



Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 09:39 am BST

PDB ID : 1SUS
Title : Crystal structure of alfalfa feruoyl coenzyme A 3-O-methyltransferase
Authors : Ferrer, J.-L.; Zubieta, C.; Dixon, R.A.; Noel, J.P.
Deposited on : 2004-03-26
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

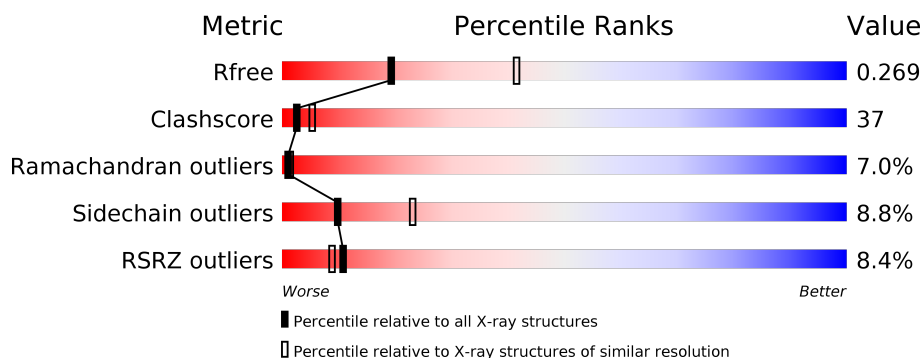
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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

Mol	Chain	Length	Quality of chain
1	A	247	<div> <div>2%</div> <div> <div></div> <div>50%</div> <div>32%</div> <div>9%</div> <div>8%</div> </div> </div>
1	B	247	<div> <div>4%</div> <div> <div></div> <div>59%</div> <div>27%</div> <div>5%</div> <div>8%</div> </div> </div>
1	C	247	<div> <div>8%</div> <div> <div></div> <div>37%</div> <div>45%</div> <div>9%</div> <div>8%</div> </div> </div>
1	D	247	<div> <div>17%</div> <div> <div></div> <div>28%</div> <div>53%</div> <div>10%</div> <div>8%</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SAH	B	302	-	-	-	X
3	SAH	C	303	-	-	-	X
4	SPF	A	401	X	-	X	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7447 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.

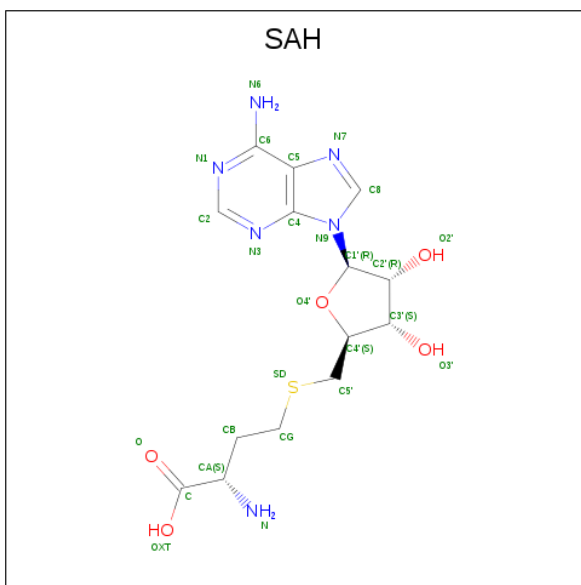
- Molecule 1 is a protein called Caffeoyle-CoA O-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	0	0	0
			1807	1162	301	335	9			
1	B	227	Total	C	N	O	S	0	0	0
			1807	1162	301	335	9			
1	C	227	Total	C	N	O	S	0	0	0
			1807	1162	301	335	9			
1	D	227	Total	C	N	O	S	0	0	0
			1789	1150	295	335	9			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

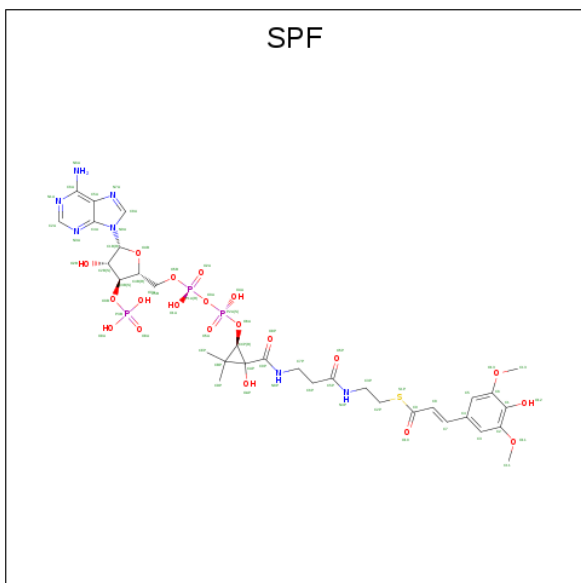
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ca	0	0
			1	1		
2	A	1	Total	Ca	0	0
			1	1		
2	D	1	Total	Ca	0	0
			1	1		
2	C	1	Total	Ca	0	0
			1	1		

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C₁₄H₂₀N₆O₅S).



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

- Molecule 4 is SINAPOYL COENZYME A (three-letter code: SPF) (formula: $\text{C}_{32}\text{H}_{44}\text{N}_7\text{O}_{20}\text{P}_3\text{S}$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	0	0
			63	32	7	20	3	1		

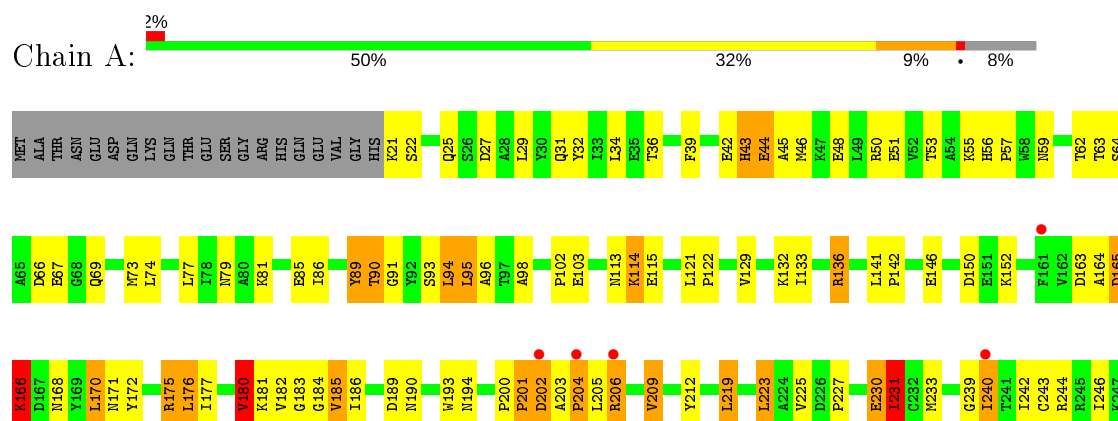
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	16	Total	O	0	0
			16	16		
5	B	34	Total	O	0	0
			34	34		
5	C	11	Total	O	0	0
			11	11		
5	D	5	Total	O	0	0
			5	5		

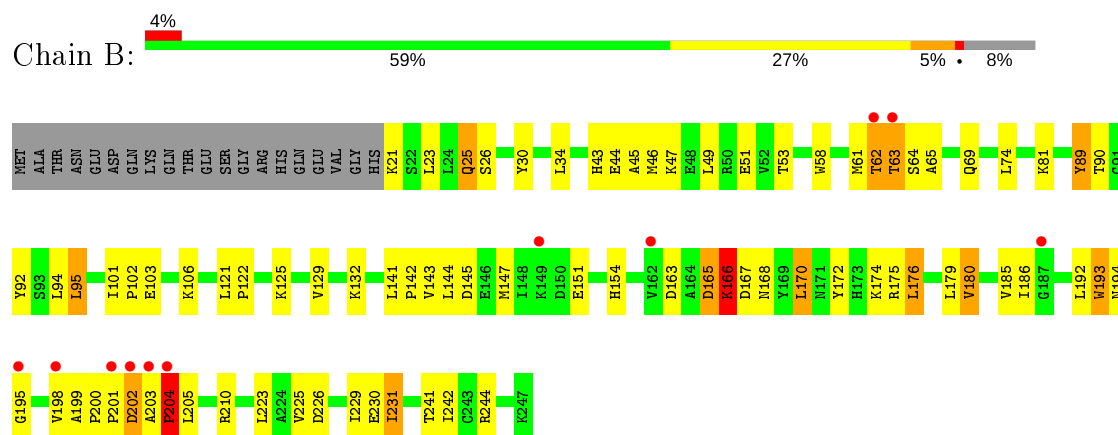
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

