:LYS:HB3	2.02	0.41
2:B:91:ILE:HG12	2:B:94:TYR:HB2	2.03	0.41
1:A:142:LEU:O	2:G:76:ILE:HD11	2.18	0.41
1:A:327:GLU:CD	2:G:11:LYS:HZ3	2.28	0.41
1:A:358:ARG:CG	1:A:358:ARG:NH1	2.73	0.41
1:A:362:HIS:HB2	1:A:365:TRP:CD1	2.56	0.41
1:E:201:LYS:HE3	1:E:314:ARG:NE	2.36	0.41
2:G:56:LYS:H	2:G:56:LYS:HG2	1.54	0.41
2:J:43:GLY:O	2:J:47:ILE:HG13	2.21	0.41
1:A:175:ASN:HB2	1:A:363:ASP:OD2	2.21	0.41
1:A:205:VAL:HG21	1:A:342:ILE:HG23	2.02	0.41
1:A:240:ILE:HG13	1:A:268:TRP:CZ3	2.56	0.41
1:A:336:GLU:OE2	1:A:362:HIS:NE2	2.50	0.41
1:E:289:LYS:HE3	1:E:289:LYS:HB2	1.84	0.41
1:K:262:ILE:HG13	1:K:303:LEU:HD21	2.03	0.41
1:K:371:GLU:HG3	3:K:401:SAM:O2'	2.20	0.41
2:B:58:GLY:HA2	2:B:98:LYS:HA	2.03	0.41
2:B:103:GLU:O	2:B:107:ILE:HG13	2.20	0.41
2:D:62:TRP:HA	2:D:65:MET:CG	2.51	0.41
2:D:111:ASN:HA	2:D:114:LYS:HG2	2.03	0.41
2:G:79:GLU:HG2	2:G:80:LEU:N	2.35	0.41
2:J:60:GLY:C	2:J:62:TRP:H	2.27	0.41
1:A:346:CYS:O	1:A:351:TYR:OH	2.28	0.41
1:K:276:ILE:HB	1:K:302:CYS:HB3	2.03	0.41
1:E:233:GLU:OE2	1:E:233:GLU:N	2.54	0.40
1:E:329:ARG:HG3	1:E:329:ARG:HH11	1.86	0.40
1:K:207:MET:HG2	1:K:250:PHE:HB2	2.03	0.40
2:B:89:THR:OG1	2:B:128:VAL:N	2.46	0.40
1:H:282:THR:H	1:H:286:LYS:HA	1.85	0.40
1:H:295:LEU:HD23	1:H:295:LEU:HA	1.81	0.40
2:D:36:VAL:HG11	2:D:41:TYR:HA	2.03	0.40
2:D:52:GLU:HG3	2:D:53:GLN:H	1.84	0.40
2:G:6:ARG:HA	2:G:9:TYR:HB3	2.02	0.40
2:B:70:LEU:CD1	2:B:72:GLN:O	2.70	0.40
1:E:196:MET:HE2	1:E:202:MET:HE2	2.03	0.40
2:B:44:GLU:HG3	2:B:45:GLU:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:74:SER:OG	2:B:78:LEU:HD23	2.08	0.40
2:D:24:LYS:HG2	2:D:30:ASN:HB2	2.04	0.40
2:D:43:GLY:O	2:D:47:ILE:HG13	2.21	0.40
2:D:48:GLN:N	2:D:51:ILE:HD11	2.36	0.40
2:G:42:TRP:HZ2	2:G:50:LEU:HD22	1.86	0.40
1:A:142:LEU:CD1	2:G:75:GLU:HB3	2.39	0.40
1:A:142:LEU:CD2	1:A:146:ILE:HB	2.50	0.40
2:G:74:SER:O	2:G:78:LEU:HD21	2.22	0.40

All (5) 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)
2:D:121:LEU:O	2:J:75:GLU:CA[1_655]	1.43	0.77
2:D:122:LYS:CA	2:J:75:GLU:CB[1_655]	1.90	0.30
2:D:121:LEU:O	2:J:75:GLU:C[1_655]	2.10	0.10
1:A:258:TYR:OH	1:H:258:TYR:OH[2_455]	2.12	0.08
2:D:122:LYS:CE	2:J:79:GLU:OE2[1_655]	2.15	0.05

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	212/247 (86%)	195 (92%)	17 (8%)	0	100	100
1	E	212/247 (86%)	199 (94%)	13 (6%)	0	100	100
1	H	212/247 (86%)	202 (95%)	10 (5%)	0	100	100
1	K	212/247 (86%)	201 (95%)	11 (5%)	0	100	100
2	B	123/128 (96%)	113 (92%)	10 (8%)	0	100	100
2	D	123/128 (96%)	112 (91%)	9 (7%)	2 (2%)	7	34
2	G	122/128 (95%)	116 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	122/128 (95%)	112 (92%)	10 (8%)	0	100	100
All	All	1338/1500 (89%)	1250 (93%)	86 (6%)	2 (0%)	48	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	92	GLN
2	D	93	PRO

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	185/219 (84%)	181 (98%)	4 (2%)	45	62
1	E	185/219 (84%)	184 (100%)	1 (0%)	81	80
1	H	184/219 (84%)	184 (100%)	0	100	100
1	K	185/219 (84%)	184 (100%)	1 (0%)	81	80
2	B	96/117 (82%)	89 (93%)	7 (7%)	13	39
2	D	73/117 (62%)	66 (90%)	7 (10%)	8	30
2	G	75/117 (64%)	71 (95%)	4 (5%)	20	46
2	J	58/117 (50%)	56 (97%)	2 (3%)	32	54
All	All	1041/1344 (78%)	1015 (98%)	26 (2%)	42	60

