



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 17, 2021 – 12:06 AM EDT

PDB ID : 1SVU
Title : Structure of the Q237W mutant of HhaI DNA methyltransferase: an insight into protein-protein interactions
Authors : Dong, A.; Zhou, L.; Zhang, X.; Stickel, S.; Roberts, R.J.; Cheng, X.
Deposited on : 2004-03-30
Resolution : 2.66 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

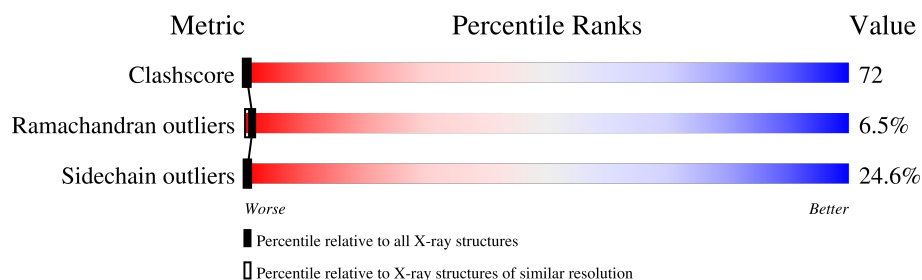
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.66 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	327	
1	B	327	

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	SAH	B	402	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4985 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.

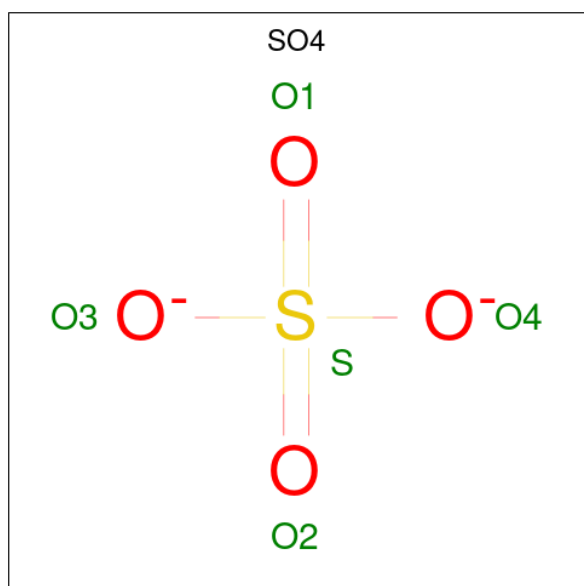
- Molecule 1 is a protein called Modification methylase HhaI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2438	1563	411	452	12			
1	B	314	Total	C	N	O	S	0	0	0
			2443	1560	414	456	13			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	237	TRP	GLN	engineered mutation	UNP P05102
B	237	TRP	GLN	engineered mutation	UNP P05102

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



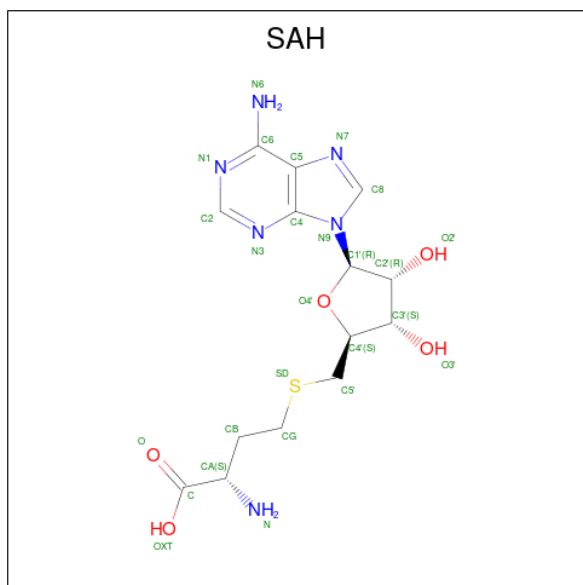
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
3	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 4 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	X	0	0
			8	8		
4	B	9	Total	X	0	0
			9	9		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	11	Total	O	0	0
			11	11		

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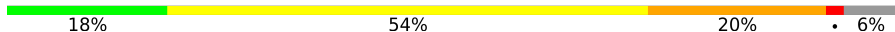
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	14	Total	O	0	0
			14	14		

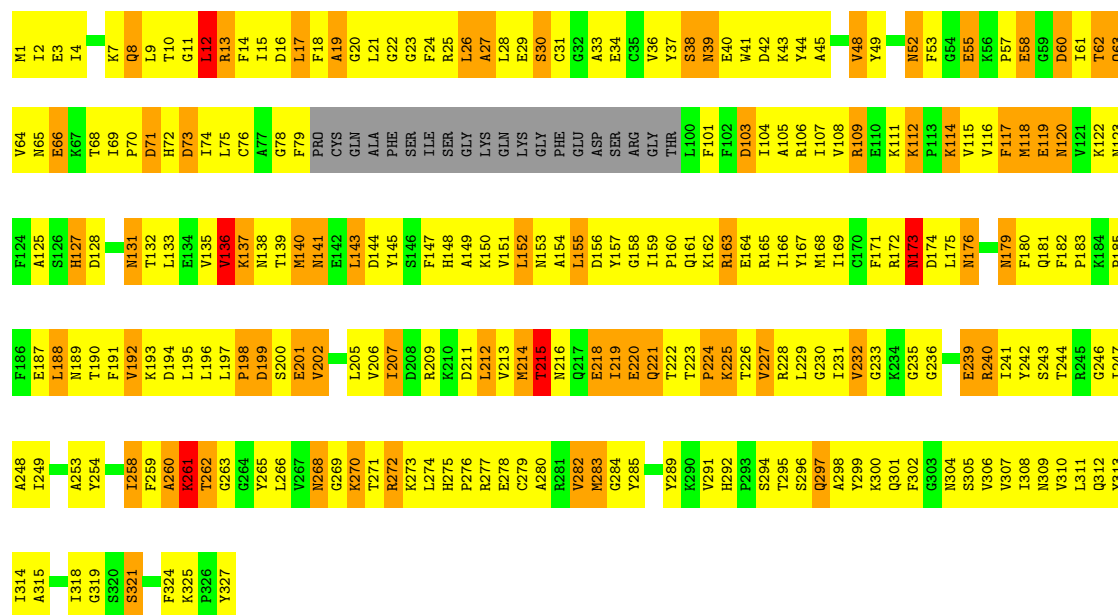
3 Residue-property plots

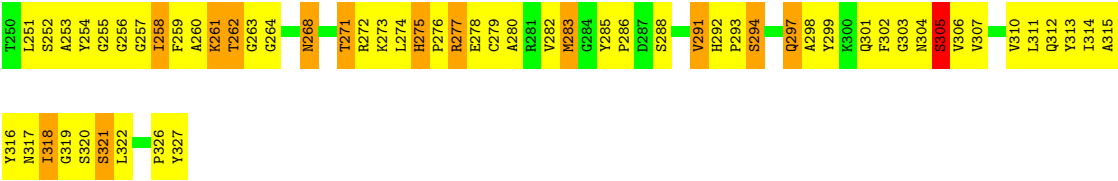
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: Modification methylase HhaI

Chain A: 





4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	155.00Å 47.00Å 122.70Å 90.00° 121.00° 90.00°	Depositor
Resolution (Å)	24.54 – 2.66	Depositor
% Data completeness (in resolution range)	91.6 (24.54-2.66)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.189 , 0.266	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4985	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SAH, UNX, SO4

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	0.46	0/2491	0.67	0/3364
1	B	0.45	0/2496	0.68	2/3378 (0.1%)
All	All	0.45	0/4987	0.67	2/6742 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	78	GLY	N-CA-C	-5.24	99.99	113.10
1	B	238	GLY	N-CA-C	-5.01	100.58	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	254	TYR	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2438	0	2398	340	0
1	B	2443	0	2361	370	0
2	A	10	0	0	1	0
3	A	26	0	19	5	0
3	B	26	0	19	10	0
4	A	8	0	0	0	0
4	B	9	0	0	0	0
5	A	11	0	0	2	0
5	B	14	0	0	1	0
All	All	4985	0	4797	707	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 72.