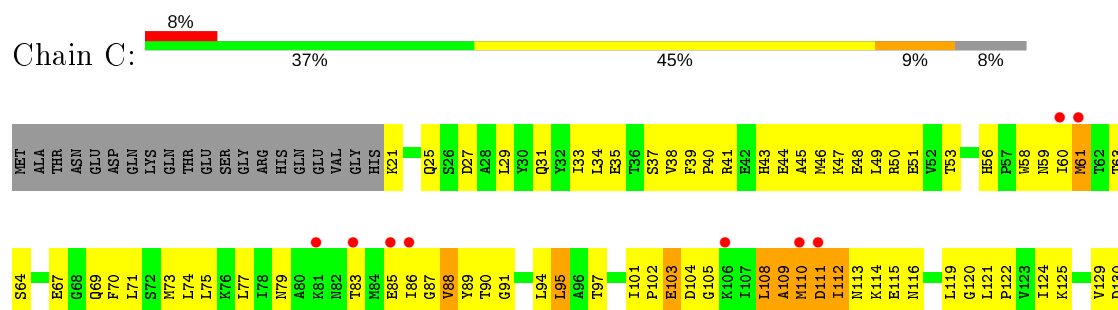
• Molecule 1: Caffeoyl-CoA O-methyltransferase

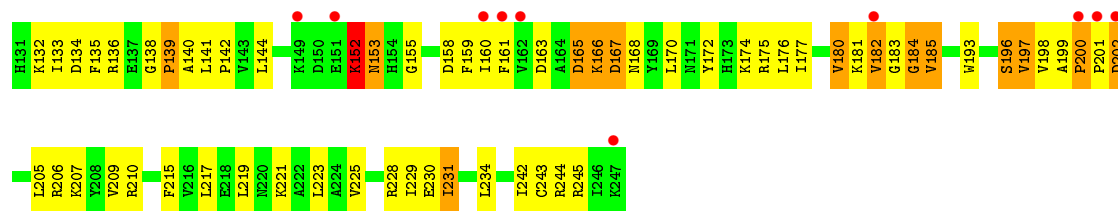


• Molecule 1: Caffeoyl-CoA O-methyltransferase

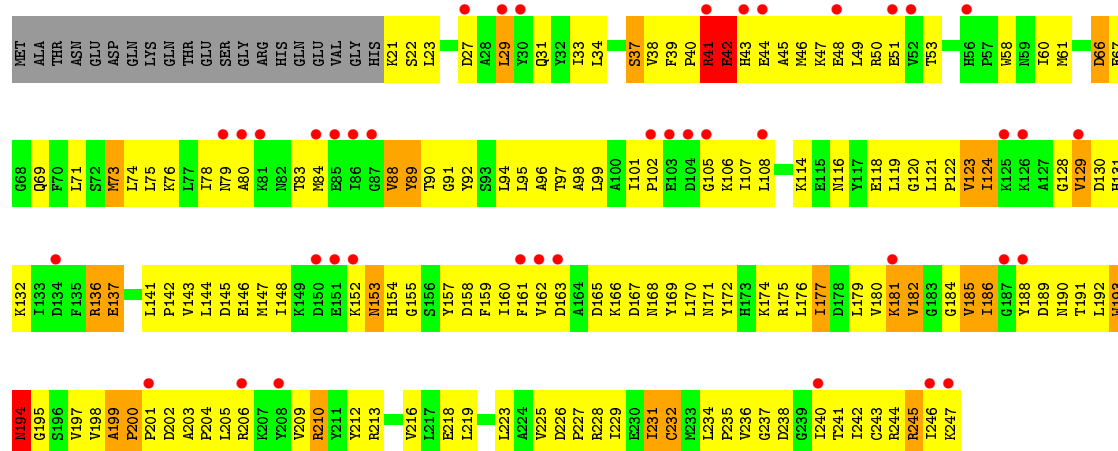


• Molecule 1: Caffeoyl-CoA O-methyltransferase





● Molecule 1: Caffeoyl-CoA O-methyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	60.85Å 136.49Å 332.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.70 25.08 – 2.72	Depositor EDS
% Data completeness (in resolution range)	93.7 (25.00-2.70) 93.9 (25.08-2.72)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 2.72Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.245 , 0.289 0.228 , 0.269	Depositor DCC
R_{free} test set	1789 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	69.4	Xtriage
Anisotropy	0.196	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 63.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7447	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% 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: CA, SAH, SPF

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	0.45	0/1844	0.72	2/2496 (0.1%)
1	B	0.46	0/1844	0.72	1/2496 (0.0%)
1	C	0.38	0/1844	0.63	0/2496
1	D	0.30	0/1824	0.53	0/2472
All	All	0.40	0/7356	0.66	3/9960 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	64	SER	N-CA-C	-5.29	96.71	111.00
1	A	184	GLY	N-CA-C	5.28	126.30	113.10
1	A	180	VAL	CB-CA-C	-5.25	101.43	111.40

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	1807	0	1831	104	0
1	B	1807	0	1831	70	0
1	C	1807	0	1831	157	0
1	D	1789	0	1799	207	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	26	0	19	4	0
3	B	26	0	19	2	0
3	C	26	0	19	6	0
3	D	26	0	19	5	0
4	A	63	0	38	23	0
5	A	16	0	0	0	0
5	B	34	0	0	0	0
5	C	11	0	0	0	0
5	D	5	0	0	1	0
All	All	7447	0	7406	541	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 37.