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	183	VAL
1	A	184	THR
1	A	358	ARG
1	A	371	GLU
1	E	329	ARG
1	K	359	ASN

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Mol	Chain	Res	Type
2	B	70	LEU
2	B	74	SER
2	B	75	GLU
2	B	78	LEU
2	B	81	ARG
2	B	93	PRO
2	B	100	THR
2	D	51	ILE
2	D	71	GLU
2	D	77	GLU
2	D	80	LEU
2	D	81	ARG
2	D	100	THR
2	D	101	LYS
2	G	76	ILE
2	G	78	LEU
2	G	80	LEU
2	G	93	PRO
2	J	78	LEU
2	J	79	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	155	GLN
1	A	189	GLN
1	A	312	ASN
1	A	344	GLN
1	A	350	ASN
1	E	244	GLN
1	E	245	GLN
1	E	267	ASN
1	E	291	HIS
1	E	297	HIS
1	E	364	ASN
1	H	236	GLN
1	H	241	GLN
1	K	144	GLN
1	K	236	GLN
1	K	237	ASN
1	K	359	ASN
2	B	40	GLN

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Mol	Chain	Res	Type
2	B	61	ASN
2	D	31	HIS
2	G	111	ASN
2	J	111	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	SAM	H	401	-	27,29,29	1.66	6 (22%)	34,42,42	2.29	10 (29%)
3	SAM	A	401	-	27,29,29	2.17	8 (29%)	34,42,42	2.80	12 (35%)
3	SAM	E	401	-	27,29,29	2.04	10 (37%)	34,42,42	2.19	10 (29%)
3	SAM	K	401	-	27,29,29	1.58	6 (22%)	34,42,42	2.28	12 (35%)

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
3	SAM	H	401	-	-	9/17/33/33	0/3/3/3
3	SAM	A	401	-	-	8/17/33/33	0/3/3/3
3	SAM	E	401	-	-	10/17/33/33	0/3/3/3
3	SAM	K	401	-	-	8/17/33/33	0/3/3/3

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	SAM	C5-N7	-6.32	1.27	1.39
3	E	401	SAM	C5-N7	-5.22	1.29	1.39
3	A	401	SAM	C4-N9	-4.28	1.28	1.37
3	E	401	SAM	C4-N9	-4.18	1.29	1.37
3	H	401	SAM	C5-N7	-4.00	1.31	1.39
3	K	401	SAM	C5-C4	3.90	1.46	1.39
3	A	401	SAM	C4-N3	-3.59	1.27	1.34
3	H	401	SAM	C5-C4	3.43	1.45	1.39
3	A	401	SAM	C8-N9	-3.30	1.31	1.37
3	H	401	SAM	C4-N9	-2.86	1.31	1.37
3	K	401	SAM	C4-N9	-2.68	1.32	1.37
3	E	401	SAM	C3'-C4'	-2.67	1.46	1.53
3	E	401	SAM	C8-N9	-2.65	1.33	1.37
3	A	401	SAM	C2'-C3'	-2.63	1.46	1.53
3	E	401	SAM	C2'-C3'	-2.61	1.46	1.53
3	K	401	SAM	C5-N7	-2.55	1.34	1.39
3	A	401	SAM	OXT-C	-2.44	1.22	1.30
3	E	401	SAM	O4'-C4'	-2.43	1.39	1.45
3	E	401	SAM	C4-N3	-2.39	1.30	1.34
3	E	401	SAM	CE-SD	-2.32	1.64	1.78
3	H	401	SAM	OXT-C	-2.31	1.23	1.30
3	A	401	SAM	CE-SD	-2.30	1.64	1.78
3	K	401	SAM	CE-SD	-2.28	1.64	1.78
3	E	401	SAM	O3'-C3'	-2.22	1.37	1.43
3	H	401	SAM	CE-SD	-2.21	1.64	1.78
3	A	401	SAM	C6-N1	-2.20	1.29	1.35
3	E	401	SAM	OXT-C	-2.19	1.23	1.30
3	K	401	SAM	C8-N7	2.19	1.35	1.31
3	K	401	SAM	C8-N9	-2.09	1.34	1.37
3	H	401	SAM	C8-N9	-2.07	1.34	1.37