All (707) 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:B:212:LEU:HA	1:B:232:VAL:HG22	1.31	1.12
1:B:4:ILE:HD12	1:B:30:SER:HB2	1.32	1.12
1:A:155:LEU:HA	1:A:159:ILE:O	1.50	1.08
1:B:260:ALA:O	1:B:261:LYS:CB	2.05	1.03
1:A:231:ILE:HD12	1:A:235:GLY:HA3	1.42	1.01
1:B:137:LYS:HG2	1:B:141:ASN:HD21	1.25	1.00
1:B:260:ALA:O	1:B:261:LYS:HB2	1.18	0.99
1:A:196:LEU:HD22	1:A:272:ARG:HH22	1.28	0.96
1:B:177:ILE:C	1:B:178:GLN:HE21	1.70	0.95
1:B:9:LEU:HD22	1:B:12:LEU:HD12	1.47	0.94
1:A:12:LEU:H	1:A:12:LEU:HD23	1.32	0.94
1:B:256:GLY:C	1:B:260:ALA:HB2	1.91	0.91
1:B:223:THR:HG22	1:B:225:LYS:HG2	1.54	0.89
1:B:15:ILE:HD11	1:B:75:LEU:HD12	1.54	0.87
1:A:207:ILE:HG21	1:A:258:ILE:HD11	1.56	0.87
1:B:82:GLN:HE22	1:B:100:LEU:HB3	1.39	0.87
1:A:196:LEU:HD22	1:A:272:ARG:NH2	1.89	0.86
1:A:294:SER:HB3	1:A:297:GLN:HB2	1.57	0.86
1:A:1:MET:HG3	1:A:312:GLN:OE1	1.75	0.86
1:A:15:ILE:HB	1:A:37:TYR:HB3	1.57	0.86
1:A:198:PRO:O	1:A:201:GLU:HG2	1.77	0.85
1:B:222:THR:HA	1:B:245:ARG:HB3	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:228:ARG:NH1	1:B:240:ARG:HH11	1.75	0.84
1:A:276:PRO:HD3	1:A:299:TYR:CE1	2.12	0.83
1:B:241:ILE:HD11	1:B:259:PHE:HE1	1.44	0.83
1:A:188:LEU:HD11	1:A:190:THR:O	1.76	0.83
1:B:241:ILE:HD11	1:B:259:PHE:CE1	2.14	0.81
1:B:160:PRO:HA	1:B:247:ILE:HG22	1.63	0.81
1:A:152:LEU:HD23	5:A:614:HOH:O	1.80	0.80
1:A:297:GLN:HA	1:A:297:GLN:NE2	1.94	0.80
1:A:172:ARG:HH11	1:A:172:ARG:HG2	1.46	0.80
1:B:50:GLU:HA	1:B:55:GLU:O	1.82	0.79
1:B:66:GLU:O	1:B:69:ILE:HB	1.82	0.78
1:A:207:ILE:HG22	1:A:209:ARG:HG3	1.66	0.78
1:B:206:VAL:HA	1:B:272:ARG:HB3	1.65	0.78
1:B:215:THR:H	1:B:230:GLY:HA2	1.49	0.78
1:A:152:LEU:HD12	1:A:167:TYR:CD1	2.19	0.77
1:A:215:THR:OG1	1:A:230:GLY:HA2	1.84	0.77
1:B:177:ILE:HG23	1:B:179:ASN:HD21	1.49	0.77
1:A:275:HIS:CD2	1:A:276:PRO:HD2	2.18	0.77
1:B:69:ILE:HG12	1:B:107:ILE:HD13	1.67	0.77
1:A:66:GLU:H	1:A:66:GLU:CD	1.88	0.77
1:A:163:ARG:HH21	1:A:283:MET:HE2	1.50	0.77
1:B:228:ARG:HH12	1:B:240:ARG:NH1	1.83	0.77
1:B:122:LYS:HD3	1:B:123:ASN:N	2.00	0.76
1:B:277:ARG:O	1:B:280:ALA:HB3	1.86	0.76
1:B:4:ILE:HD13	1:B:31:CYS:SG	2.25	0.75
1:B:238:GLY:O	1:B:258:ILE:HG23	1.86	0.75
1:B:137:LYS:HG2	1:B:141:ASN:ND2	1.99	0.74
1:A:66:GLU:HA	1:A:69:ILE:HD12	1.69	0.74
1:B:188:LEU:HD11	1:B:190:THR:O	1.86	0.74
1:B:280:ALA:HA	1:B:302:PHE:CE2	2.23	0.74
1:B:63:GLN:O	1:B:64:VAL:HG23	1.88	0.74
1:B:226:THR:HG21	1:B:249:ILE:HA	1.68	0.74
1:A:268:ASN:O	1:A:270:LYS:N	2.20	0.73
1:B:276:PRO:O	1:B:279:CYS:HB2	1.88	0.73
1:A:297:GLN:HE21	1:A:297:GLN:CA	2.01	0.72
1:A:69:ILE:HD13	1:A:107:ILE:HG23	1.72	0.72
1:A:172:ARG:NH1	1:A:174:ASP:HB2	2.04	0.72
1:A:12:LEU:H	1:A:12:LEU:CD2	1.97	0.72
1:A:297:GLN:HA	1:A:297:GLN:HE21	1.54	0.72
1:B:100:LEU:HA	1:B:103:ASP:OD1	1.90	0.71
1:B:228:ARG:HH12	1:B:240:ARG:HH11	1.35	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:ASN:HA	5:B:424:HOH:O	1.90	0.70
1:A:144:ASP:C	1:A:173:ASN:HD21	1.94	0.70
1:A:153:ASN:OD1	1:A:155:LEU:HD23	1.91	0.70
1:B:48:VAL:HA	1:B:51:MET:HG3	1.74	0.70
1:B:12:LEU:O	1:B:13:ARG:HG3	1.90	0.70
1:B:212:LEU:CA	1:B:232:VAL:HG22	2.16	0.70
1:B:227:VAL:O	1:B:242:TYR:HA	1.92	0.70
1:B:188:LEU:HD12	1:B:190:THR:H	1.57	0.70
1:A:198:PRO:O	1:A:200:SER:N	2.26	0.69
1:B:163:ARG:NH1	1:B:283:MET:HE1	2.07	0.69
1:B:28:LEU:HB3	1:B:33:ALA:HB3	1.74	0.69
1:B:101:PHE:C	1:B:103:ASP:H	1.95	0.69
1:A:12:LEU:HA	1:A:73:ASP:OD1	1.93	0.69
1:B:147:PHE:HE2	1:B:149:ALA:HB2	1.57	0.69
1:B:177:ILE:HG23	1:B:179:ASN:ND2	2.08	0.69
1:A:70:PRO:O	1:A:111:LYS:HD2	1.92	0.69
1:A:198:PRO:HD2	1:A:201:GLU:OE1	1.93	0.69
1:B:14:PHE:CG	1:B:28:LEU:HD12	2.28	0.69
1:A:202:VAL:HG21	1:A:272:ARG:HH21	1.57	0.68
1:B:149:ALA:HA	1:B:167:TYR:O	1.93	0.68
1:B:291:VAL:HG12	1:B:302:PHE:HE1	1.58	0.68
1:B:137:LYS:HA	1:B:147:PHE:CD1	2.28	0.68
1:A:75:LEU:HD13	1:A:108:VAL:CG2	2.23	0.68
1:B:15:ILE:HG22	1:B:36:VAL:HG23	1.75	0.68
1:A:214:MET:O	1:A:216:ASN:N	2.26	0.68
1:A:101:PHE:CZ	1:A:136:VAL:HG22	2.28	0.68
1:B:240:ARG:C	1:B:241:ILE:HD12	2.15	0.68
1:B:46:GLN:HB3	1:B:56:LYS:HE2	1.75	0.67
1:A:8:GLN:O	1:A:9:LEU:HD23	1.94	0.67
1:A:153:ASN:ND2	1:A:163:ARG:O	2.27	0.67
1:A:17:LEU:HD11	1:A:107:ILE:HD13	1.77	0.67
1:A:75:LEU:HD13	1:A:108:VAL:HG23	1.77	0.67
1:A:206:VAL:HG12	1:A:207:ILE:N	2.10	0.66
1:A:259:PHE:O	1:A:263:GLY:HA2	1.95	0.66
1:A:44:TYR:O	1:A:48:VAL:HG22	1.95	0.66
1:B:138:ASN:HA	1:B:141:ASN:HD22	1.61	0.66
1:B:215:THR:H	1:B:230:GLY:CA	2.09	0.66
1:A:53:PHE:O	1:A:55:GLU:HG2	1.95	0.66
1:A:196:LEU:HD23	1:A:278:GLU:CD	2.16	0.66
1:A:139:THR:O	1:A:143:LEU:HB2	1.96	0.66
1:B:19:ALA:HB1	1:B:49:TYR:CE1	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:ASP:O	1:B:213:VAL:HG23	1.95	0.65
1:A:12:LEU:HD23	1:A:12:LEU:N	2.07	0.65
1:A:163:ARG:NH2	1:A:283:MET:HE2	2.11	0.65
1:A:276:PRO:HD3	1:A:299:TYR:HE1	1.61	0.65
1:B:231:ILE:HD12	1:B:235:GLY:HA3	1.78	0.65
1:A:228:ARG:CZ	1:A:240:ARG:HD3	2.26	0.65
1:A:69:ILE:HD13	1:A:107:ILE:CG2	2.27	0.65
1:A:137:LYS:O	1:A:140:MET:HB2	1.97	0.65
1:B:245:ARG:HH11	1:B:245:ARG:CG	2.10	0.65
1:B:8:GLN:O	1:B:9:LEU:HD23	1.97	0.65
1:A:136:VAL:HG12	1:A:137:LYS:N	2.11	0.64
1:B:215:THR:HG23	1:B:230:GLY:HA2	1.79	0.64
1:B:256:GLY:C	1:B:260:ALA:CB	2.65	0.64
1:A:120:ASN:H	1:A:166:ILE:HG22	1.62	0.64
1:A:324:PHE:CE1	1:B:320:SER:HB3	2.32	0.64
1:A:228:ARG:NH2	1:A:240:ARG:HH11	1.96	0.64
1:B:228:ARG:CZ	1:B:240:ARG:HH11	2.09	0.64
1:B:297:GLN:O	1:B:301:GLN:HG3	1.97	0.64
1:B:212:LEU:HD23	1:B:213:VAL:N	2.11	0.64
1:A:199:ASP:HA	1:A:202:VAL:CG2	2.28	0.64
1:B:147:PHE:HE2	1:B:149:ALA:CB	2.11	0.64
1:A:163:ARG:NE	1:A:283:MET:HE1	2.13	0.64
1:A:172:ARG:HG2	1:A:172:ARG:NH1	2.13	0.64
1:B:130:GLY:C	1:B:132:THR:H	1.99	0.64
1:A:163:ARG:HH21	1:A:283:MET:CE	2.10	0.63
1:B:109:ARG:HA	1:B:112:LYS:HE2	1.79	0.63
1:B:103:ASP:O	1:B:107:ILE:HG13	1.98	0.63
1:B:228:ARG:HD3	1:B:231:ILE:HG22	1.80	0.63
1:B:2:ILE:HG12	1:B:312:GLN:OE1	1.99	0.63
1:A:78:GLY:O	3:A:401:SAH:HG1	1.99	0.63
1:B:153:ASN:OD1	1:B:155:LEU:HD23	1.99	0.63
1:B:50:GLU:OE1	1:B:56:LYS:HG3	1.99	0.62
1:A:163:ARG:HE	1:A:283:MET:HE1	1.64	0.62
1:A:297:GLN:NE2	1:A:297:GLN:CA	2.60	0.62
1:A:74:ILE:HA	1:A:115:VAL:O	1.99	0.62
1:A:205:LEU:HD13	1:A:273:LYS:O	1.99	0.62