All (541) 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)
4:A:401:SPF:C3P	4:A:401:SPF:C2P	1.77	1.62
1:D:141:LEU:HD21	1:D:175:ARG:HH21	1.15	1.07
1:B:165:ASP:O	1:B:166:LYS:HB2	1.57	1.03
1:A:165:ASP:O	1:A:166:LYS:HB2	1.59	0.98
1:C:141:LEU:H	1:C:141:LEU:HD12	1.33	0.92
1:A:193:TRP:CH2	4:A:401:SPF:H4	2.05	0.92
1:C:182:VAL:HG13	1:C:183:GLY:H	1.34	0.92
1:D:181:LYS:HA	1:D:245:ARG:HG3	1.54	0.90
1:D:185:VAL:HG13	1:D:186:ILE:H	1.37	0.89
1:C:185:VAL:HA	1:C:243:CYS:O	1.72	0.88
1:C:53:THR:OG1	1:C:90:THR:HG21	1.73	0.88
1:B:53:THR:HB	1:B:90:THR:HG21	1.56	0.88
1:C:61:MET:HE3	1:C:61:MET:H	1.38	0.86
1:D:141:LEU:HD21	1:D:175:ARG:NH2	1.90	0.86
1:A:193:TRP:HH2	4:A:401:SPF:H4	1.39	0.86
1:D:185:VAL:HG13	1:D:186:ILE:N	1.90	0.85
1:C:110:MET:HG3	1:C:111:ASP:OD1	1.76	0.85
1:C:181:LYS:HG3	1:C:182:VAL:H	1.39	0.84
1:A:113:ASN:O	1:A:114:LYS:HB3	1.75	0.84
1:A:53:THR:OG1	1:A:90:THR:HG21	1.76	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:112:ILE:HG12	1:C:113:ASN:H	1.43	0.84
1:D:21:LYS:HG2	1:D:22:SER:H	1.42	0.82
1:D:124:ILE:HG22	1:D:130:ASP:HB3	1.62	0.82
1:D:146:GLU:HG3	1:D:147:MET:HG3	1.62	0.81
1:A:180:VAL:HG21	1:A:186:ILE:HD11	1.63	0.81
1:C:165:ASP:O	1:C:166:LYS:HB2	1.79	0.80
1:D:193:TRP:HE1	1:D:209:VAL:HA	1.46	0.80
4:A:401:SPF:N4P	4:A:401:SPF:C2P	2.45	0.80
1:C:198:VAL:HG12	1:C:199:ALA:H	1.45	0.79
1:D:152:LYS:HA	1:D:152:LYS:HE2	1.62	0.79
4:A:401:SPF:C3P	4:A:401:SPF:S1P	2.72	0.78
1:C:61:MET:N	1:C:61:MET:HE3	1.98	0.78
1:D:159:PHE:HA	1:D:185:VAL:HG11	1.64	0.78
1:D:231:ILE:HA	1:D:242:ILE:O	1.84	0.78
1:B:198:VAL:HG11	1:B:205:LEU:HD11	1.66	0.77
1:A:163:ASP:OD1	4:A:401:SPF:H133	1.85	0.77
1:B:89:TYR:O	1:B:90:THR:HB	1.84	0.77
1:C:205:LEU:HD21	1:C:210:ARG:NH2	1.99	0.77
1:D:34:LEU:HA	1:D:38:VAL:HG22	1.66	0.77
1:C:44:GLU:N	1:C:44:GLU:OE1	2.18	0.77
1:D:166:LYS:HB2	1:D:212:TYR:CD1	2.20	0.76
1:A:129:VAL:HG23	1:A:132:LYS:HE3	1.67	0.75
1:A:136:ARG:HG2	1:A:136:ARG:HH11	1.51	0.75
1:A:185:VAL:HA	1:A:243:CYS:O	1.87	0.75
1:A:85:GLU:OE2	1:A:93:SER:HB2	1.85	0.74
1:D:219:LEU:O	1:D:223:LEU:HB2	1.87	0.74
1:D:205:LEU:CD1	1:D:213:ARG:HH21	2.01	0.74
1:C:125:LYS:HD2	1:C:130:ASP:OD1	1.88	0.73
1:D:199:ALA:HB3	1:D:203:ALA:HB2	1.70	0.73
1:D:228:ARG:HH21	1:D:245:ARG:HH21	1.37	0.73
1:A:67:GLU:OE2	1:A:240:ILE:HD12	1.89	0.72
1:B:49:LEU:O	1:B:53:THR:HG22	1.88	0.72
1:A:42:GLU:OE2	1:A:50:ARG:NH2	2.22	0.72
1:D:205:LEU:HD13	1:D:213:ARG:HH21	1.53	0.71
1:D:184:GLY:O	1:D:185:VAL:HB	1.89	0.71
1:D:229:ILE:HA	1:D:244:ARG:O	1.90	0.71
1:B:230:GLU:O	1:B:231:ILE:HG12	1.91	0.70
1:C:45:ALA:HA	1:C:48:GLU:HB2	1.73	0.70
1:C:121:LEU:N	1:C:122:PRO:HD2	2.07	0.70
1:C:231:ILE:HA	1:C:242:ILE:O	1.91	0.70
1:D:47:LYS:O	1:D:51:GLU:HG3	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:141:LEU:CD2	1:D:175:ARG:HH21	2.00	0.69
1:D:202:ASP:O	1:D:204:PRO:HD3	1.92	0.69
1:D:38:VAL:HG12	1:D:69:GLN:NE2	2.07	0.69
1:C:43:HIS:HB2	1:C:46:MET:HG2	1.74	0.68
1:C:60:ILE:HG23	1:C:61:MET:H	1.59	0.68
1:D:200:PRO:C	1:D:202:ASP:H	1.95	0.68
1:B:203:ALA:N	1:B:204:PRO:CD	2.57	0.68
1:C:110:MET:O	1:C:111:ASP:HB3	1.93	0.68
1:C:44:GLU:O	1:C:45:ALA:HB3	1.94	0.68
1:C:228:ARG:HH21	1:C:245:ARG:HH21	1.41	0.67
1:A:94:LEU:HD13	1:A:133:ILE:HD13	1.77	0.67
1:A:42:GLU:HG3	1:A:42:GLU:O	1.94	0.67
1:D:180:VAL:HG23	1:D:181:LYS:N	2.10	0.67
1:A:98:ALA:HB1	1:A:129:VAL:HG22	1.77	0.67
1:D:205:LEU:H	1:D:205:LEU:HD23	1.59	0.67
1:D:159:PHE:HD1	1:D:185:VAL:HG21	1.58	0.67
1:D:159:PHE:HD1	1:D:185:VAL:CG2	2.08	0.66
1:B:202:ASP:OD1	1:B:204:PRO:HB2	1.95	0.66
1:C:133:ILE:N	1:C:133:ILE:HD12	2.09	0.66
1:A:193:TRP:CH2	4:A:401:SPF:C3	2.78	0.66
1:A:44:GLU:HG3	1:A:45:ALA:N	2.09	0.66
1:B:230:GLU:HG3	1:B:244:ARG:CZ	2.25	0.66
1:A:212:TYR:CE2	4:A:401:SPF:H111	2.30	0.66
1:C:165:ASP:O	1:C:166:LYS:HE2	1.96	0.65
1:D:101:ILE:HD12	1:D:101:ILE:O	1.97	0.65
1:D:180:VAL:HG23	1:D:181:LYS:H	1.61	0.65
1:A:163:ASP:O	3:A:301:SAH:H5'1	1.96	0.65
1:C:120:GLY:C	1:C:122:PRO:HD2	2.17	0.65
1:D:160:ILE:O	1:D:186:ILE:HA	1.97	0.65
1:C:111:ASP:OD1	1:C:140:ALA:HB2	1.96	0.65
1:A:63:THR:HG23	3:A:301:SAH:OXT	1.96	0.65
1:C:43:HIS:HD2	1:C:46:MET:HG3	1.62	0.65
1:D:176:LEU:HA	1:D:179:LEU:HD23	1.79	0.64
1:B:180:VAL:HG21	1:B:186:ILE:HD11	1.78	0.64
1:D:38:VAL:HG12	1:D:69:GLN:HE21	1.61	0.64
1:C:87:GLY:HA2	3:C:303:SAH:H2	1.79	0.64
1:C:46:MET:HE1	1:C:95:LEU:HD13	1.80	0.64
1:B:230:GLU:HG3	1:B:244:ARG:NH2	2.13	0.64
1:D:170:LEU:HD12	1:D:218:GLU:HG2	1.79	0.64
1:A:43:HIS:O	1:A:44:GLU:HB3	1.97	0.64
1:B:89:TYR:HB3	3:B:302:SAH:HB2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:182:VAL:HG13	1:C:183:GLY:N	2.11	0.64
1:D:83:THR:O	1:D:108:LEU:HD23	1.98	0.63
1:C:37:SER:O	1:C:69:GLN:NE2	2.31	0.63
1:C:198:VAL:HG12	1:C:199:ALA:N	2.14	0.62
1:C:108:LEU:O	1:C:110:MET:N	2.28	0.62
1:C:112:ILE:HG12	1:C:113:ASN:N	2.14	0.62
4:A:401:SPF:C5P	4:A:401:SPF:C2P	2.76	0.62
1:D:89:TYR:O	1:D:90:THR:HB	1.98	0.62
1:C:31:GLN:O	1:C:35:GLU:HG2	1.99	0.62
1:C:197:VAL:HG23	1:C:197:VAL:O	1.98	0.62
1:D:200:PRO:O	1:D:202:ASP:N	2.33	0.62
1:D:228:ARG:NH2	1:D:245:ARG:HH21	1.97	0.62
1:D:128:GLY:O	1:D:129:VAL:HG12	1.99	0.61
1:B:163:ASP:OD2	3:B:302:SAH:HG1	1.99	0.61
1:C:141:LEU:H	1:C:141:LEU:CD1	2.09	0.61
1:A:180:VAL:CG2	1:A:186:ILE:HD11	2.29	0.61
1:B:170:LEU:HD12	1:B:174:LYS:HE2	1.81	0.61
1:D:34:LEU:HA	1:D:38:VAL:CG2	2.30	0.61
1:C:217:LEU:O	1:C:221:LYS:HG2	2.00	0.61
1:D:34:LEU:HB3	1:D:39:PHE:CE1	2.36	0.61
1:B:200:PRO:N	1:B:201:PRO:HD2	2.16	0.61
1:C:86:ILE:HG12	1:C:110:MET:HG2	1.81	0.61
1:C:119:LEU:O	1:C:119:LEU:HD23	2.01	0.60
1:D:105:GLY:O	1:D:132:LYS:HD3	2.01	0.60
1:D:160:ILE:HD13	1:D:176:LEU:HD11	1.83	0.60
1:C:200:PRO:O	1:C:202:ASP:N	2.35	0.60
1:A:206:ARG:HE	1:A:206:ARG:N	1.99	0.60
1:D:38:VAL:HG23	1:D:39:PHE:H	1.66	0.60
1:D:95:LEU:HD23	1:D:95:LEU:O	2.01	0.60
1:A:163:ASP:OD1	4:A:401:SPF:C13	2.50	0.60
1:C:130:ASP:HA	1:C:133:ILE:HD13	1.84	0.60
1:D:177:ILE:HD12	1:D:228:ARG:CZ	2.30	0.60
1:B:205:LEU:HB2	1:B:210:ARG:NH1	2.17	0.60
1:D:146:GLU:HG3	1:D:147:MET:N	2.17	0.60
1:D:38:VAL:HG23	1:D:39:PHE:HD1	1.67	0.59
1:D:246:ILE:HG13	1:D:247:LYS:N	2.18	0.59
1:A:171:ASN:O	1:A:175:ARG:HD3	2.03	0.59
1:A:231:ILE:HA	1:A:242:ILE:O	2.02	0.59
1:D:46:MET:O	1:D:50:ARG:HG3	2.03	0.59
1:A:113:ASN:O	1:A:114:LYS:CB	2.47	0.59
1:A:136:ARG:HG2	1:A:136:ARG:NH1	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:106:LYS:HA	1:D:132:LYS:HB3	1.83	0.59
1:C:43:HIS:CD2	1:C:46:MET:HG3	2.37	0.59
1:A:55:LYS:O	1:A:55:LYS:HD3	2.03	0.59
1:C:45:ALA:CA	1:C:48:GLU:HB2	2.33	0.58
4:A:401:SPF:C3P	4:A:401:SPF:O10	2.51	0.58
1:C:47:LYS:O	1:C:51:GLU:HG3	2.04	0.58
4:A:401:SPF:H132	4:A:401:SPF:O12	2.03	0.58
1:B:165:ASP:OD1	1:B:168:ASN:HB2	2.04	0.58
1:A:201:PRO:O	1:A:202:ASP:HB3	2.02	0.58
1:C:60:ILE:HG23	1:C:61:MET:HE3	1.85	0.58
1:C:103:GLU:HA	1:C:132:LYS:HE2	1.85	0.57
1:C:95:LEU:HG	1:C:124:ILE:HG12	1.85	0.57
1:A:21:LYS:HE2	4:A:401:SPF:OAP	2.04	0.57
1:C:103:GLU:HA	1:C:132:LYS:CE	2.33	0.57
1:D:177:ILE:HD13	1:D:177:ILE:O	2.05	0.57
1:D:212:TYR:O	1:D:216:VAL:HG23	2.04	0.57
1:D:184:GLY:HA2	1:D:245:ARG:HB2	1.86	0.57
1:D:165:ASP:C	1:D:166:LYS:HD2	2.25	0.57
1:C:141:LEU:HB2	1:C:142:PRO:HD3	1.87	0.57
1:D:38:VAL:HG23	1:D:39:PHE:N	2.20	0.57
1:A:46:MET:SD	1:A:95:LEU:HD13	2.45	0.56
1:C:228:ARG:NH2	1:C:245:ARG:HH21	2.03	0.56
1:D:114:LYS:HE3	1:D:137:GLU:HG2	1.87	0.56
1:D:141:LEU:HB3	1:D:142:PRO:HD3	1.87	0.56
1:D:21:LYS:HG2	1:D:22:SER:N	2.19	0.56
1:D:184:GLY:O	1:D:185:VAL:CB	2.53	0.56
1:D:185:VAL:CG1	1:D:186:ILE:N	2.62	0.56
1:A:21:LYS:N	4:A:401:SPF:O5P	2.39	0.56
1:C:103:GLU:HA	1:C:132:LYS:NZ	2.20	0.56
1:C:67:GLU:O	1:C:71:LEU:HD22	2.06	0.56
1:D:84:MET:HB3	1:D:160:ILE:HG12	1.88	0.56
1:B:203:ALA:O	1:B:205:LEU:N	2.31	0.55
1:A:74:LEU:O	1:A:74:LEU:HD12	2.07	0.55
1:D:27:ASP:O	1:D:31:GLN:HB2	2.06	0.55
1:D:71:LEU:O	1:D:75:LEU:HD13	2.06	0.55
1:B:203:ALA:N	1:B:204:PRO:HD2	2.21	0.55
1:A:193:TRP:HH2	4:A:401:SPF:C3	2.15	0.55
1:D:99:LEU:HD23	1:D:129:VAL:HG11	1.89	0.55