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	SAM	C5-C4-N3	-7.28	116.70	126.72
3	H	401	SAM	C5-C4-N3	-7.27	116.71	126.72
3	K	401	SAM	C2'-C1'-N9	-6.59	96.94	113.30
3	A	401	SAM	CG-SD-C5'	5.57	117.05	103.43
3	A	401	SAM	O3'-C3'-C2'	-5.42	94.45	111.82
3	E	401	SAM	C5-C4-N3	-5.37	119.32	126.72
3	A	401	SAM	N3-C4-N9	5.35	136.27	127.17
3	E	401	SAM	O3'-C3'-C4'	-5.30	95.85	111.08
3	A	401	SAM	O2'-C2'-C3'	-5.20	95.16	111.82
3	H	401	SAM	N3-C4-N9	4.94	135.57	127.17
3	K	401	SAM	C5-C4-N3	-4.44	120.60	126.72
3	K	401	SAM	CG-SD-C5'	4.23	113.78	103.43
3	A	401	SAM	N6-C6-N1	4.04	127.38	118.38
3	A	401	SAM	C6-C5-C4	3.92	122.53	117.18
3	E	401	SAM	N3-C4-N9	3.80	133.64	127.17
3	K	401	SAM	N3-C4-N9	3.73	133.52	127.17
3	H	401	SAM	O4'-C4'-C3'	-3.73	97.76	105.15
3	K	401	SAM	C4-N9-C8	3.55	109.47	105.74
3	E	401	SAM	N3-C2-N1	-3.51	123.26	128.58
3	E	401	SAM	C2-N3-C4	3.40	120.14	111.83
3	H	401	SAM	C2-N3-C4	3.39	120.10	111.83
3	H	401	SAM	C4-C5-N7	-3.10	107.04	110.58
3	A	401	SAM	C3'-C2'-C1'	3.09	107.31	101.46
3	E	401	SAM	O3'-C3'-C2'	-3.07	101.98	111.82
3	H	401	SAM	CG-SD-C5'	3.06	110.91	103.43
3	K	401	SAM	C4-C5-N7	-3.02	107.13	110.58
3	H	401	SAM	O4'-C4'-C5'	2.98	116.41	108.88
3	A	401	SAM	C2-N3-C4	2.90	118.91	111.83
3	E	401	SAM	O2'-C2'-C3'	-2.81	102.82	111.82
3	H	401	SAM	O3'-C3'-C4'	-2.79	103.08	111.08
3	K	401	SAM	N3-C2-N1	-2.73	124.45	128.58
3	A	401	SAM	C5-C6-N6	-2.72	116.55	123.29
3	K	401	SAM	C2-N3-C4	2.70	118.43	111.83
3	K	401	SAM	C2-N1-C6	2.62	123.03	118.73
3	K	401	SAM	O3'-C3'-C2'	-2.58	103.54	111.82
3	K	401	SAM	N9-C8-N7	-2.38	110.56	113.94
3	E	401	SAM	O4'-C4'-C3'	-2.34	100.51	105.15
3	H	401	SAM	C6-C5-C4	2.23	120.22	117.18
3	K	401	SAM	C5-N7-C8	2.22	106.94	103.45
3	E	401	SAM	N6-C6-N1	2.21	123.30	118.38
3	H	401	SAM	O3'-C3'-C2'	2.17	118.79	111.82
3	A	401	SAM	C6-C5-N7	-2.14	127.96	132.09
3	E	401	SAM	CG-SD-C5'	2.12	108.62	103.43

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	A	401	SAM	O4'-C1'-N9	-2.04	104.16	108.09

There are no chirality outliers.

All (35) torsion outliers are listed below:

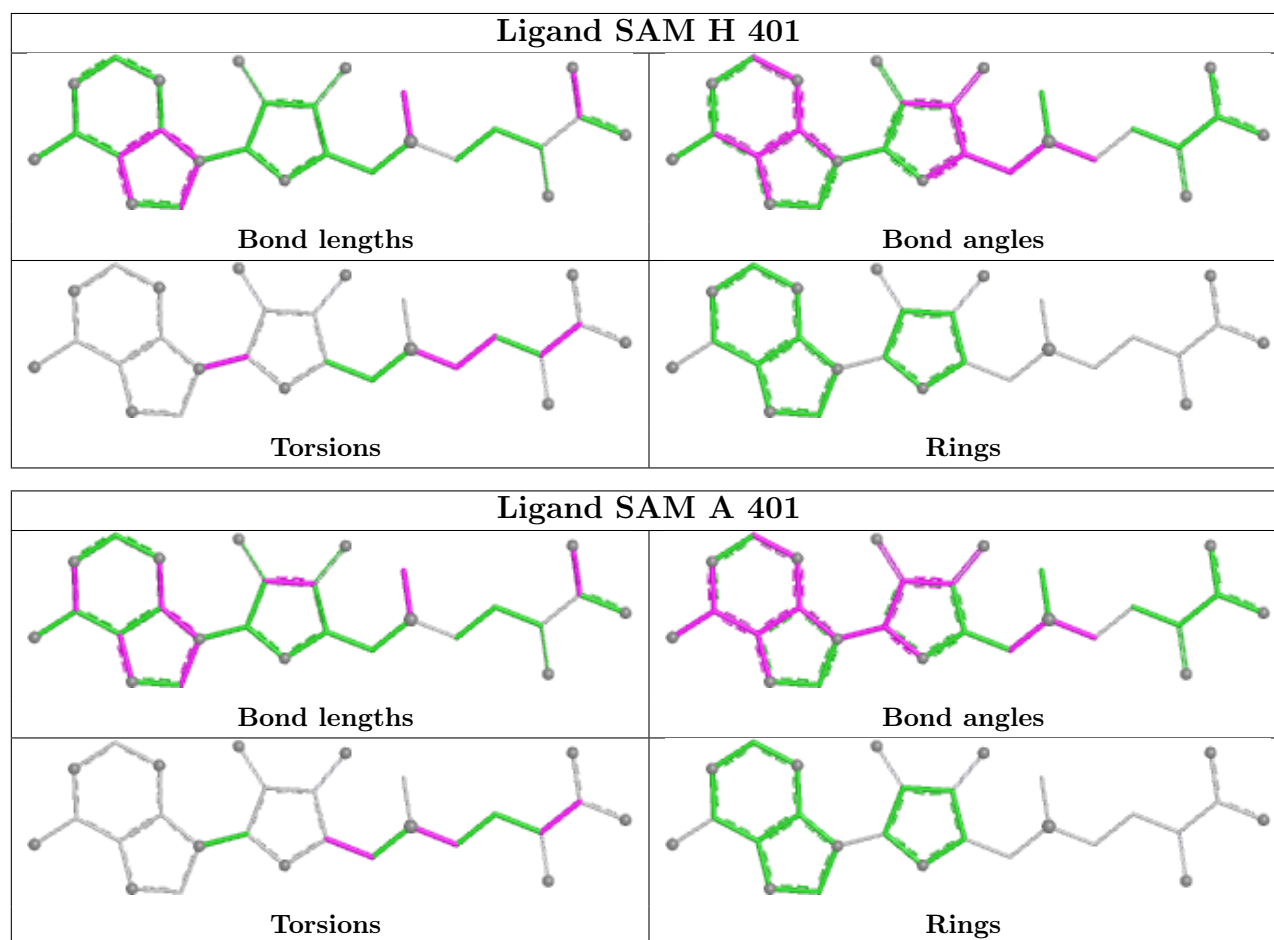
Mol	Chain	Res	Type	Atoms
3	A	401	SAM	O-C-CA-N
3	A	401	SAM	CB-CG-SD-CE
3	A	401	SAM	CB-CG-SD-C5'
3	A	401	SAM	O4'-C4'-C5'-SD
3	A	401	SAM	C3'-C4'-C5'-SD
3	E	401	SAM	O-C-CA-N
3	E	401	SAM	CB-CG-SD-CE
3	E	401	SAM	C4'-C5'-SD-CE
3	E	401	SAM	C2'-C1'-N9-C8
3	H	401	SAM	O-C-CA-N
3	H	401	SAM	CA-CB-CG-SD
3	H	401	SAM	CB-CG-SD-CE
3	K	401	SAM	O-C-CA-N
3	K	401	SAM	N-CA-CB-CG
3	E	401	SAM	OXT-C-CA-N
3	H	401	SAM	OXT-C-CA-N
3	K	401	SAM	OXT-C-CA-N
3	H	401	SAM	C2'-C1'-N9-C4
3	A	401	SAM	OXT-C-CA-N
3	H	401	SAM	C2'-C1'-N9-C8
3	K	401	SAM	C-CA-CB-CG
3	E	401	SAM	C2'-C1'-N9-C4
3	K	401	SAM	CA-CB-CG-SD
3	K	401	SAM	O-C-CA-CB
3	H	401	SAM	O-C-CA-CB
3	H	401	SAM	OXT-C-CA-CB
3	E	401	SAM	CB-CG-SD-C5'
3	H	401	SAM	CB-CG-SD-C5'
3	K	401	SAM	CB-CG-SD-C5'
3	E	401	SAM	O-C-CA-CB
3	K	401	SAM	OXT-C-CA-CB
3	E	401	SAM	OXT-C-CA-CB
3	E	401	SAM	O4'-C1'-N9-C8
3	A	401	SAM	OXT-C-CA-CB
3	A	401	SAM	O-C-CA-CB