1:B:167:TYR:CZ	1:B:310:VAL:HG11	2.34	0.62
1:A:115:VAL:HG22	1:A:171:PHE:CD2	2.34	0.62
1:B:108:VAL:CG1	1:B:143:LEU:HD12	2.29	0.62
1:A:119:GLU:HG2	1:A:166:ILE:O	2.00	0.62
1:B:147:PHE:CE2	1:B:149:ALA:HB2	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:236:GLY:N	1:B:239:GLU:HB3	2.15	0.62
1:B:24:PHE:CG	1:B:76:CYS:HB3	2.35	0.62
1:B:223:THR:CG2	1:B:225:LYS:HG2	2.29	0.62
1:A:40:GLU:OE2	3:A:401:SAH:H1'	2.00	0.61
1:B:12:LEU:HD11	1:B:322:LEU:HD12	1.82	0.61
1:B:22:GLY:HA3	1:B:53:PHE:HE1	1.64	0.61
1:B:108:VAL:HG12	1:B:143:LEU:HD12	1.83	0.61
1:B:228:ARG:HA	1:B:241:ILE:O	2.01	0.61
1:B:39:ASN:ND2	1:B:61:ILE:HD13	2.16	0.61
1:A:127:HIS:ND1	1:A:128:ASP:N	2.49	0.61
1:A:276:PRO:CD	1:A:299:TYR:HE1	2.14	0.60
1:B:130:GLY:O	1:B:132:THR:N	2.34	0.60
1:A:173:ASN:ND2	1:A:173:ASN:H	1.98	0.60
1:B:229:LEU:HD21	1:B:243:SER:HB2	1.83	0.60
1:A:212:LEU:HA	1:A:232:VAL:HG23	1.84	0.60
1:B:13:ARG:CZ	1:B:36:VAL:HG11	2.31	0.60
1:A:220:GLU:C	1:A:221:GLN:HG3	2.21	0.60
1:B:40:GLU:OE2	3:B:402:SAH:H1'	2.01	0.60
1:A:42:ASP:HB3	1:A:45:ALA:CB	2.31	0.60
1:A:71:ASP:OD1	1:A:111:LYS:NZ	2.34	0.60
1:A:76:CYS:HA	1:A:117:PHE:O	2.01	0.60
1:A:196:LEU:CD2	1:A:272:ARG:HH22	2.08	0.60
1:A:229:LEU:HD13	1:A:266:LEU:HD22	1.82	0.60
1:A:265:TYR:CD1	1:A:274:LEU:HG	2.37	0.59
1:B:79:PHE:HB2	1:B:80:PRO:HD2	1.83	0.59
1:B:161:GLN:NE2	1:B:282:VAL:HG12	2.16	0.59
1:B:118:MET:HB2	1:B:168:MET:HE3	1.85	0.59
1:B:122:LYS:HD3	1:B:122:LYS:C	2.23	0.59
1:A:229:LEU:HD11	1:A:243:SER:HB3	1.84	0.59
1:B:168:MET:C	1:B:169:ILE:HD13	2.23	0.59
1:B:251:LEU:HD21	1:B:279:CYS:HA	1.84	0.59
1:A:202:VAL:HG21	1:A:272:ARG:NH2	2.17	0.59
1:B:276:PRO:HD3	1:B:299:TYR:CE1	2.37	0.59
1:A:151:VAL:HG11	1:A:164:GLU:HG2	1.83	0.59
1:B:71:ASP:HA	1:B:111:LYS:HE2	1.85	0.59
1:A:28:LEU:O	1:A:31:CYS:N	2.36	0.59
1:A:120:ASN:O	1:A:165:ARG:HD2	2.03	0.59
1:A:327:TYR:HB2	1:B:317:ASN:OD1	2.02	0.59
1:B:257:GLY:N	1:B:260:ALA:HB2	2.18	0.59
1:B:62:THR:HG22	1:B:63:GLN:NE2	2.18	0.59
1:A:141:ASN:C	1:A:143:LEU:N	2.55	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:PRO:HG3	5:A:614:HOH:O	2.03	0.58
1:A:314:ILE:O	1:A:318:ILE:HG13	2.02	0.58
1:B:138:ASN:O	1:B:142:GLU:HB2	2.03	0.58
1:B:226:THR:HG22	1:B:247:ILE:O	2.03	0.58
1:A:14:PHE:CG	1:A:28:LEU:HD12	2.38	0.58
1:A:16:ASP:O	1:A:38:SER:HA	2.03	0.58
1:A:154:ALA:HB2	1:A:307:VAL:HG21	1.85	0.58
1:A:114:LYS:HG2	1:A:175:LEU:HD11	1.84	0.58
1:A:144:ASP:C	1:A:173:ASN:ND2	2.57	0.58
1:A:205:LEU:O	1:A:272:ARG:HB2	2.04	0.58
1:A:308:ILE:HG22	1:A:312:GLN:OE1	2.03	0.58
1:B:192:VAL:O	1:B:196:LEU:HG	2.03	0.58
1:A:2:ILE:HB	1:A:312:GLN:NE2	2.18	0.58
1:B:168:MET:O	1:B:169:ILE:HD13	2.02	0.58
1:A:202:VAL:HG11	1:A:272:ARG:CZ	2.33	0.58
1:A:137:LYS:HG3	1:A:138:ASN:N	2.17	0.58
1:A:196:LEU:HD23	1:A:278:GLU:OE2	2.03	0.58
1:A:28:LEU:O	1:A:31:CYS:HB2	2.03	0.58
1:A:66:GLU:HA	1:A:69:ILE:CD1	2.33	0.58
1:B:113:PRO:HD2	1:B:145:TYR:OH	2.04	0.58
1:B:21:LEU:HD12	1:B:305:SER:HB2	1.85	0.57
1:B:161:GLN:HE21	1:B:282:VAL:HG12	1.69	0.57
1:A:73:ASP:HB3	1:A:114:LYS:HE3	1.85	0.57
1:B:146:SER:O	1:B:170:CYS:HB3	2.04	0.57
1:B:291:VAL:HG12	1:B:302:PHE:CE1	2.39	0.57
1:B:297:GLN:OE1	1:B:297:GLN:HA	2.02	0.57
1:A:73:ASP:OD2	1:A:73:ASP:N	2.37	0.57
1:A:147:PHE:CZ	1:A:168:MET:HG2	2.39	0.57
1:A:261:LYS:N	1:A:261:LYS:HD2	2.18	0.57
1:B:222:THR:HG22	1:B:245:ARG:HG3	1.85	0.57
1:B:212:LEU:HD23	1:B:212:LEU:C	2.25	0.57
1:A:202:VAL:HG11	1:A:272:ARG:NH2	2.20	0.57
1:A:212:LEU:HD23	1:A:213:VAL:N	2.20	0.57
1:A:260:ALA:O	1:A:262:THR:N	2.38	0.57
1:B:20:GLY:HA3	3:B:402:SAH:HA	1.85	0.57
1:A:14:PHE:CD1	1:A:28:LEU:HD12	2.40	0.57
1:B:204:HIS:CE1	1:B:205:LEU:HD23	2.40	0.57
1:B:306:VAL:HG22	1:B:307:VAL:N	2.20	0.57
1:A:79:PHE:HE2	1:A:118:MET:HG2	1.70	0.57
1:B:116:VAL:HG21	1:B:140:MET:HE1	1.87	0.57
1:B:206:VAL:HA	1:B:272:ARG:CB	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:LEU:HD23	1:A:213:VAL:H	1.67	0.56
1:B:76:CYS:HA	1:B:117:PHE:O	2.05	0.56
1:B:241:ILE:HA	1:B:264:GLY:O	2.04	0.56
1:A:141:ASN:C	1:A:143:LEU:H	2.08	0.56
1:B:205:LEU:HD13	1:B:273:LYS:CG	2.35	0.56
1:A:181:GLN:OE1	1:B:326:PRO:HG2	2.05	0.56
1:B:98:GLY:H	1:B:102:PHE:CB	2.18	0.56
1:B:178:GLN:HE21	1:B:178:GLN:N	2.04	0.56
1:B:306:VAL:HG13	1:B:311:LEU:HD22	1.87	0.56
1:A:28:LEU:HD11	1:A:76:CYS:SG	2.46	0.56
1:A:161:GLN:NE2	1:A:282:VAL:HG13	2.20	0.56
1:A:7:LYS:C	1:A:9:LEU:H	2.09	0.56
1:A:206:VAL:HG12	1:A:207:ILE:H	1.71	0.56
1:A:279:CYS:O	1:A:282:VAL:HG12	2.06	0.56
1:A:325:LYS:O	1:B:316:TYR:HE2	1.88	0.56
1:B:13:ARG:HG2	1:B:34:GLU:OE1	2.06	0.56
1:B:155:LEU:HA	1:B:159:ILE:O	2.06	0.56
1:B:17:LEU:O	1:B:18:PHE:HB2	2.05	0.56
1:B:9:LEU:HD22	1:B:12:LEU:CD1	2.30	0.55
1:A:105:ALA:O	1:A:106:ARG:C	2.45	0.55
1:A:120:ASN:N	1:A:166:ILE:HG22	2.21	0.55
1:B:14:PHE:CD2	1:B:28:LEU:HD12	2.41	0.55
1:A:223:THR:CG2	1:A:225:LYS:HG2	2.36	0.55
1:A:15:ILE:HD11	1:A:17:LEU:HG	1.88	0.55
1:B:275:HIS:ND1	1:B:276:PRO:HD2	2.21	0.55
1:B:19:ALA:O	3:B:402:SAH:HA	2.07	0.55
1:B:160:PRO:CA	1:B:247:ILE:HG22	2.34	0.55
1:A:308:ILE:O	1:A:312:GLN:HG3	2.06	0.55
1:B:205:LEU:O	1:B:272:ARG:HB2	2.07	0.55
1:A:153:ASN:HA	1:A:163:ARG:O	2.07	0.55
1:A:158:GLY:HA2	1:A:188:LEU:HB2	1.89	0.55
1:A:147:PHE:CE2	1:A:149:ALA:HB2	2.42	0.55
1:B:22:GLY:HA3	1:B:53:PHE:CE1	2.41	0.55
1:A:191:PHE:O	1:A:194:ASP:HB2	2.07	0.54
1:A:306:VAL:HG22	1:A:307:VAL:N	2.23	0.54
1:B:136:VAL:HG12	1:B:147:PHE:HE1	1.71	0.54
1:B:206:VAL:HG12	1:B:207:ILE:N	2.20	0.54
1:B:160:PRO:HB3	1:B:190:THR:O	2.06	0.54
1:B:215:THR:OG1	1:B:230:GLY:HA2	2.07	0.54
1:A:214:MET:C	1:A:216:ASN:N	2.61	0.54
1:B:144:ASP:OD1	1:B:173:ASN:HB2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:ALA:HB3	1:B:282:VAL:HG11	1.89	0.54
1:A:219:ILE:HD12	1:A:227:VAL:HG21	1.90	0.54
1:B:119:GLU:HG2	1:B:166:ILE:O	2.08	0.54
1:A:42:ASP:HB3	1:A:45:ALA:HB2	1.89	0.54
1:A:70:PRO:O	1:A:72:HIS:HD2	1.91	0.54
1:B:125:ALA:HA	1:B:133:LEU:HD23	1.89	0.54
1:B:294:SER:OG	1:B:297:GLN:HB2	2.08	0.54
1:A:306:VAL:CG2	1:A:307:VAL:N	2.71	0.53
1:A:151:VAL:CG1	1:A:164:GLU:HG2	2.37	0.53
1:A:169:ILE:HD11	1:A:314:ILE:HG21	1.91	0.53
1:A:199:ASP:HA	1:A:202:VAL:HG23	1.90	0.53
1:B:82:GLN:NE2	1:B:100:LEU:HB3	2.15	0.53
1:B:46:GLN:HB3	1:B:56:LYS:CE	2.38	0.53