1:B:165:ASP:O	1:B:166:LYS:CB	2.43	0.55
1:B:226:ASP:HB3	1:B:229:ILE:HG12	1.89	0.55
1:D:182:VAL:H	1:D:245:ARG:HH11	1.53	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:88:VAL:O	1:C:89:TYR:HB3	2.06	0.55
1:D:200:PRO:C	1:D:202:ASP:N	2.60	0.55
4:A:401:SPF:O10	4:A:401:SPF:H32	2.07	0.55
4:A:401:SPF:O12	4:A:401:SPF:C11	2.55	0.55
1:D:234:LEU:HB3	1:D:236:VAL:HG23	1.89	0.55
1:B:34:LEU:HD22	1:B:65:ALA:HB3	1.89	0.54
1:C:183:GLY:O	1:C:185:VAL:N	2.40	0.54
1:C:163:ASP:OD2	3:C:303:SAH:HA	2.07	0.54
1:D:158:ASP:O	1:D:185:VAL:HG11	2.07	0.54
1:D:39:PHE:HB2	1:D:40:PRO:HD3	1.89	0.54
1:C:89:TYR:O	1:C:90:THR:HB	2.08	0.54
1:D:83:THR:CG2	1:D:159:PHE:HB3	2.38	0.54
1:D:48:GLU:OE1	1:D:123:VAL:HG13	2.08	0.54
1:C:206:ARG:O	1:C:209:VAL:HG22	2.07	0.54
1:A:43:HIS:O	1:A:44:GLU:CB	2.55	0.54
1:C:70:PHE:CZ	1:C:234:LEU:HD12	2.43	0.54
1:D:160:ILE:HD12	1:D:180:VAL:HG13	1.89	0.54
1:D:162:VAL:HG12	1:D:169:TYR:HE1	1.71	0.54
1:D:184:GLY:CA	1:D:245:ARG:H	2.21	0.54
1:B:165:ASP:HB2	1:B:167:ASP:OD1	2.08	0.53
1:A:172:TYR:HB3	1:A:176:LEU:HD22	1.89	0.53
1:A:182:VAL:O	1:A:183:GLY:C	2.47	0.53
1:A:142:PRO:O	1:A:146:GLU:HG3	2.09	0.53
1:C:205:LEU:HD23	1:C:205:LEU:H	1.73	0.53
1:D:189:ASP:O	1:D:190:ASN:HB2	2.08	0.53
1:C:56:HIS:HE1	1:C:58:TRP:HB2	1.73	0.53
1:A:165:ASP:O	1:A:166:LYS:HE2	2.08	0.53
1:A:32:TYR:O	1:A:36:THR:HG23	2.09	0.53
1:D:166:LYS:HA	1:D:169:TYR:CD2	2.43	0.53
1:D:181:LYS:HB3	1:D:245:ARG:HH12	1.73	0.53
1:C:166:LYS:HE3	1:C:193:TRP:CZ3	2.44	0.53
1:A:59:ASN:O	1:A:62:THR:HG22	2.09	0.53
1:B:199:ALA:O	1:B:202:ASP:HB3	2.09	0.53
1:C:49:LEU:HD22	1:C:95:LEU:HD12	1.90	0.53
1:C:73:MET:HE3	1:C:77:LEU:HG	1.91	0.52
1:A:230:GLU:OE1	1:A:246:ILE:HG21	2.09	0.52
1:C:46:MET:CE	1:C:95:LEU:HD13	2.38	0.52
1:D:206:ARG:HB2	1:D:209:VAL:HG12	1.90	0.52
1:D:73:MET:HA	1:D:73:MET:CE	2.39	0.52
1:C:121:LEU:N	1:C:122:PRO:CD	2.73	0.52
1:C:141:LEU:HD12	1:C:141:LEU:N	2.14	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:ASP:OD1	1:A:152:LYS:HB2	2.09	0.52
1:D:165:ASP:HB3	3:D:304:SAH:N7	2.25	0.52
1:D:29:LEU:O	1:D:33:ILE:HG13	2.09	0.52
1:D:53:THR:HG22	1:D:53:THR:O	2.09	0.52
1:A:193:TRP:CZ3	4:A:401:SPF:C3	2.93	0.52
1:D:83:THR:HG22	1:D:159:PHE:HB3	1.91	0.52
1:D:128:GLY:C	1:D:130:ASP:H	2.14	0.52
1:D:74:LEU:O	1:D:78:ILE:HG12	2.10	0.52
1:D:42:GLU:OE2	1:D:47:LYS:HE3	2.09	0.51
1:C:39:PHE:HB2	1:C:40:PRO:HD3	1.92	0.51
1:D:21:LYS:HE3	1:D:22:SER:O	2.10	0.51
1:C:46:MET:O	1:C:50:ARG:HB2	2.10	0.51
1:D:98:ALA:HB1	1:D:129:VAL:HG13	1.92	0.51
1:B:121:LEU:N	1:B:122:PRO:HD2	2.25	0.51
1:A:244:ARG:HD3	1:C:73:MET:HE1	1.93	0.51
1:A:180:VAL:HG21	1:A:186:ILE:CD1	2.37	0.51
1:A:239:GLY:C	1:A:240:ILE:HD13	2.31	0.51
1:C:56:HIS:CE1	1:C:58:TRP:HB2	2.46	0.51
1:C:110:MET:O	1:C:136:ARG:HB2	2.11	0.51
1:B:223:LEU:HD23	1:B:241:THR:HG21	1.93	0.51
1:C:85:GLU:O	1:C:110:MET:HB3	2.11	0.51
1:C:34:LEU:HD23	1:C:38:VAL:HG21	1.93	0.51
1:A:32:TYR:CE1	1:A:36:THR:HG21	2.46	0.51
1:C:184:GLY:O	1:C:185:VAL:HB	2.09	0.50
1:C:46:MET:CE	1:C:95:LEU:HD22	2.40	0.50
1:A:231:ILE:O	1:A:231:ILE:HG13	2.10	0.50
1:C:64:SER:HB2	1:C:67:GLU:HG3	1.92	0.50
1:B:25:GLN:O	1:B:26:SER:HB3	2.11	0.50
1:D:170:LEU:HD23	1:D:170:LEU:O	2.11	0.50
1:B:205:LEU:HB2	1:B:210:ARG:HH12	1.76	0.50
1:B:121:LEU:HG	1:B:125:LYS:HE3	1.92	0.50
1:D:188:TYR:CD1	1:D:223:LEU:HD21	2.46	0.50
1:B:225:VAL:O	1:B:225:VAL:HG12	2.11	0.50
1:D:162:VAL:HG12	1:D:169:TYR:CE1	2.46	0.50
1:D:95:LEU:HD23	1:D:99:LEU:HG	1.94	0.50
1:C:196:SER:O	1:C:198:VAL:HG23	2.11	0.50
1:D:159:PHE:CD1	1:D:185:VAL:HG21	2.44	0.50
1:D:185:VAL:HG22	1:D:186:ILE:N	2.27	0.50
1:D:191:THR:HG21	1:D:241:THR:OG1	2.11	0.49
1:A:98:ALA:HB1	1:A:129:VAL:CG2	2.41	0.49
1:C:89:TYR:HA	1:C:116:ASN:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:TYR:HB3	1:B:176:LEU:HD22	1.94	0.49
1:B:231:ILE:HA	1:B:242:ILE:O	2.13	0.49
1:A:206:ARG:HB2	1:A:209:VAL:HG13	1.94	0.49
1:B:46:MET:HE3	1:B:92:TYR:CE1	2.47	0.49
1:D:118:GLU:O	1:D:122:PRO:HD3	2.12	0.49
3:A:301:SAH:HG2	4:A:401:SPF:H131	1.94	0.49
1:D:193:TRP:NE1	1:D:209:VAL:HA	2.21	0.49
1:D:234:LEU:O	1:D:236:VAL:N	2.37	0.49
1:C:49:LEU:CD2	1:C:95:LEU:HD12	2.43	0.49
1:D:166:LYS:N	1:D:166:LYS:HD2	2.27	0.49
1:D:200:PRO:HB2	1:D:202:ASP:OD2	2.12	0.49
1:B:180:VAL:CG2	1:B:186:ILE:HD11	2.41	0.49
1:D:122:PRO:C	1:D:124:ILE:H	2.15	0.49
1:D:95:LEU:O	1:D:99:LEU:HG	2.13	0.49
1:D:144:LEU:HD11	1:D:176:LEU:HD13	1.95	0.49
1:D:229:ILE:HD12	1:D:243:CYS:SG	2.53	0.49
1:B:106:LYS:HE2	1:B:106:LYS:HA	1.95	0.48
1:C:133:ILE:CD1	1:C:133:ILE:N	2.75	0.48
1:D:176:LEU:CA	1:D:179:LEU:HD23	2.42	0.48
1:D:180:VAL:O	1:D:181:LYS:O	2.31	0.48
1:C:43:HIS:HB3	1:C:44:GLU:OE1	2.12	0.48
1:D:108:LEU:HG	1:D:157:TYR:OH	2.13	0.48
1:D:166:LYS:HA	1:D:169:TYR:CE2	2.49	0.48
1:D:185:VAL:HG22	1:D:186:ILE:H	1.77	0.48
1:A:176:LEU:O	1:A:180:VAL:HG23	2.13	0.48
1:A:170:LEU:CD2	1:A:219:LEU:HA	2.43	0.48
1:B:151:GLU:HA	1:B:154:HIS:CD2	2.48	0.48
1:B:62:THR:HG23	1:B:63:THR:N	2.28	0.48
1:D:121:LEU:N	1:D:122:PRO:CD	2.76	0.48
1:D:219:LEU:C	1:D:219:LEU:HD13	2.33	0.48
1:D:22:SER:OG	1:D:23:LEU:N	2.46	0.48
1:D:184:GLY:HA2	1:D:245:ARG:H	1.79	0.48
1:A:240:ILE:HD13	1:A:240:ILE:N	2.29	0.48
1:D:116:ASN:O	1:D:119:LEU:HB3	2.13	0.48
1:A:231:ILE:HG12	1:C:41:ARG:HD3	1.96	0.48
1:D:84:MET:HB2	1:D:157:TYR:CE2	2.49	0.48
1:A:200:PRO:HG2	1:A:203:ALA:HB2	1.96	0.48
1:A:230:GLU:O	1:A:231:ILE:HG12	2.14	0.48
1:B:30:TYR:CE1	1:B:34:LEU:HD11	2.49	0.48
1:C:152:LYS:HA	1:C:152:LYS:HE3	1.95	0.48
1:D:192:LEU:O	1:D:193:TRP:C	2.52	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:75:LEU:HD21	1:D:97:THR:HG23	1.96	0.48
1:A:244:ARG:HB2	1:C:73:MET:CE	2.44	0.47
1:B:230:GLU:OE2	1:B:244:ARG:NH2	2.46	0.47
1:C:196:SER:OG	1:C:197:VAL:N	2.45	0.47
1:D:165:ASP:OD2	3:D:304:SAH:N6	2.47	0.47
1:D:226:ASP:HB3	1:D:229:ILE:HG12	1.96	0.47
1:D:41:ARG:HA	1:D:41:ARG:CZ	2.44	0.47
1:D:41:ARG:HG3	1:D:41:ARG:HH11	1.79	0.47
1:C:115:GLU:OE1	1:C:115:GLU:HA	2.14	0.47
1:A:25:GLN:NE2	1:C:21:LYS:NZ	2.62	0.47
1:C:158:ASP:O	1:C:184:GLY:O	2.33	0.47
1:C:229:ILE:HA	1:C:244:ARG:O	2.15	0.47
1:A:233:MET:CE	1:C:37:SER:HB2	2.44	0.47
1:A:53:THR:OG1	1:A:90:THR:CG2	2.56	0.47
1:D:160:ILE:HB	1:D:186:ILE:HG12	1.97	0.47
1:C:85:GLU:OE2	1:C:94:LEU:HB2	2.15	0.47
1:C:182:VAL:HG22	1:C:183:GLY:N	2.28	0.47
1:D:225:VAL:O	1:D:227:PRO:HD3	2.15	0.47
1:B:143:VAL:HG12	1:B:147:MET:HE2	1.97	0.47
1:C:111:ASP:OD2	1:C:138:GLY:O	2.33	0.47
1:C:181:LYS:CG	1:C:182:VAL:H	2.16	0.47
1:D:209:VAL:HG13	1:D:210:ARG:N	2.29	0.47
1:D:89:TYR:C	1:D:91:GLY:H	2.18	0.47
1:C:133:ILE:H	1:C:133:ILE:HD12	1.78	0.46
1:D:163:ASP:OD2	3:D:304:SAH:HB1	2.16	0.46
1:D:114:LYS:HE3	1:D:137:GLU:CG	2.44	0.46
1:D:159:PHE:HA	1:D:185:VAL:CG1	2.41	0.46
1:D:180:VAL:CG2	1:D:181:LYS:N	2.78	0.46
1:C:109:ALA:O	1:C:110:MET:C	2.53	0.46
1:C:112:ILE:HG13	3:C:303:SAH:N3	2.29	0.46
1:C:167:ASP:HB3	1:C:215:PHE:CE1	2.50	0.46
1:C:176:LEU:O	1:C:180:VAL:HG22	2.14	0.46
1:C:88:VAL:HG13	1:C:91:GLY:HA2	1.96	0.46
1:A:185:VAL:H	1:A:244:ARG:HA	1.79	0.46
1:C:60:ILE:CG2	1:C:61:MET:HE3	2.45	0.46
1:D:107:ILE:C	1:D:108:LEU:HD22	2.36	0.46
1:D:179:LEU:HD22	1:D:179:LEU:N	2.30	0.46
1:B:47:LYS:O	1:B:51:GLU:HG3	2.16	0.46
1:C:230:GLU:O	1:C:231:ILE:HG12	2.15	0.46
1:D:129:VAL:HA	1:D:131:HIS:CE1	2.51	0.46
1:A:163:ASP:OD2	3:A:301:SAH:HB1	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:180:VAL:CG2	1:D:181:LYS:H	2.28	0.46
1:D:185:VAL:CG1	1:D:186:ILE:H	2.09	0.46
1:A:177:ILE:O	1:A:177:ILE:HG13	2.16	0.46
1:A:46:MET:HE1	1:A:96:ALA:HB2	1.97	0.46
1:A:56:HIS:ND1	1:A:57:PRO:HD2	2.30	0.46
1:B:172:TYR:HB3	1:B:176:LEU:CD2	2.45	0.46
1:B:45:ALA:HB1	1:B:95:LEU:HD11	1.98	0.46
1:B:200:PRO:CD	1:B:201:PRO:HD2	2.45	0.46
1:C:44:GLU:HG2	1:C:44:GLU:O	2.16	0.46
1:D:181:LYS:HB3	1:D:245:ARG:NH1	2.30	0.46
1:A:200:PRO:HA	1:A:201:PRO:HD3	1.80	0.46
1:A:225:VAL:HG12	1:A:225:VAL:O	2.15	0.46
1:B:176:LEU:O	1:B:180:VAL:HG22	2.15	0.46
1:C:88:VAL:HG12	1:C:89:TYR:N	2.31	0.46
1:D:136:ARG:HH11	1:D:136:ARG:HG2	1.81	0.46