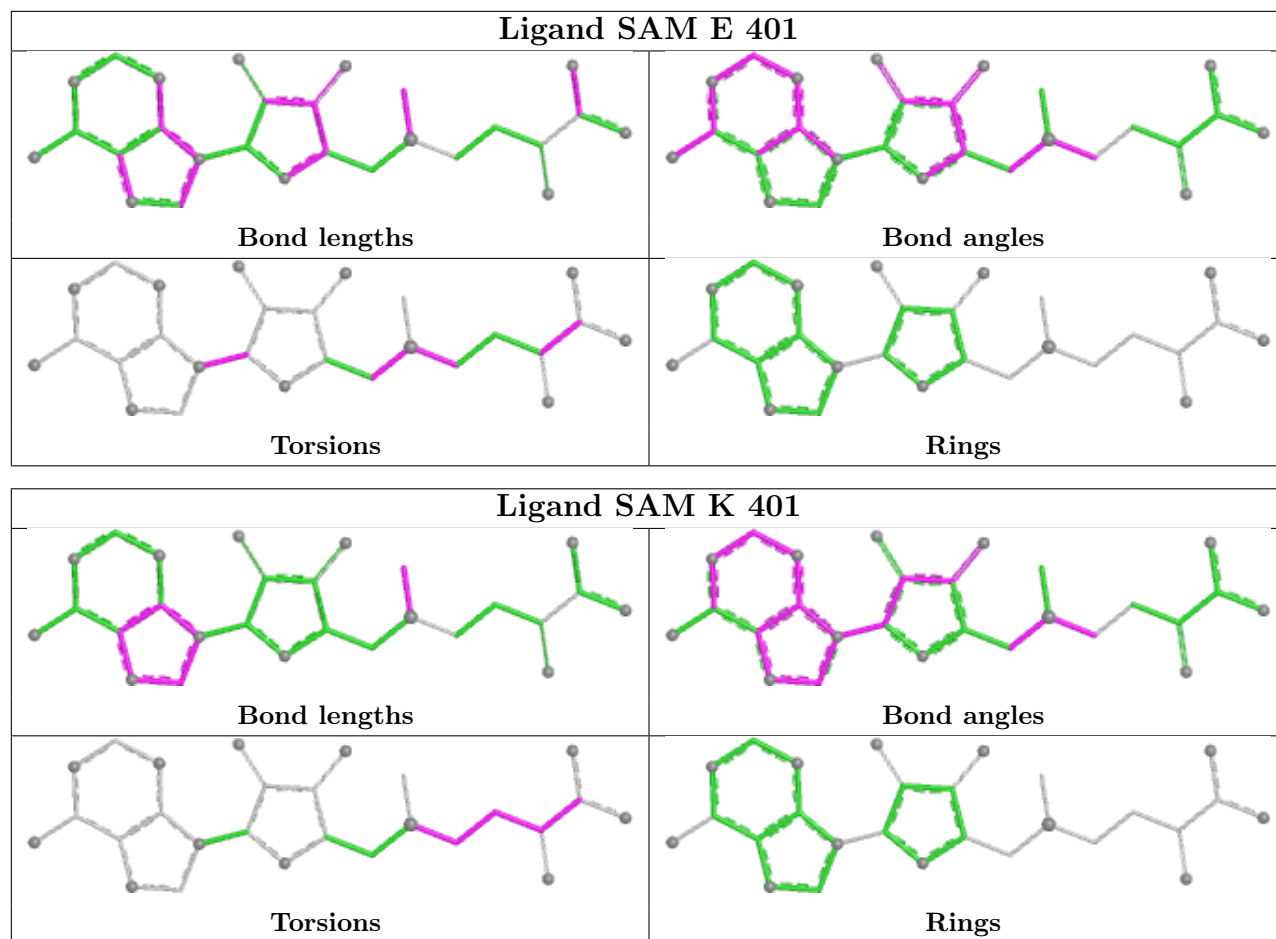
There are no ring outliers.