1:B:154:ALA:HB2	1:B:307:VAL:HG21	1.90	0.53
1:A:306:VAL:HG21	1:A:311:LEU:HD13	1.90	0.53
1:A:202:VAL:HB	1:A:272:ARG:NE	2.23	0.53
1:A:276:PRO:HD3	1:A:299:TYR:CZ	2.44	0.53
1:A:212:LEU:HD22	1:A:214:MET:SD	2.49	0.53
1:A:285:TYR:CE1	1:A:308:ILE:HD11	2.43	0.53
1:A:308:ILE:N	1:A:308:ILE:HD13	2.23	0.53
1:A:176:ASN:CG	1:A:176:ASN:O	2.48	0.53
1:A:198:PRO:O	1:A:199:ASP:C	2.47	0.53
1:A:232:VAL:O	1:A:239:GLU:HG2	2.08	0.53
1:B:75:LEU:HD23	1:B:75:LEU:O	2.09	0.53
1:B:136:VAL:HG12	1:B:147:PHE:CE1	2.44	0.53
1:A:12:LEU:HB3	1:A:73:ASP:HB2	1.90	0.53
1:A:119:GLU:HA	1:A:166:ILE:O	2.09	0.53
1:A:154:ALA:HB1	1:A:159:ILE:HG21	1.92	0.53
1:A:298:ALA:O	1:A:301:GLN:HB2	2.08	0.53
1:B:228:ARG:HD3	1:B:240:ARG:HB3	1.91	0.53
1:A:108:VAL:HG12	1:A:143:LEU:HD13	1.89	0.52
1:B:63:GLN:O	1:B:64:VAL:CG2	2.56	0.52
1:A:131:ASN:O	1:A:132:THR:C	2.47	0.52
1:A:202:VAL:O	1:A:205:LEU:HB2	2.10	0.52
1:A:169:ILE:HG13	1:A:180:PHE:CZ	2.44	0.52
1:A:233:GLY:C	1:A:235:GLY:H	2.12	0.52
1:B:125:ALA:HA	1:B:133:LEU:CD2	2.39	0.52
1:B:150:LYS:HD3	1:B:152:LEU:CD2	2.40	0.52
1:B:285:TYR:OH	1:B:305:SER:OG	2.22	0.52
1:A:261:LYS:HD2	1:A:261:LYS:H	1.74	0.52
1:B:20:GLY:HA3	3:B:402:SAH:CA	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:PHE:O	1:B:120:ASN:ND2	2.42	0.52
1:A:214:MET:C	1:A:216:ASN:H	2.13	0.52
1:A:73:ASP:O	1:A:74:ILE:HG13	2.10	0.52
1:A:154:ALA:O	1:A:159:ILE:HB	2.09	0.52
1:A:37:TYR:CG	1:A:38:SER:N	2.78	0.52
1:A:163:ARG:NH2	1:A:283:MET:CE	2.71	0.52
1:B:275:HIS:ND1	1:B:276:PRO:CD	2.73	0.52
1:A:128:ASP:HB3	1:A:131:ASN:HB2	1.92	0.52
1:A:153:ASN:O	1:A:156:ASP:HB2	2.09	0.52
1:B:9:LEU:CD2	1:B:12:LEU:HD12	2.30	0.52
1:B:304:ASN:O	1:B:305:SER:O	2.28	0.52
1:A:66:GLU:CD	1:A:66:GLU:N	2.59	0.52
1:A:274:LEU:HD22	1:A:278:GLU:HB3	1.91	0.52
1:A:324:PHE:HE1	1:B:320:SER:C	2.13	0.52
1:B:66:GLU:CD	1:B:66:GLU:H	2.13	0.52
1:B:157:TYR:HA	1:B:186:PHE:CE2	2.45	0.52
1:B:228:ARG:NH2	1:B:240:ARG:HH11	2.08	0.52
1:A:199:ASP:O	1:A:200:SER:C	2.46	0.51
1:B:4:ILE:CD1	1:B:30:SER:HB2	2.23	0.51
1:B:41:TRP:HA	1:B:46:GLN:NE2	2.25	0.51
1:B:14:PHE:CB	1:B:28:LEU:HD12	2.41	0.51
1:B:44:TYR:HB3	1:B:292:HIS:CD2	2.46	0.51
1:B:215:THR:HG21	1:B:231:ILE:HG23	1.91	0.51
1:B:245:ARG:NH1	1:B:245:ARG:HG2	2.25	0.51
1:B:272:ARG:HG3	1:B:272:ARG:HH11	1.76	0.51
1:B:294:SER:O	1:B:297:GLN:N	2.43	0.51
1:B:174:ASP:C	1:B:176:ASN:H	2.14	0.51
1:B:228:ARG:HH22	1:B:240:ARG:NH1	2.08	0.51
1:A:17:LEU:HD11	1:A:107:ILE:CD1	2.41	0.51
1:B:161:GLN:HB2	1:B:282:VAL:CG1	2.39	0.51
1:B:9:LEU:HD13	1:B:33:ALA:HB2	1.93	0.51
1:B:41:TRP:H	3:B:402:SAH:C2	2.22	0.51
1:B:151:VAL:C	1:B:152:LEU:HD23	2.30	0.51
1:A:193:LYS:HB3	1:A:244:THR:O	2.09	0.51
1:A:229:LEU:CD1	1:A:243:SER:HB3	2.40	0.51
1:B:15:ILE:O	1:B:15:ILE:HG13	2.11	0.51
1:A:7:LYS:O	1:A:9:LEU:N	2.41	0.51
1:A:13:ARG:HA	1:A:34:GLU:O	2.11	0.51
1:A:20:GLY:HA3	3:A:401:SAH:HA	1.92	0.51
1:A:62:THR:HB	1:A:63:GLN:HE21	1.75	0.51
1:B:150:LYS:HD3	1:B:152:LEU:HD21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:152:LEU:HB2	1:B:167:TYR:CE1	2.47	0.50
1:B:223:THR:HG23	1:B:224:PRO:HD2	1.93	0.50
1:B:314:ILE:O	1:B:317:ASN:N	2.44	0.50
1:A:60:ASP:O	1:A:64:VAL:HG23	2.11	0.50
1:A:122:LYS:HB2	1:A:164:GLU:HB3	1.93	0.50
1:B:143:LEU:O	1:B:144:ASP:CB	2.59	0.50
1:B:149:ALA:HB2	1:B:168:MET:HG2	1.93	0.50
1:B:161:GLN:N	1:B:247:ILE:HB	2.26	0.50
1:B:179:ASN:ND2	1:B:179:ASN:N	2.59	0.50
1:B:186:PHE:N	1:B:186:PHE:CD2	2.79	0.50
1:A:223:THR:HG21	1:A:225:LYS:HE3	1.93	0.50
1:A:236:GLY:C	1:A:240:ARG:HH21	2.15	0.50
1:B:39:ASN:ND2	1:B:59:GLY:O	2.44	0.50
1:B:61:ILE:HG23	1:B:106:ARG:NH2	2.26	0.50
1:A:27:ALA:HB2	1:A:311:LEU:HB3	1.94	0.50
1:A:75:LEU:C	1:A:75:LEU:HD23	2.32	0.50
1:A:205:LEU:HD11	1:A:275:HIS:CA	2.42	0.50
1:B:108:VAL:HG12	1:B:143:LEU:CD1	2.41	0.50
1:A:19:ALA:HB3	1:A:40:GLU:HB2	1.94	0.50
1:B:5:LYS:O	1:B:7:LYS:HD3	2.11	0.50
1:B:101:PHE:O	1:B:104:ILE:N	2.42	0.50
1:B:125:ALA:O	1:B:130:GLY:HA2	2.11	0.50
1:B:188:LEU:CD1	1:B:190:THR:H	2.22	0.50
1:A:283:MET:O	1:A:307:VAL:HA	2.12	0.50
1:B:9:LEU:HB2	1:B:31:CYS:O	2.12	0.50
1:B:40:GLU:OE1	3:B:402:SAH:O3'	2.27	0.50
1:B:12:LEU:HD13	1:B:74:ILE:HD11	1.93	0.50
1:A:109:ARG:HB2	1:A:143:LEU:HD21	1.94	0.49
1:B:46:GLN:HB3	1:B:56:LYS:HG2	1.94	0.49
1:B:171:PHE:HZ	1:B:180:PHE:CD1	2.30	0.49
1:B:262:THR:CG2	1:B:273:LYS:HB2	2.41	0.49
1:A:101:PHE:CE1	1:A:136:VAL:HG22	2.47	0.49
1:A:172:ARG:HH11	1:A:174:ASP:HB2	1.76	0.49
1:A:310:VAL:O	1:A:314:ILE:HG13	2.12	0.49
1:B:236:GLY:C	1:B:239:GLU:HB2	2.33	0.49
1:B:298:ALA:O	1:B:302:PHE:HD1	1.96	0.49
1:B:61:ILE:C	1:B:63:GLN:N	2.64	0.49
1:B:71:ASP:CA	1:B:111:LYS:HE2	2.42	0.49
1:B:82:GLN:HE22	1:B:100:LEU:CB	2.18	0.49
1:A:125:ALA:HA	1:A:133:LEU:HD22	1.93	0.49
1:A:315:ALA:O	1:A:318:ILE:HB	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:305:SER:HA	3:B:402:SAH:C	2.42	0.49
1:A:285:TYR:HH	1:A:305:SER:HG	1.60	0.49
1:B:14:PHE:O	1:B:36:VAL:HG22	2.13	0.49
1:A:145:TYR:N	1:A:173:ASN:HD21	2.10	0.49
1:A:223:THR:HG22	1:A:225:LYS:HG2	1.94	0.49
1:B:17:LEU:HD12	1:B:75:LEU:HD11	1.94	0.49
1:B:64:VAL:O	1:B:106:ARG:NH1	2.39	0.49
1:A:137:LYS:CG	1:A:138:ASN:N	2.76	0.49
1:B:41:TRP:HA	1:B:46:GLN:HE21	1.78	0.49
1:B:249:ILE:HD11	1:B:262:THR:O	2.12	0.49
1:B:318:ILE:HG22	1:B:319:GLY:N	2.28	0.49
1:A:9:LEU:HB2	1:A:31:CYS:O	2.12	0.49
1:B:101:PHE:C	1:B:103:ASP:N	2.62	0.49
1:B:222:THR:HG22	1:B:245:ARG:CG	2.43	0.49
1:A:21:LEU:HD22	1:A:289:TYR:OH	2.13	0.49
1:B:202:VAL:O	1:B:205:LEU:N	2.45	0.49
1:A:48:VAL:HG13	1:A:292:HIS:HB2	1.94	0.49
1:A:108:VAL:O	1:A:108:VAL:CG1	2.61	0.49
1:A:254:TYR:N	1:A:261:LYS:HZ1	2.11	0.49
1:A:206:VAL:O	1:A:207:ILE:HG13	2.13	0.48
1:B:61:ILE:HG22	1:B:62:THR:N	2.27	0.48
1:B:275:HIS:ND1	1:B:276:PRO:N	2.61	0.48
1:A:103:ASP:O	1:A:106:ARG:HB3	2.13	0.48
1:A:229:LEU:HD13	1:A:266:LEU:CD2	2.43	0.48
1:B:72:HIS:CE1	1:B:75:LEU:HB2	2.48	0.48
1:B:152:LEU:HD13	1:B:157:TYR:CZ	2.49	0.48
1:A:61:ILE:HA	1:A:64:VAL:HG23	1.95	0.48
1:A:294:SER:O	1:A:297:GLN:N	2.46	0.48
1:A:148:HIS:O	1:A:168:MET:HA	2.13	0.48
1:B:49:TYR:CD2	1:B:57:PRO:HD3	2.49	0.48
1:B:255:GLY:O	1:B:261:LYS:NZ	2.47	0.48
1:A:145:TYR:HA	1:A:171:PHE:O	2.13	0.48
1:B:152:LEU:HB3	1:B:157:TYR:CE1	2.49	0.48