1:D:232:CYS:HB3	1:D:242:ILE:HG13	1.98	0.46
1:B:43:HIS:CD2	1:B:45:ALA:H	2.35	0.45
1:A:27:ASP:O	1:A:31:GLN:HG2	2.16	0.45
1:D:120:GLY:O	1:D:124:ILE:HG13	2.16	0.45
1:D:131:HIS:CD2	1:D:132:LYS:HZ3	2.34	0.45
1:D:161:PHE:CE1	1:D:189:ASP:HB2	2.51	0.45
1:C:29:LEU:O	1:C:33:ILE:HG13	2.16	0.45
1:D:80:ALA:HB1	1:D:83:THR:CG2	2.47	0.45
1:B:46:MET:SD	1:B:95:LEU:HD13	2.56	0.45
1:D:114:LYS:O	1:D:118:GLU:HG3	2.17	0.45
1:D:123:VAL:O	1:D:123:VAL:HG12	2.16	0.45
1:D:143:VAL:O	1:D:146:GLU:HG2	2.15	0.45
1:D:185:VAL:O	1:D:243:CYS:O	2.33	0.45
1:B:165:ASP:OD1	1:B:166:LYS:N	2.48	0.45
1:D:144:LEU:O	1:D:148:ILE:HG12	2.17	0.45
1:A:165:ASP:HB2	1:A:168:ASN:HB2	1.98	0.45
1:A:225:VAL:O	1:A:227:PRO:HD3	2.17	0.45
1:C:101:ILE:HB	1:C:102:PRO:HD2	1.99	0.45
1:D:229:ILE:HB	1:D:243:CYS:HB3	1.99	0.45
1:A:202:ASP:C	1:A:204:PRO:HD3	2.37	0.45
1:A:89:TYR:O	1:A:91:GLY:N	2.41	0.45
1:C:133:ILE:HG22	1:C:134:ASP:N	2.31	0.45
1:D:101:ILE:HA	5:D:310:HOH:O	2.16	0.45
1:D:205:LEU:HD12	1:D:209:VAL:HG22	1.99	0.45
1:A:189:ASP:O	1:A:190:ASN:HB2	2.16	0.45
1:A:225:VAL:CG1	1:A:225:VAL:O	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:GLU:OE1	1:C:244:ARG:NH1	2.50	0.45
1:D:160:ILE:HD13	1:D:176:LEU:CD1	2.47	0.45
1:D:53:THR:CG2	1:D:90:THR:HG21	2.46	0.45
1:A:166:LYS:C	1:A:168:ASN:H	2.20	0.45
1:D:198:VAL:HG22	1:D:199:ALA:N	2.32	0.45
1:C:205:LEU:HD21	1:C:210:ARG:HH21	1.79	0.44
1:B:176:LEU:O	1:B:180:VAL:CG2	2.65	0.44
1:C:114:LYS:HG3	1:C:115:GLU:H	1.82	0.44
1:C:144:LEU:HD23	1:C:175:ARG:HB2	1.98	0.44
1:D:165:ASP:OD1	1:D:168:ASN:HB2	2.17	0.44
1:B:81:LYS:HG2	1:B:102:PRO:CG	2.47	0.44
1:D:108:LEU:N	1:D:108:LEU:HD22	2.33	0.44
1:D:38:VAL:HG11	1:D:66:ASP:HA	1.99	0.44
1:C:109:ALA:CB	1:C:133:ILE:HG23	2.47	0.44
1:D:145:ASP:OD1	1:D:175:ARG:HD2	2.17	0.44
1:A:129:VAL:HG23	1:A:132:LYS:CE	2.44	0.44
1:A:22:SER:O	1:C:25:GLN:NE2	2.46	0.44
1:B:193:TRP:O	1:B:195:GLY:N	2.45	0.44
1:C:209:VAL:HG23	1:C:210:ARG:N	2.32	0.44
1:D:181:LYS:CB	1:D:245:ARG:NH1	2.81	0.44
1:D:60:ILE:HG13	1:D:60:ILE:O	2.17	0.44
1:A:165:ASP:CB	1:A:168:ASN:HB2	2.48	0.44
1:A:244:ARG:HB2	1:C:73:MET:HE1	2.00	0.44
1:B:143:VAL:HG12	1:B:147:MET:CE	2.48	0.44
1:C:44:GLU:CD	1:C:44:GLU:H	2.19	0.44
1:C:67:GLU:O	1:C:71:LEU:CD2	2.65	0.44
1:D:58:TRP:HB3	1:D:61:MET:CE	2.48	0.44
1:C:198:VAL:CG1	1:C:199:ALA:H	2.25	0.43
1:C:61:MET:CE	1:C:61:MET:H	2.21	0.43
1:D:172:TYR:O	1:D:176:LEU:HB2	2.18	0.43
1:D:154:HIS:HB3	1:D:181:LYS:HE2	1.99	0.43
1:D:190:ASN:HD22	1:D:190:ASN:N	2.13	0.43
1:B:101:ILE:HB	1:B:102:PRO:HD2	2.00	0.43
1:D:194:ASN:HB3	1:D:195:GLY:H	1.65	0.43
1:D:192:LEU:HB2	1:D:238:ASP:O	2.18	0.43
1:B:43:HIS:HD2	1:B:45:ALA:H	1.67	0.43
1:C:133:ILE:H	1:C:133:ILE:CD1	2.32	0.43
1:D:101:ILE:HD12	1:D:101:ILE:C	2.39	0.43
1:A:103:GLU:OE1	1:A:103:GLU:HA	2.18	0.43
4:A:401:SPF:O12	4:A:401:SPF:H113	2.18	0.43
1:C:182:VAL:O	1:C:245:ARG:O	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:128:GLY:C	1:D:130:ASP:N	2.72	0.43
1:D:155:GLY:C	1:D:157:TYR:H	2.22	0.43
1:C:125:LYS:HD2	1:C:130:ASP:CG	2.39	0.43
1:D:189:ASP:OD2	1:D:190:ASN:ND2	2.52	0.43
1:D:45:ALA:HB1	1:D:95:LEU:HD11	2.01	0.43
1:A:170:LEU:HD22	1:A:219:LEU:HD23	2.00	0.43
1:A:42:GLU:CG	1:A:42:GLU:O	2.65	0.43
1:C:111:ASP:CB	1:C:136:ARG:O	2.67	0.43
1:C:86:ILE:HG12	1:C:110:MET:CG	2.46	0.43
1:D:234:LEU:C	1:D:236:VAL:H	2.19	0.43
1:A:48:GLU:O	1:A:51:GLU:HB2	2.19	0.43
1:B:192:LEU:HA	1:B:192:LEU:HD23	1.88	0.43
1:C:109:ALA:HB2	1:C:133:ILE:HG23	2.00	0.43
1:C:228:ARG:NH2	1:C:245:ARG:NH2	2.67	0.43
1:D:49:LEU:HD23	1:D:92:TYR:HA	2.00	0.43
1:A:56:HIS:CG	1:A:57:PRO:HD2	2.54	0.42
1:C:112:ILE:HA	3:C:303:SAH:C2	2.48	0.42
1:D:141:LEU:HD23	1:D:141:LEU:O	2.18	0.42
1:A:163:ASP:O	4:A:401:SPF:H131	2.19	0.42
1:A:73:MET:O	1:A:77:LEU:HG	2.19	0.42
1:A:86:ILE:HG22	1:A:164:ALA:HB2	2.01	0.42
1:C:112:ILE:HG22	1:C:135:PHE:CZ	2.55	0.42
1:C:46:MET:HE1	1:C:95:LEU:HB3	2.00	0.42
1:C:153:ASN:HA	1:C:153:ASN:HD22	1.55	0.42
1:C:75:LEU:CD1	1:C:97:THR:HG23	2.50	0.42
1:D:231:ILE:HG22	1:D:243:CYS:SG	2.59	0.42
1:A:200:PRO:O	1:A:202:ASP:N	2.53	0.42
1:B:201:PRO:O	1:B:203:ALA:N	2.53	0.42
1:C:163:ASP:OD1	3:C:303:SAH:HG1	2.18	0.42
1:D:166:LYS:HE3	1:D:193:TRP:CZ3	2.54	0.42
1:D:67:GLU:OE2	1:D:240:ILE:HG13	2.18	0.42
1:C:103:GLU:HA	1:C:132:LYS:HZ1	1.83	0.42
1:C:160:ILE:HD12	1:C:180:VAL:HG13	2.01	0.42
1:C:182:VAL:O	1:C:245:ARG:HB3	2.20	0.42
1:C:160:ILE:CD1	1:C:180:VAL:HG13	2.49	0.42
1:D:197:VAL:O	1:D:197:VAL:HG22	2.19	0.42
1:A:194:ASN:OD1	4:A:401:SPF:H22	2.20	0.42
1:B:200:PRO:HD2	1:B:201:PRO:HD2	2.00	0.42
1:B:61:MET:HB2	1:B:62:THR:H	1.57	0.42
1:D:165:ASP:OD1	1:D:165:ASP:C	2.58	0.42
1:A:121:LEU:N	1:A:122:PRO:CD	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:TYR:O	1:B:90:THR:CB	2.58	0.42
1:C:209:VAL:CG2	1:C:210:ARG:N	2.83	0.42
1:D:128:GLY:O	1:D:130:ASP:N	2.53	0.42
1:D:184:GLY:HA3	1:D:245:ARG:H	1.83	0.41
1:B:21:LYS:O	1:B:21:LYS:HG2	2.21	0.41
1:C:43:HIS:HB2	1:C:46:MET:CG	2.47	0.41
1:D:232:CYS:SG	1:D:234:LEU:HD21	2.60	0.41
1:A:201:PRO:O	1:A:202:ASP:CB	2.68	0.41
1:A:94:LEU:HD23	1:A:94:LEU:HA	1.84	0.41
1:C:165:ASP:HB2	1:C:168:ASN:HD22	1.85	0.41
1:C:207:LYS:HB3	1:C:207:LYS:HE3	1.93	0.41
1:D:159:PHE:HA	1:D:185:VAL:HG21	2.01	0.41
1:D:163:ASP:OD1	1:D:189:ASP:HB3	2.20	0.41
1:D:43:HIS:O	1:D:44:GLU:HB3	2.20	0.41
1:D:46:MET:CE	1:D:96:ALA:HB2	2.50	0.41
1:A:175:ARG:N	1:A:175:ARG:CD	2.84	0.41
1:A:166:LYS:HE2	4:A:401:SPF:H112	2.01	0.41
1:D:61:MET:SD	3:D:304:SAH:SD	3.19	0.41
1:B:89:TYR:CD2	1:B:89:TYR:O	2.73	0.41
1:C:108:LEU:C	1:C:110:MET:N	2.74	0.41
1:C:159:PHE:CZ	1:C:161:PHE:HB2	2.54	0.41
1:C:219:LEU:C	1:C:219:LEU:HD13	2.41	0.41
1:C:58:TRP:O	1:C:59:ASN:C	2.58	0.41
1:A:81:LYS:HG3	1:A:102:PRO:CG	2.51	0.41
1:B:81:LYS:HG2	1:B:102:PRO:HG3	2.02	0.41
1:C:155:GLY:HA3	1:C:181:LYS:HD2	2.03	0.41
1:D:177:ILE:HD13	1:D:177:ILE:C	2.41	0.41
1:C:114:LYS:HG3	1:C:115:GLU:N	2.36	0.41
1:B:145:ASP:OD1	1:B:175:ARG:NE	2.53	0.41
1:C:165:ASP:O	1:C:166:LYS:CB	2.56	0.41
1:C:60:ILE:HG23	1:C:61:MET:N	2.31	0.41
1:D:88:VAL:O	3:D:304:SAH:HA	2.21	0.41
1:B:141:LEU:HB3	1:B:142:PRO:HD3	2.01	0.41
1:C:114:LYS:O	1:C:115:GLU:OE1	2.39	0.41
1:C:75:LEU:HD11	1:C:97:THR:HG23	2.02	0.41
1:D:171:ASN:O	1:D:172:TYR:C	2.58	0.41
1:D:205:LEU:CD1	1:D:213:ARG:NH2	2.79	0.41
1:A:34:LEU:HB3	1:A:39:PHE:CE2	2.55	0.41
1:B:193:TRP:HA	1:B:193:TRP:CE3	2.56	0.41
1:C:38:VAL:O	1:C:39:PHE:C	2.58	0.41
1:C:63:THR:O	1:C:63:THR:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:23:LEU:HD12	1:D:237:GLY:O	2.21	0.41
1:B:129:VAL:O	1:B:132:LYS:HG3	2.21	0.41
1:B:23:LEU:HD21	1:B:194:ASN:HA	2.03	0.41
1:D:89:TYR:O	1:D:90:THR:CB	2.68	0.41
1:D:95:LEU:C	1:D:95:LEU:HD23	2.40	0.41
1:A:181:LYS:HE3	1:A:181:LYS:HB3	1.78	0.40
1:D:180:VAL:CG2	1:D:186:ILE:HD11	2.51	0.40
1:D:180:VAL:HG21	1:D:186:ILE:HD11	2.03	0.40
1:A:64:SER:HB2	1:A:66:ASP:OD1	2.21	0.40
1:B:43:HIS:HD2	1:B:44:GLU:N	2.19	0.40
1:C:225:VAL:HG12	1:C:225:VAL:O	2.21	0.40
1:D:84:MET:O	1:D:160:ILE:HA	2.21	0.40
1:D:98:ALA:HB1	1:D:129:VAL:CG1	2.51	0.40
1:D:152:LYS:HA	1:D:152:LYS:CE	2.43	0.40
1:D:189:ASP:O	1:D:190:ASN:CB	2.70	0.40
1:D:33:ILE:O	1:D:37:SER:HB3	2.21	0.40
1:D:49:LEU:HD11	1:D:90:THR:HG23	2.03	0.40
1:D:98:ALA:O	1:D:101:ILE:HG13	2.21	0.40
1:A:206:ARG:HE	1:A:206:ARG:CA	2.35	0.40
1:A:223:LEU:HA	1:A:223:LEU:HD12	1.89	0.40
1:C:163:ASP:CG	3:C:303:SAH:HG1	2.42	0.40
1:D:76:LYS:C	1:D:78:ILE:H	2.24	0.40
1:A:165:ASP:O	1:A:166:LYS:CB	2.43	0.40
1:B:200:PRO:N	1:B:201:PRO:CD	2.85	0.40
1:B:202:ASP:C	1:B:204:PRO:HD2	2.41	0.40
1:C:120:GLY:C	1:C:122:PRO:CD	2.87	0.40
1:C:168:ASN:HB3	1:C:172:TYR:CE2	2.56	0.40
1:D:170:LEU:HD12	1:D:218:GLU:CG	2.49	0.40
1:D:92:TYR:C	1:D:94:LEU:H	2.24	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	225/247 (91%)	195 (87%)	19 (8%)	11 (5%)	2	4
1	B	225/247 (91%)	197 (88%)	20 (9%)	8 (4%)	3	7
1	C	225/247 (91%)	176 (78%)	28 (12%)	21 (9%)	0	0
1	D	225/247 (91%)	157 (70%)	45 (20%)	23 (10%)	0	0
All	All	900/988 (91%)	725 (81%)	112 (12%)	63 (7%)	1	1