4 monomers are involved in 55 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	401	SAM	15	0
3	A	401	SAM	5	0
3	E	401	SAM	9	0
3	K	401	SAM	26	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	218/247 (88%)	0.84	24 (11%)	10 11	2, 12, 115, 146	0
1	E	218/247 (88%)	1.15	35 (16%)	4 6	4, 27, 134, 142	0
1	H	218/247 (88%)	1.04	28 (12%)	7 9	19, 39, 132, 153	0
1	K	218/247 (88%)	1.24	40 (18%)	3 4	23, 53, 158, 171	0
2	B	125/128 (97%)	1.34	28 (22%)	2 2	15, 67, 88, 98	0
2	D	125/128 (97%)	2.20	56 (44%)	0 1	31, 90, 159, 177	0
2	G	124/128 (96%)	2.23	62 (50%)	0 0	55, 112, 148, 163	0
2	J	124/128 (96%)	2.63	85 (68%)	0 0	95, 140, 180, 189	0
All	All	1370/1500 (91%)	1.44	358 (26%)	1 2	2, 47, 154, 189	0

All (358) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	89	THR	9.3
2	G	125	VAL	8.4
1	E	160	GLU	8.4
1	K	153	TYR	8.0
2	D	128	VAL	7.7
1	E	152	HIS	7.3
2	D	90	ASP	6.7
2	D	123	TYR	6.5
1	E	157	PHE	6.3
2	D	59	VAL	6.3
1	K	146	ILE	6.2
1	K	145	ASP	6.1
1	K	149	ARG	6.0
2	J	83	CYS	6.0
2	D	77	GLU	5.8
2	D	88	THR	5.8

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Mol	Chain	Res	Type	RSRZ
2	G	122	LYS	5.7
2	J	127	VAL	5.7
1	E	153	TYR	5.5
2	J	71	GLU	5.3
2	D	96	ASP	5.3
2	B	80	LEU	5.3
2	D	89	THR	5.3
2	D	118	LEU	5.2
2	B	59	VAL	5.2
2	J	77	GLU	5.2
1	H	145	ASP	5.1
2	D	124	GLY	5.1
2	G	90	ASP	5.0
1	E	155	GLN	5.0
1	E	154	LYS	5.0
1	E	142	LEU	5.0
2	J	90	ASP	4.9
2	G	127	VAL	4.9
2	D	122	LYS	4.8
1	E	150	ILE	4.8
2	J	128	VAL	4.7
2	J	126	PHE	4.7
2	J	45	GLU	4.7
2	G	124	GLY	4.7
1	A	143	LEU	4.6
2	J	80	LEU	4.6
2	G	120	LYS	4.6
2	D	79	GLU	4.6
2	G	119	SER	4.6
1	E	161	GLN	4.5
2	G	123	TYR	4.4
2	D	117	GLN	4.4
2	G	98	LYS	4.4
2	D	87	LYS	4.4
2	D	93	PRO	4.3
2	B	86	PHE	4.3
1	H	140	GLN	4.3
2	J	91	ILE	4.3
1	H	147	GLU	4.3
1	A	156	LEU	4.3
2	D	69	LEU	4.3
1	K	191	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	149	ARG	4.2
2	D	92	GLN	4.2
2	J	109	GLN	4.2
2	J	40	GLN	4.2
1	E	146	ILE	4.2
1	K	142	LEU	4.1
2	D	62	TRP	4.1
2	G	84	LEU	4.0
2	G	101	LYS	4.0
2	B	103	GLU	4.0
2	G	42	TRP	4.0
2	J	60	GLY	4.0
1	H	148	LYS	4.0
1	E	149	ARG	4.0
2	J	66	GLN	4.0
1	A	148	LYS	3.9
2	G	75	GLU	3.9
2	B	93	PRO	3.9
2	D	83	CYS	3.9
1	A	154	LYS	3.9
2	D	95	MET	3.9
2	D	91	ILE	3.9
1	A	145	ASP	3.9
2	J	55	GLU	3.8
1	K	203	PHE	3.8
2	J	89	THR	3.8
1	K	152	HIS	3.8
2	D	45	GLU	3.8
1	K	143	LEU	3.7
1	E	145	ASP	3.7
1	H	149	ARG	3.7
2	B	96	ASP	3.7
2	D	116	GLN	3.7
1	A	142	LEU	3.7
2	J	106	GLN	3.7
2	B	67	LYS	3.7
2	G	92	GLN	3.7
2	G	99	PHE	3.7
2	G	118	LEU	3.7
2	J	68	GLY	3.6
2	J	42	TRP	3.6
1	E	162	ASN	3.6