1:B:211:ASP:OD1	1:B:211:ASP:N	2.42	0.48
1:B:215:THR:CG2	1:B:230:GLY:HA2	2.42	0.48
1:B:6:ASP:HB2	1:B:316:TYR:HE1	1.78	0.48
1:B:14:PHE:CZ	1:B:25:ARG:HA	2.49	0.48
1:A:227:VAL:HB	1:A:243:SER:OG	2.13	0.48
1:A:310:VAL:CG1	1:A:314:ILE:HD11	2.44	0.48
1:A:2:ILE:HG12	1:A:309:ASN:ND2	2.29	0.48
1:A:209:ARG:HH21	1:A:211:ASP:CG	2.15	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:ILE:N	1:A:241:ILE:HD12	2.29	0.48
1:B:165:ARG:HA	1:B:165:ARG:HD2	1.64	0.48
1:A:120:ASN:H	1:A:166:ILE:CG2	2.26	0.48
1:A:206:VAL:CG1	1:A:207:ILE:N	2.76	0.48
1:B:205:LEU:HD13	1:B:273:LYS:HG3	1.94	0.48
1:A:127:HIS:ND1	1:A:127:HIS:C	2.68	0.47
1:A:240:ARG:C	1:A:241:ILE:HD12	2.34	0.47
1:B:253:ALA:HB2	1:B:303:GLY:HA3	1.94	0.47
1:A:62:THR:HB	1:A:63:GLN:NE2	2.28	0.47
1:A:275:HIS:ND1	1:A:277:ARG:HB3	2.29	0.47
1:A:105:ALA:HA	1:A:108:VAL:HB	1.96	0.47
1:A:25:ARG:O	1:A:29:GLU:HB2	2.14	0.47
1:B:28:LEU:HD11	1:B:76:CYS:SG	2.54	0.47
1:A:9:LEU:HG	1:A:31:CYS:HB3	1.96	0.47
1:A:55:GLU:O	1:A:57:PRO:HD3	2.14	0.47
1:A:152:LEU:HB3	1:A:157:TYR:HE1	1.80	0.47
1:A:314:ILE:HG13	1:A:314:ILE:H	1.55	0.47
1:B:152:LEU:HD23	1:B:152:LEU:N	2.29	0.47
1:B:152:LEU:HB3	1:B:157:TYR:HE1	1.79	0.47
1:B:263:GLY:O	1:B:273:LYS:HA	2.14	0.47
1:B:280:ALA:HB2	1:B:302:PHE:CZ	2.49	0.47
1:A:127:HIS:ND1	1:A:128:ASP:HB2	2.29	0.47
1:B:141:ASN:O	1:B:144:ASP:N	2.38	0.47
1:A:12:LEU:HB3	1:A:73:ASP:CB	2.45	0.47
1:A:52:ASN:ND2	1:A:289:TYR:CZ	2.83	0.47
1:B:205:LEU:HD13	1:B:273:LYS:HG2	1.97	0.47
1:B:179:ASN:HD22	1:B:180:PHE:N	2.13	0.47
1:B:121:VAL:O	1:B:124:PHE:HB2	2.15	0.46
1:B:188:LEU:HD12	1:B:188:LEU:C	2.35	0.46
1:A:45:ALA:O	1:A:48:VAL:HG23	2.15	0.46
1:A:162:LYS:HB2	1:A:226:THR:HG21	1.97	0.46
1:A:163:ARG:HE	1:A:283:MET:CE	2.28	0.46
1:A:211:ASP:OD1	1:A:232:VAL:HG22	2.16	0.46
1:B:206:VAL:CG1	1:B:207:ILE:N	2.77	0.46
1:A:271:THR:HG23	1:A:271:THR:O	2.16	0.46
1:B:14:PHE:HZ	1:B:25:ARG:CG	2.29	0.46
1:B:66:GLU:OE1	1:B:106:ARG:HD2	2.16	0.46
1:B:160:PRO:HA	1:B:247:ILE:CG2	2.38	0.46
1:A:39:ASN:HA	1:A:58:GLU:O	2.16	0.46
1:A:61:ILE:HA	1:A:64:VAL:CG2	2.45	0.46
1:A:108:VAL:HG12	1:A:108:VAL:O	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:ILE:HD13	1:B:61:ILE:HA	1.65	0.46
3:B:402:SAH:HG1	3:B:402:SAH:H4'	1.87	0.46
1:A:27:ALA:O	1:A:30:SER:OG	2.27	0.46
1:A:42:ASP:HB3	1:A:45:ALA:HB3	1.96	0.46
1:B:252:SER:O	1:B:261:LYS:HG2	2.15	0.46
1:A:9:LEU:CG	1:A:31:CYS:HB3	2.46	0.46
1:B:240:ARG:O	1:B:241:ILE:HD12	2.16	0.46
1:B:275:HIS:O	1:B:276:PRO:C	2.54	0.46
3:B:402:SAH:O3'	3:B:402:SAH:HG2	2.15	0.46
1:A:218:GLU:HG3	1:A:219:ILE:N	2.31	0.46
1:B:67:LYS:HG2	1:B:110:GLU:OE2	2.16	0.46
1:B:72:HIS:CE1	1:B:113:PRO:HB3	2.50	0.46
1:A:280:ALA:O	1:A:283:MET:N	2.36	0.46
1:B:66:GLU:HA	1:B:69:ILE:HD13	1.97	0.46
1:A:1:MET:CE	1:A:26:LEU:HB3	2.46	0.46
1:A:42:ASP:O	1:A:45:ALA:HB3	2.16	0.46
1:A:197:LEU:HB3	1:A:201:GLU:HG3	1.98	0.46
1:B:14:PHE:HA	1:B:74:ILE:O	2.16	0.46
1:B:137:LYS:O	1:B:140:MET:HB2	2.15	0.45
1:B:211:ASP:O	1:B:212:LEU:C	2.53	0.45
1:A:105:ALA:O	1:A:109:ARG:N	2.49	0.45
1:B:192:VAL:HG23	1:B:246:GLY:O	2.15	0.45
1:A:228:ARG:NH2	1:A:240:ARG:NH1	2.63	0.45
1:A:280:ALA:HA	1:A:302:PHE:CE2	2.52	0.45
1:B:12:LEU:HD22	1:B:73:ASP:CB	2.47	0.45
1:B:15:ILE:HD11	1:B:75:LEU:CD1	2.38	0.45
1:B:47:GLU:O	1:B:51:MET:HG2	2.17	0.45
1:B:280:ALA:O	1:B:283:MET:HB2	2.16	0.45
1:A:62:THR:C	1:A:63:GLN:NE2	2.70	0.45
1:A:66:GLU:HB2	1:A:107:ILE:HA	1.99	0.45
1:A:157:TYR:CE2	1:A:185:PRO:HA	2.52	0.45
1:B:24:PHE:HE1	1:B:78:GLY:N	2.14	0.45
1:B:39:ASN:ND2	1:B:61:ILE:CD1	2.79	0.45
1:B:212:LEU:HD12	1:B:271:THR:HG21	1.98	0.45
1:B:253:ALA:HB2	1:B:303:GLY:C	2.37	0.45
1:A:12:LEU:HB3	1:A:73:ASP:OD1	2.15	0.45
1:A:199:ASP:O	1:A:202:VAL:N	2.42	0.45
1:A:223:THR:HG23	1:A:224:PRO:HD2	1.98	0.45
1:B:122:LYS:C	1:B:124:PHE:H	2.20	0.45
1:A:297:GLN:O	1:A:298:ALA:C	2.55	0.45
1:B:153:ASN:CG	1:B:155:LEU:HD23	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:168:MET:HE3	1:B:168:MET:HB2	1.57	0.45
1:A:114:LYS:HE3	1:A:114:LYS:HB2	1.79	0.45
1:A:143:LEU:HA	1:A:143:LEU:HD23	1.57	0.45
1:A:221:GLN:HB2	1:A:222:THR:H	1.54	0.45
1:B:118:MET:HB2	1:B:168:MET:CE	2.47	0.45
1:B:314:ILE:O	1:B:315:ALA:C	2.54	0.45
1:A:141:ASN:OD1	1:A:141:ASN:N	2.48	0.45
1:B:9:LEU:O	1:B:12:LEU:HB2	2.17	0.45
1:B:60:ASP:HB3	1:B:63:GLN:HB2	1.98	0.45
1:B:148:HIS:O	1:B:168:MET:HA	2.17	0.45
1:B:256:GLY:HA2	1:B:260:ALA:HB1	1.99	0.45
1:A:207:ILE:HG22	1:A:207:ILE:O	2.17	0.45
1:B:104:ILE:O	1:B:107:ILE:HB	2.16	0.45
1:B:236:GLY:N	1:B:239:GLU:CB	2.80	0.45
1:A:192:VAL:O	1:A:194:ASP:N	2.50	0.44
1:B:153:ASN:ND2	1:B:164:GLU:OE2	2.50	0.44
1:A:191:PHE:N	1:A:191:PHE:CD1	2.83	0.44
1:A:260:ALA:O	1:A:263:GLY:N	2.42	0.44
1:B:174:ASP:O	1:B:176:ASN:N	2.50	0.44
1:B:205:LEU:HD12	1:B:273:LYS:O	2.17	0.44
1:B:215:THR:CB	1:B:230:GLY:HA2	2.48	0.44
1:A:120:ASN:CA	1:A:166:ILE:HG22	2.47	0.44
1:A:253:ALA:HB3	1:A:304:ASN:OD1	2.17	0.44
1:B:12:LEU:C	1:B:13:ARG:HG3	2.38	0.44
1:B:275:HIS:O	1:B:278:GLU:N	2.50	0.44
1:A:9:LEU:HB2	1:A:31:CYS:HB3	2.00	0.44
1:A:49:TYR:O	1:A:53:PHE:N	2.49	0.44
1:B:37:TYR:OH	1:B:58:GLU:OE2	2.35	0.44
1:A:18:PHE:CE1	1:A:79:PHE:HB3	2.52	0.44
1:A:22:GLY:O	1:A:23:GLY:C	2.56	0.44
1:A:205:LEU:HD11	1:A:275:HIS:HA	1.99	0.44
1:A:276:PRO:N	1:A:299:TYR:HE1	2.16	0.44
1:A:315:ALA:HA	1:A:318:ILE:HD12	1.99	0.44
1:A:179:ASN:ND2	1:A:321:SER:OG	2.51	0.44
1:B:313:TYR:O	1:B:314:ILE:C	2.55	0.44
1:A:61:ILE:HG23	1:A:103:ASP:OD2	2.17	0.44
1:A:214:MET:CE	1:A:230:GLY:HA3	2.47	0.44
1:A:259:PHE:O	1:A:260:ALA:O	2.34	0.44
1:B:103:ASP:HA	1:B:106:ARG:HE	1.83	0.44
1:B:174:ASP:C	1:B:176:ASN:N	2.71	0.44
1:B:275:HIS:HB3	1:B:278:GLU:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:VAL:O	1:A:116:VAL:HG12	2.18	0.44
1:A:152:LEU:HD22	1:A:157:TYR:OH	2.16	0.44
1:A:278:GLU:O	1:A:279:CYS:C	2.55	0.44
1:B:56:LYS:HA	1:B:57:PRO:HD2	1.64	0.44
1:B:14:PHE:CZ	1:B:25:ARG:HG3	2.53	0.43
1:B:50:GLU:HB2	1:B:56:LYS:HG3	2.00	0.43
1:A:172:ARG:HH12	1:A:174:ASP:HB2	1.78	0.43
1:A:179:ASN:HD22	1:A:179:ASN:H	1.65	0.43
1:A:183:PRO:HB3	1:A:313:TYR:HB3	2.00	0.43
1:A:192:VAL:HG23	1:A:246:GLY:O	2.17	0.43
1:B:72:HIS:HE1	1:B:75:LEU:HB2	1.82	0.43
1:B:131:ASN:O	1:B:135:VAL:HG23	2.18	0.43