All (63) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	89	TYR
1	A	165	ASP
1	A	202	ASP
1	A	231	ILE
1	B	166	LYS
1	B	204	PRO
1	B	231	ILE
1	C	110	MET
1	C	112	ILE
1	C	182	VAL
1	C	184	GLY
1	C	201	PRO
1	C	202	ASP
1	C	231	ILE
1	D	181	LYS
1	D	185	VAL
1	D	231	ILE
1	A	44	GLU
1	A	114	LYS
1	A	166	LYS
1	B	63	THR
1	B	89	TYR
1	B	202	ASP
1	C	105	GLY
1	C	111	ASP
1	C	152	LYS
1	C	166	LYS
1	C	196	SER
1	D	37	SER
1	D	42	GLU
1	D	102	PRO
1	D	123	VAL
1	D	129	VAL

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Mol	Chain	Res	Type
1	D	153	ASN
1	D	182	VAL
1	A	43	HIS
1	B	193	TRP
1	C	109	ALA
1	C	139	PRO
1	C	200	PRO
1	D	41	ARG
1	D	89	TYR
1	D	193	TRP
1	D	232	CYS
1	C	104	ASP
1	C	165	ASP
1	C	185	VAL
1	C	197	VAL
1	D	186	ILE
1	D	194	ASN
1	D	201	PRO
1	A	185	VAL
1	A	204	PRO
1	C	88	VAL
1	B	62	THR
1	D	79	ASN
1	D	200	PRO
1	C	129	VAL
1	D	88	VAL
1	D	199	ALA
1	D	235	PRO
1	D	124	ILE
1	A	201	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	196/214 (92%)	174 (89%)	22 (11%)	6 13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	196/214 (92%)	180 (92%)	16 (8%)	11	26
1	C	196/214 (92%)	179 (91%)	17 (9%)	10	23
1	D	192/214 (90%)	178 (93%)	14 (7%)	14	33
All	All	780/856 (91%)	711 (91%)	69 (9%)	10	23