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Mol	Chain	Res	Type	RSRZ
2	D	125	VAL	3.6
2	B	90	ASP	3.6
1	E	313	GLY	3.6
2	J	107	ILE	3.6
2	J	44	GLU	3.6
2	J	52	GLU	3.6
2	J	84	LEU	3.5
2	J	97	LYS	3.5
2	G	62	TRP	3.5
2	G	83	CYS	3.5
1	K	154	LYS	3.4
2	J	7	GLU	3.4
2	J	8	GLU	3.4
2	B	92	GLN	3.4
2	G	116	GLN	3.4
2	D	68	GLY	3.4
2	J	19	ASP	3.4
2	G	25	PRO	3.4
2	J	38	LYS	3.4
1	H	143	LEU	3.4
1	A	323	VAL	3.4
2	J	59	VAL	3.4
2	J	110	GLN	3.3
1	E	159	LYS	3.3
2	J	37	LYS	3.3
2	G	50	LEU	3.3
1	A	150	ILE	3.3
2	G	109	GLN	3.3
2	J	81	ARG	3.3
2	D	75	GLU	3.3
1	K	144	GLN	3.2
2	D	66	GLN	3.2
2	J	32	GLN	3.2
2	D	94	TYR	3.2
2	J	49	TYR	3.2
1	A	146	ILE	3.2
2	D	55	GLU	3.2
2	G	16	ALA	3.2
2	J	85	LEU	3.2
2	J	6	ARG	3.2
2	J	9	TYR	3.2
2	J	123	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
2	D	70	LEU	3.2
2	G	51	ILE	3.1
1	H	156	LEU	3.1
2	J	54	LEU	3.1
2	J	20	ASN	3.1
1	H	142	LEU	3.1
2	G	126	PHE	3.1
1	A	155	GLN	3.1
2	D	115	ALA	3.1
1	K	150	ILE	3.1
1	K	147	GLU	3.1
1	A	140	GLN	3.0
1	H	141	GLY	3.0
2	J	122	LYS	3.0
2	B	94	TYR	3.0
2	G	20	ASN	3.0
2	J	121	LEU	3.0
1	H	150	ILE	3.0
2	G	117	GLN	3.0
2	J	67	LYS	3.0
2	D	86	PHE	3.0
2	B	75	GLU	3.0
2	D	113	GLU	3.0
2	G	91	ILE	3.0
1	H	273	VAL	3.0
2	G	121	LEU	3.0
2	J	93	PRO	3.0
1	A	151	LEU	3.0
2	J	118	LEU	3.0
2	J	10	ALA	3.0
2	J	21	HIS	3.0
1	E	237	ASN	3.0
2	D	119	SER	3.0
2	J	120	LYS	2.9
2	B	83	CYS	2.9
1	H	171	MET	2.9
1	E	147	GLU	2.9
1	H	228	ASP	2.9
2	D	111	ASN	2.9
2	J	101	LYS	2.9
1	A	328	ARG	2.9
2	J	46	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
2	J	92	GLN	2.9
1	E	165	ALA	2.9
1	H	154	LYS	2.9
1	E	151	LEU	2.8
1	E	158	PHE	2.8
2	J	56	LYS	2.8
1	H	205	VAL	2.8
2	G	96	ASP	2.8
1	A	327	GLU	2.8
1	K	368	ILE	2.8
2	D	80	LEU	2.8
2	J	53	GLN	2.8
2	J	99	PHE	2.8
2	G	35	LEU	2.8
2	G	112	ILE	2.8
1	E	310	VAL	2.8
2	G	59	VAL	2.8
1	E	143	LEU	2.8
2	G	47	ILE	2.8
2	J	119	SER	2.8
2	J	61	ASN	2.8
2	J	108	ALA	2.8
2	G	82	THR	2.8
2	G	114	LYS	2.8
2	J	76	ILE	2.7
1	K	178	PRO	2.7
2	B	120	LYS	2.7
1	A	141	GLY	2.7
2	J	79	GLU	2.7
2	J	103	GLU	2.7
2	G	94	TYR	2.7
1	K	160	GLU	2.7
1	K	361	LEU	2.7
2	G	80	LEU	2.7
2	J	96	ASP	2.7
1	E	156	LEU	2.7
2	D	53	GLN	2.7
2	D	63	LYS	2.7
2	J	25	PRO	2.7
2	D	54	LEU	2.7
2	J	125	VAL	2.6
2	B	71	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
2	J	35	LEU	2.6
1	H	146	ILE	2.6
1	A	144	GLN	2.6
2	G	33	TYR	2.6
2	G	52	GLU	2.6
2	G	85	LEU	2.6
1	K	328	ARG	2.6
1	E	174	ASP	2.6
2	J	112	ILE	2.6
2	G	43	GLY	2.6
2	J	47	ILE	2.6
2	G	46	LYS	2.6
1	K	140	GLN	2.6
1	H	160	GLU	2.6
2	D	67	LYS	2.6
2	D	120	LYS	2.6
2	D	58	GLY	2.6
2	J	73	THR	2.5
2	D	127	VAL	2.5
1	H	191	LEU	2.5
2	D	76	ILE	2.5
2	G	113	GLU	2.5
2	B	84	LEU	2.5
1	E	288	ALA	2.5
1	K	331	GLN	2.5
2	B	19	ASP	2.5
1	E	314	ARG	2.5
2	G	128	VAL	2.5
1	E	252	TRP	2.5
2	B	64	GLN	2.5
2	D	60	GLY	2.5
2	D	103	GLU	2.5
2	J	102	ILE	2.4
2	D	23	CYS	2.4
2	D	32	GLN	2.4
2	J	29	VAL	2.4
2	J	114	LYS	2.4
2	J	16	ALA	2.4
2	G	95	MET	2.4
1	K	295	LEU	2.4
2	G	53	GLN	2.4
1	E	141	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
2	J	82	THR	2.4
1	E	164	ILE	2.4
1	K	177	ILE	2.4
2	D	15	LEU	2.4
2	J	57	ILE	2.4
2	B	106	GLN	2.3
2	J	39	GLY	2.3
2	D	82	THR	2.3
1	H	286	LYS	2.3
1	H	152	HIS	2.3
2	J	34	PHE	2.3
2	D	85	LEU	2.3
1	A	171	MET	2.3
1	K	157	PHE	2.3
2	G	68	GLY	2.3
2	G	29	VAL	2.3
2	B	79	GLU	2.3
1	K	369	GLY	2.3
2	G	30	ASN	2.2
1	A	158	PHE	2.2
1	K	327	GLU	2.2
2	B	60	GLY	2.2
2	G	108	ALA	2.2
2	B	68	GLY	2.2
2	B	89	THR	2.2
1	K	206	ILE	2.2
2	B	104	ILE	2.2
1	A	157	PHE	2.2
2	J	62	TRP	2.2
1	E	140	GLN	2.2
2	B	72	GLN	2.2
2	J	69	LEU	2.2
2	B	39	GLY	2.2
2	G	58	GLY	2.2
2	G	60	GLY	2.2
1	K	156	LEU	2.2
2	J	94	TYR	2.2
1	K	283	VAL	2.2
2	D	71	GLU	2.2
1	K	319	ILE	2.2
1	H	248	PHE	2.2
2	G	24	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
2	J	13	MET	2.2
2	G	27	GLY	2.2
1	H	144	GLN	2.1
1	E	283	VAL	2.1
2	J	36	VAL	2.1
1	E	185	LYS	2.1
1	E	350	ASN	2.1
2	G	81	ARG	2.1
1	E	213	GLN	2.1
1	K	141	GLY	2.1
1	K	151	LEU	2.1
2	G	15	LEU	2.1
1	H	169	ARG	2.1
2	B	91	ILE	2.1
1	K	198	HIS	2.1
2	J	11	LYS	2.1
1	K	365	TRP	2.1
2	B	70	LEU	2.1
2	D	16	ALA	2.1
1	E	289	LYS	2.1
2	D	64	GLN	2.1
2	G	63	LYS	2.1
1	K	208	MET	2.1
2	D	44	GLU	2.1
2	G	67	LYS	2.1
2	G	74	SER	2.1
1	K	175	ASN	2.1
1	K	325	PHE	2.1
1	K	350	ASN	2.1
1	K	174	ASP	2.1
1	H	164	ILE	2.1
1	H	256	ALA	2.1
2	J	111	ASN	2.1
1	A	167	GLY	2.0
1	A	232	ASP	2.0
1	K	159	LYS	2.0
2	D	43	GLY	2.0
1	H	328	ARG	2.0
1	K	240	ILE	2.0
2	J	28	THR	2.0
1	A	160	GLU	2.0
1	H	158	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
2	G	34	PHE	2.0
1	H	289	LYS	2.0
2	J	41	TYR	2.0
2	B	121	LEU	2.0
2	J	75	GLU	2.0
1	A	229	SER	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