1:B:209:ARG:HB3	1:B:211:ASP:OD1	2.18	0.43
1:B:237:TRP:NE1	1:B:240:ARG:NH2	2.65	0.43
1:A:161:GLN:HE22	1:A:282:VAL:HG13	1.81	0.43
1:B:151:VAL:HA	1:B:165:ARG:O	2.18	0.43
1:B:292:HIS:ND1	1:B:293:PRO:HD2	2.33	0.43
1:A:48:VAL:O	1:A:49:TYR:C	2.56	0.43
1:A:192:VAL:O	1:A:193:LYS:C	2.57	0.43
1:A:111:LYS:O	1:A:112:LYS:C	2.57	0.43
1:A:160:PRO:HB3	1:A:190:THR:O	2.18	0.43
1:A:253:ALA:HB1	1:A:300:LYS:HG3	2.00	0.43
1:B:45:ALA:O	1:B:46:GLN:C	2.56	0.43
1:A:7:LYS:HD2	1:A:30:SER:O	2.18	0.43
1:A:17:LEU:O	1:A:18:PHE:HB2	2.19	0.43
1:B:45:ALA:O	1:B:48:VAL:N	2.52	0.43
1:A:262:THR:HG1	1:A:274:LEU:HB2	1.84	0.43
1:B:312:GLN:O	1:B:313:TYR:C	2.56	0.43
1:B:318:ILE:O	1:B:322:LEU:HG	2.18	0.43
1:A:69:ILE:HG22	1:A:70:PRO:O	2.19	0.43
1:A:137:LYS:HA	1:A:147:PHE:CD1	2.54	0.43
1:B:151:VAL:HG22	1:B:166:ILE:HA	2.00	0.43
1:B:203:GLU:C	1:B:205:LEU:H	2.22	0.43
1:B:228:ARG:NH1	1:B:240:ARG:HG2	2.34	0.43
1:A:9:LEU:HB3	1:A:33:ALA:HB2	2.00	0.43
1:A:174:ASP:OD1	1:A:174:ASP:N	2.51	0.43
1:A:227:VAL:O	1:A:242:TYR:HA	2.19	0.43
1:B:212:LEU:C	1:B:212:LEU:CD2	2.86	0.43
1:B:228:ARG:NH2	1:B:240:ARG:NH1	2.66	0.43
1:B:306:VAL:CG2	1:B:307:VAL:N	2.82	0.43
1:A:155:LEU:HG	1:A:156:ASP:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:THR:O	1:A:246:GLY:HA2	2.18	0.42
1:B:25:ARG:NH2	1:B:55:GLU:CD	2.72	0.42
1:B:204:HIS:ND1	1:B:205:LEU:HD23	2.34	0.42
1:B:14:PHE:CZ	1:B:35:CYS:HB2	2.54	0.42
1:B:147:PHE:CZ	1:B:168:MET:HG2	2.54	0.42
1:A:119:GLU:OE1	1:A:119:GLU:C	2.57	0.42
1:B:12:LEU:HD22	1:B:73:ASP:HB3	2.01	0.42
1:B:177:ILE:HG21	1:B:321:SER:HB3	2.01	0.42
1:B:251:LEU:HD11	1:B:274:LEU:CD1	2.49	0.42
1:A:310:VAL:HG13	1:A:314:ILE:HD11	2.02	0.42
1:A:40:GLU:CD	3:A:401:SAH:H1'	2.40	0.42
1:A:192:VAL:HG22	1:A:247:ILE:HA	2.01	0.42
1:B:130:GLY:C	1:B:132:THR:N	2.67	0.42
1:A:275:HIS:CG	1:A:276:PRO:HD2	2.55	0.42
1:B:25:ARG:HG3	1:B:35:CYS:HB2	2.01	0.42
1:B:226:THR:CG2	1:B:249:ILE:HA	2.45	0.42
1:A:197:LEU:HD23	1:A:197:LEU:N	2.35	0.42
1:B:253:ALA:HB2	1:B:303:GLY:CA	2.49	0.42
1:B:268:ASN:HD22	1:B:268:ASN:HA	1.56	0.42
1:A:14:PHE:HB3	1:A:74:ILE:HB	2.02	0.42
1:B:4:ILE:HD11	1:B:312:GLN:HE21	1.85	0.42
1:B:161:GLN:NE2	1:B:282:VAL:O	2.52	0.42
1:A:66:GLU:OE2	1:A:106:ARG:NH1	2.46	0.42
1:B:8:GLN:NE2	1:B:320:SER:HA	2.35	0.42
1:B:25:ARG:NH1	1:B:53:PHE:HB3	2.34	0.42
1:B:27:ALA:HA	1:B:30:SER:OG	2.19	0.42
1:B:276:PRO:HD3	1:B:299:TYR:CZ	2.54	0.42
1:B:14:PHE:HD2	1:B:33:ALA:HB1	1.85	0.42
1:B:179:ASN:N	1:B:179:ASN:HD22	2.17	0.42
1:B:236:GLY:O	1:B:239:GLU:CB	2.67	0.42
3:A:401:SAH:HG2	3:A:401:SAH:H4'	1.93	0.41
1:A:1:MET:HB2	1:A:284:GLY:O	2.21	0.41
1:A:163:ARG:HD2	1:A:307:VAL:HG23	2.02	0.41
1:A:191:PHE:O	1:A:192:VAL:C	2.58	0.41
1:A:313:TYR:HD2	1:B:327:TYR:CD1	2.38	0.41
1:B:24:PHE:O	1:B:26:LEU:N	2.52	0.41
1:B:133:LEU:O	1:B:134:GLU:C	2.59	0.41
1:B:137:LYS:HA	1:B:147:PHE:CE1	2.55	0.41
1:B:248:ALA:CB	1:B:282:VAL:HG11	2.50	0.41
1:B:283:MET:HE3	1:B:302:PHE:O	2.20	0.41
1:A:101:PHE:C	1:A:103:ASP:N	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:212:LEU:HG	1:B:232:VAL:CG2	2.50	0.41
1:A:12:LEU:CA	1:A:73:ASP:OD1	2.65	0.41
1:A:206:VAL:CG1	1:A:207:ILE:H	2.32	0.41
1:B:150:LYS:HB2	1:B:182:PHE:CE1	2.55	0.41
1:B:175:LEU:N	1:B:175:LEU:HD23	2.35	0.41
1:A:201:GLU:HG2	1:A:201:GLU:H	1.47	0.41
1:B:25:ARG:O	1:B:25:ARG:HG2	2.20	0.41
1:B:119:GLU:HG3	1:B:167:TYR:CE2	2.54	0.41
1:B:310:VAL:O	1:B:311:LEU:C	2.59	0.41
1:A:133:LEU:HA	1:A:133:LEU:HD12	1.77	0.41
1:A:150:LYS:HB3	1:A:182:PHE:CE1	2.56	0.41
1:A:188:LEU:O	1:A:189:ASN:OD1	2.39	0.41
1:A:242:TYR:CE1	1:A:249:ILE:HG12	2.55	0.41
1:B:13:ARG:HE	1:B:13:ARG:HB2	1.73	0.41
1:B:122:LYS:O	1:B:124:PHE:N	2.53	0.41
1:B:262:THR:OG1	1:B:263:GLY:N	2.54	0.41
1:A:192:VAL:HG13	1:A:248:ALA:HB2	2.02	0.41
1:A:212:LEU:CD2	1:A:213:VAL:N	2.84	0.41
1:B:42:ASP:OD2	1:B:44:TYR:HB2	2.21	0.41
1:B:188:LEU:HD12	1:B:189:ASN:N	2.35	0.41
1:B:237:TRP:N	1:B:237:TRP:CD1	2.88	0.41
1:A:1:MET:HE3	1:A:26:LEU:HD13	2.02	0.41
1:A:71:ASP:OD1	2:A:600:SO4:O2	2.38	0.41
1:A:226:THR:HG22	1:A:247:ILE:O	2.21	0.41
1:A:253:ALA:CB	1:A:300:LYS:O	2.69	0.41
1:A:272:ARG:HD2	1:A:273:LYS:O	2.21	0.41
1:B:176:ASN:CG	1:B:176:ASN:O	2.59	0.41
1:A:214:MET:HE3	1:A:230:GLY:HA3	2.03	0.41
1:A:275:HIS:O	1:A:278:GLU:N	2.54	0.41
1:B:12:LEU:HD11	1:B:322:LEU:CD1	2.48	0.41
1:B:114:LYS:CB	1:B:175:LEU:HD11	2.51	0.41
1:B:205:LEU:HD22	1:B:205:LEU:HA	1.92	0.41
1:B:249:ILE:H	1:B:249:ILE:HG13	1.49	0.41
1:B:318:ILE:CG2	1:B:319:GLY:N	2.82	0.41
1:A:9:LEU:HD23	1:A:319:GLY:HA3	2.03	0.41
1:A:15:ILE:HG22	1:A:36:VAL:CG2	2.51	0.41
1:A:24:PHE:CG	1:A:76:CYS:HB3	2.57	0.41
1:A:104:ILE:O	1:A:108:VAL:N	2.33	0.41
1:A:162:LYS:HB2	1:A:226:THR:CG2	2.51	0.41
1:A:172:ARG:O	1:A:174:ASP:N	2.54	0.41
1:A:274:LEU:HA	1:A:274:LEU:HD23	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4:ILE:CD1	1:B:312:GLN:HE21	2.34	0.41
1:B:8:GLN:HE22	1:B:320:SER:HA	1.85	0.41
1:B:211:ASP:HB2	1:B:233:GLY:H	1.85	0.41
1:A:141:ASN:O	1:A:144:ASP:N	2.40	0.40
1:B:8:GLN:HE21	1:B:8:GLN:HB3	1.72	0.40
1:B:20:GLY:C	1:B:22:GLY:H	2.25	0.40
1:B:41:TRP:N	3:B:402:SAH:C2	2.83	0.40
1:B:101:PHE:O	1:B:104:ILE:HB	2.21	0.40
1:B:160:PRO:C	1:B:247:ILE:HB	2.41	0.40
1:B:205:LEU:O	1:B:207:ILE:HD12	2.21	0.40
1:B:256:GLY:CA	1:B:260:ALA:HB1	2.52	0.40
1:A:49:TYR:CG	1:A:57:PRO:HG3	2.56	0.40
1:A:179:ASN:HD22	1:A:179:ASN:N	2.20	0.40
1:B:247:ILE:O	1:B:248:ALA:C	2.60	0.40
1:A:65:ASN:HB3	1:A:68:THR:OG1	2.21	0.40
1:A:69:ILE:HD13	1:A:107:ILE:HG12	2.02	0.40
1:B:14:PHE:CZ	1:B:25:ARG:CG	3.04	0.40
1:B:153:ASN:CG	1:B:164:GLU:HG2	2.42	0.40
1:A:230:GLY:O	1:A:241:ILE:N	2.48	0.40
1:A:275:HIS:O	1:A:278:GLU:HB2	2.21	0.40
1:B:8:GLN:HG3	1:B:316:TYR:CE1	2.57	0.40
1:B:50:GLU:CD	1:B:56:LYS:HG3	2.42	0.40
1:B:82:GLN:HB3	1:B:83:ALA:H	1.77	0.40
1:B:119:GLU:HG2	1:B:120:ASN:N	2.37	0.40
1:B:147:PHE:CE2	1:B:168:MET:HG2	2.57	0.40
1:B:314:ILE:O	1:B:318:ILE:N	2.55	0.40
1:B:14:PHE:HB3	1:B:28:LEU:HD12	2.03	0.40
1:B:27:ALA:O	1:B:30:SER:OG	2.40	0.40
1:B:262:THR:HG21	1:B:273:LYS:HB2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	303/327 (93%)	222 (73%)	56 (18%)	25 (8%)	1	0
1	B	310/327 (95%)	231 (74%)	64 (21%)	15 (5%)	2	2
All	All	613/654 (94%)	453 (74%)	120 (20%)	40 (6%)	1	0