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	LEU
1	A	69	GLN
1	A	79	ASN
1	A	90	THR
1	A	94	LEU
1	A	95	LEU
1	A	115	GLU
1	A	136	ARG
1	A	141	LEU
1	A	166	LYS
1	A	170	LEU
1	A	175	ARG
1	A	176	LEU
1	A	180	VAL
1	A	205	LEU
1	A	206	ARG
1	A	209	VAL
1	A	219	LEU
1	A	223	LEU
1	A	230	GLU
1	A	231	ILE
1	A	240	ILE
1	B	25	GLN
1	B	58	TRP
1	B	69	GLN
1	B	74	LEU
1	B	94	LEU
1	B	95	LEU
1	B	103	GLU
1	B	144	LEU
1	B	165	ASP
1	B	166	LYS
1	B	170	LEU

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Mol	Chain	Res	Type
1	B	176	LEU
1	B	179	LEU
1	B	180	VAL
1	B	185	VAL
1	B	204	PRO
1	C	27	ASP
1	C	61	MET
1	C	74	LEU
1	C	79	ASN
1	C	83	THR
1	C	95	LEU
1	C	103	GLU
1	C	108	LEU
1	C	139	PRO
1	C	152	LYS
1	C	153	ASN
1	C	167	ASP
1	C	170	LEU
1	C	174	LYS
1	C	177	ILE
1	C	180	VAL
1	C	223	LEU
1	D	29	LEU
1	D	41	ARG
1	D	42	GLU
1	D	66	ASP
1	D	73	MET
1	D	136	ARG
1	D	137	GLU
1	D	153	ASN
1	D	167	ASP
1	D	174	LYS
1	D	177	ILE
1	D	194	ASN
1	D	210	ARG
1	D	245	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	31	GLN