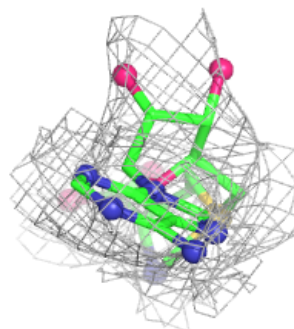
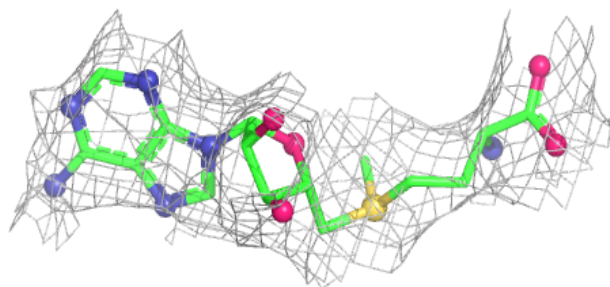
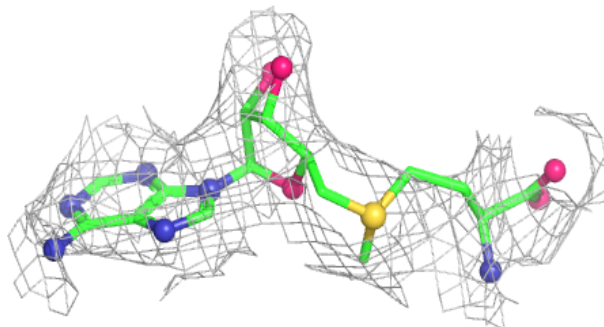
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SAM	K	401	27/27	0.85	0.15	61,74,82,83	0
3	SAM	H	401	27/27	0.90	0.12	32,41,52,55	0
3	SAM	A	401	27/27	0.92	0.13	10,14,17,17	0
3	SAM	E	401	27/27	0.94	0.12	11,14,18,19	0