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	ALA
1	A	199	ASP
1	A	215	THR
1	A	260	ALA
1	A	261	LYS
1	A	269	GLY
1	B	12	LEU
1	B	131	ASN
1	B	176	ASN
1	B	261	LYS
1	B	305	SER
1	A	8	GLN
1	A	12	LEU
1	A	27	ALA
1	A	127	HIS
1	A	135	VAL
1	A	173	ASN
1	A	218	GLU
1	A	268	ASN
1	B	123	ASN
1	A	198	PRO
1	B	25	ARG
1	B	40	GLU
1	B	57	PRO
1	B	175	LEU
1	B	204	HIS
1	B	286	PRO
1	A	60	ASP
1	A	123	ASN
1	A	225	LYS
1	A	131	ASN
1	A	136	VAL
1	B	102	PHE
1	A	38	SER
1	A	112	LYS

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Mol	Chain	Res	Type
1	A	224	PRO
1	B	112	LYS
1	A	11	GLY
1	B	202	VAL
1	A	207	ILE

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	261/283 (92%)	195 (75%)	66 (25%)	0	0
1	B	256/283 (90%)	195 (76%)	61 (24%)	0	0
All	All	517/566 (91%)	390 (75%)	127 (25%)	0	0

All (127) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLU
1	A	4	ILE
1	A	10	THR
1	A	12	LEU
1	A	13	ARG
1	A	17	LEU
1	A	26	LEU
1	A	30	SER
1	A	39	ASN
1	A	41	TRP
1	A	43	LYS
1	A	48	VAL
1	A	52	ASN
1	A	55	GLU
1	A	58	GLU
1	A	62	THR
1	A	63	GLN
1	A	66	GLU