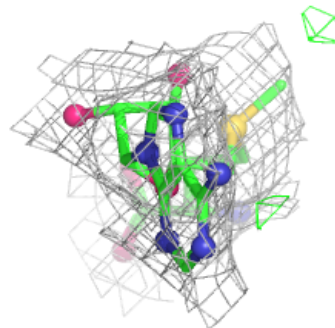
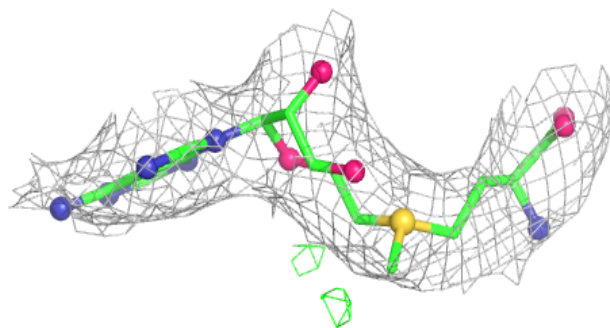
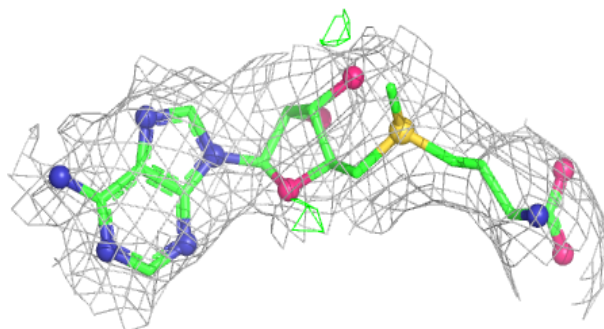
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SAM K 401:

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

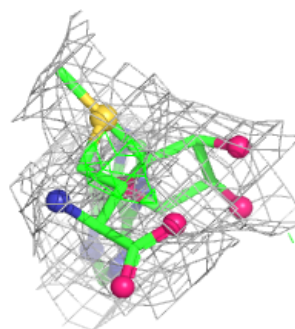
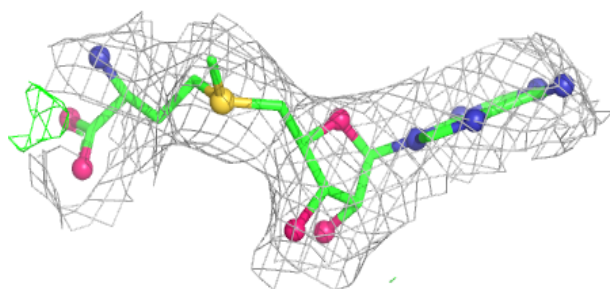
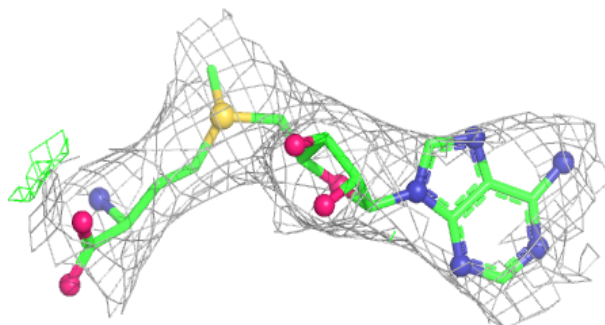
**Electron density around SAM H 401:**

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

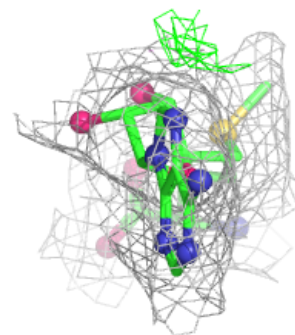
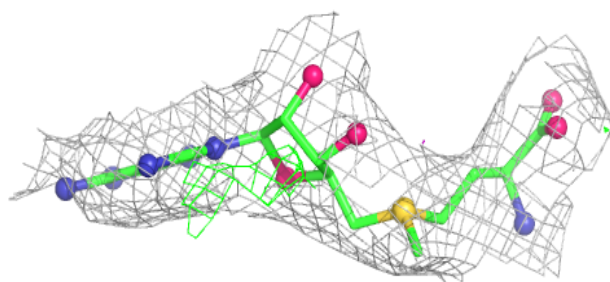
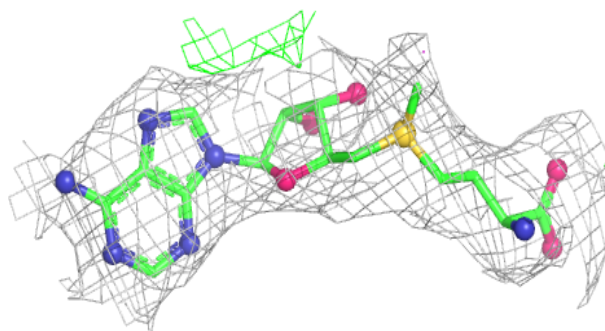


Electron density around SAM A 401:

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

**Electron density around SAM E 401:**

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



6.5 Other polymers ⓘ

There are no such residues in this entry.