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Mol	Chain	Res	Type
1	A	71	ASP
1	A	73	ASP
1	A	103	ASP
1	A	109	ARG
1	A	114	LYS
1	A	117	PHE
1	A	118	MET
1	A	119	GLU
1	A	120	ASN
1	A	136	VAL
1	A	137	LYS
1	A	140	MET
1	A	141	ASN
1	A	143	LEU
1	A	152	LEU
1	A	155	LEU
1	A	163	ARG
1	A	173	ASN
1	A	176	ASN
1	A	179	ASN
1	A	187	GLU
1	A	188	LEU
1	A	192	VAL
1	A	195	LEU
1	A	201	GLU
1	A	202	VAL
1	A	212	LEU
1	A	214	MET
1	A	215	THR
1	A	219	ILE
1	A	220	GLU
1	A	221	GLN
1	A	227	VAL
1	A	232	VAL
1	A	239	GLU
1	A	240	ARG
1	A	258	ILE
1	A	261	LYS
1	A	262	THR
1	A	270	LYS
1	A	272	ARG
1	A	282	VAL

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Mol	Chain	Res	Type
1	A	283	MET
1	A	291	VAL
1	A	295	THR
1	A	296	SER
1	A	297	GLN
1	A	321	SER
1	B	5	LYS
1	B	7	LYS
1	B	8	GLN
1	B	13	ARG
1	B	25	ARG
1	B	30	SER
1	B	38	SER
1	B	41	TRP
1	B	51	MET
1	B	56	LYS
1	B	61	ILE
1	B	65	ASN
1	B	67	LYS
1	B	81	CYS
1	B	106	ARG
1	B	111	LYS
1	B	120	ASN
1	B	122	LYS
1	B	126	SER
1	B	133	LEU
1	B	134	GLU
1	B	139	THR
1	B	142	GLU
1	B	143	LEU
1	B	155	LEU
1	B	156	ASP
1	B	162	LYS
1	B	165	ARG
1	B	166	ILE
1	B	170	CYS
1	B	178	GLN
1	B	179	ASN
1	B	181	GLN
1	B	184	LYS
1	B	188	LEU
1	B	193	LYS

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Mol	Chain	Res	Type
1	B	194	ASP
1	B	199	ASP
1	B	205	LEU
1	B	207	ILE
1	B	209	ARG
1	B	214	MET
1	B	221	GLN
1	B	227	VAL
1	B	239	GLU
1	B	245	ARG
1	B	249	ILE
1	B	258	ILE
1	B	262	THR
1	B	268	ASN
1	B	271	THR
1	B	275	HIS
1	B	277	ARG
1	B	283	MET
1	B	288	SER
1	B	291	VAL
1	B	294	SER
1	B	297	GLN
1	B	305	SER
1	B	318	ILE
1	B	321	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	A	72	HIS
1	A	161	GLN
1	A	173	ASN
1	A	176	ASN
1	A	179	ASN
1	A	221	GLN
1	A	268	ASN
1	A	297	GLN
1	B	8	GLN
1	B	63	GLN
1	B	72	HIS
1	B	82	GLN

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Mol	Chain	Res	Type
1	B	123	ASN
1	B	141	ASN
1	B	176	ASN
1	B	178	GLN
1	B	179	ASN
1	B	268	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 21 ligands modelled in this entry, 17 are unknown - 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	$\# Z > 2$
2	SO4	A	600	-	4,4,4	0.27	0	6,6,6	0.80	0
3	SAH	A	401	-	21,28,28	0.60	0	20,40,40	1.61	4 (20%)
3	SAH	B	402	-	21,28,28	0.67	0	20,40,40	1.65	5 (25%)
2	SO4	A	601	-	4,4,4	0.15	0	6,6,6	0.83	0

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	SAH	A	401	-	-	2/7/31/31	0/3/3/3
3	SAH	B	402	-	-	3/7/31/31	0/3/3/3

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	SAH	C4'-C5'-SD	-4.26	98.48	113.78
3	A	401	SAH	CB-CG-SD	4.23	122.79	113.31
3	B	402	SAH	C4'-C5'-SD	-3.97	99.53	113.78
3	B	402	SAH	C5'-SD-CG	3.66	113.25	102.27
3	B	402	SAH	CB-CG-SD	2.94	119.90	113.31
3	B	402	SAH	O4'-C1'-C2'	-2.59	103.14	106.93
3	A	401	SAH	C5'-SD-CG	-2.32	95.30	102.27
3	B	402	SAH	C5-C6-N6	2.29	123.83	120.35
3	A	401	SAH	C5-C6-N6	2.03	123.44	120.35

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	SAH	C-CA-CB-CG
3	B	402	SAH	C4'-C5'-SD-CG
3	A	401	SAH	CA-CB-CG-SD
3	B	402	SAH	CA-CB-CG-SD
3	B	402	SAH	O4'-C4'-C5'-SD

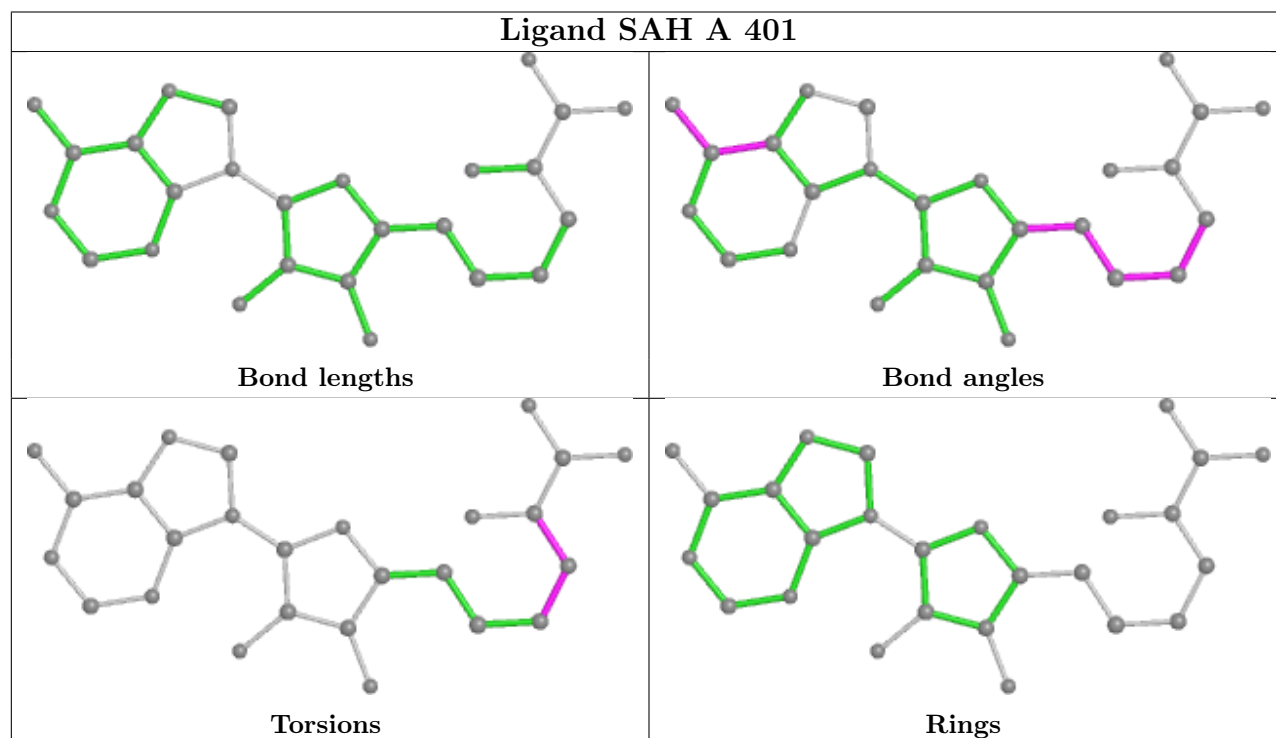
There are no ring outliers.

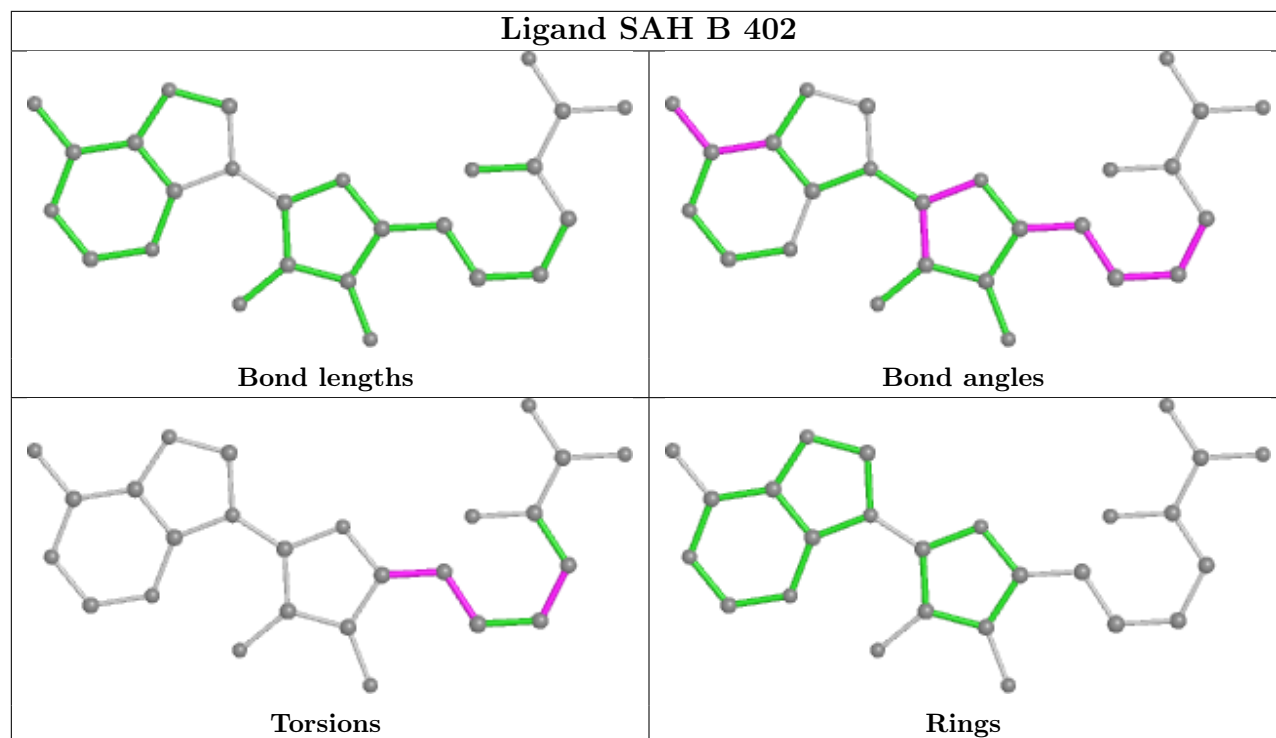
3 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	SO4	1	0
3	A	401	SAH	5	0
3	B	402	SAH	10	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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.