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Mol	Chain	Res	Type
1	B	43	HIS
1	B	116	ASN
1	C	43	HIS
1	C	69	GLN
1	C	79	ASN
1	C	113	ASN
1	C	116	ASN
1	C	153	ASN
1	C	168	ASN
1	D	31	GLN
1	D	69	GLN
1	D	116	ASN
1	D	153	ASN
1	D	190	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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
3	SAH	D	304	-	21,28,28	1.74	4 (19%)	20,40,40	2.14	8 (40%)
3	SAH	A	301	-	21,28,28	1.79	6 (28%)	20,40,40	2.42	13 (65%)
4	SPF	A	401	-	58,67,67	11.34	18 (31%)	64,102,102	4.00	24 (37%)
3	SAH	C	303	-	21,28,28	1.68	3 (14%)	20,40,40	2.18	10 (50%)
3	SAH	B	302	-	21,28,28	1.56	4 (19%)	20,40,40	2.18	9 (45%)

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	D	304	-	-	2/7/31/31	0/3/3/3
3	SAH	A	301	-	-	3/7/31/31	0/3/3/3
4	SPF	A	401	-	1/1/13/17	19/45/88/88	0/5/5/5
3	SAH	C	303	-	-	0/7/31/31	0/3/3/3
3	SAH	B	302	-	-	3/7/31/31	0/3/3/3

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	401	SPF	CAP-CCP	84.08	2.34	1.47
4	A	401	SPF	C5-C6	7.74	1.52	1.38
4	A	401	SPF	C7P-N8P	6.32	1.60	1.46
4	A	401	SPF	C2P-C3P	6.24	1.77	1.51
4	A	401	SPF	C6-C1	6.22	1.48	1.40
4	A	401	SPF	C2P-S1P	-5.78	1.57	1.81
3	D	304	SAH	O4'-C1'	5.13	1.48	1.41
4	A	401	SPF	O9P-C9P	4.89	1.31	1.22
4	A	401	SPF	C3P-N4P	4.86	1.57	1.46
4	A	401	SPF	CAP-C9P	4.81	1.64	1.52
3	C	303	SAH	O4'-C1'	4.76	1.47	1.41
4	A	401	SPF	P2A-O6A	-4.52	1.48	1.60
3	A	301	SAH	O4'-C1'	4.47	1.47	1.41
4	A	401	SPF	O5B-C5B	-4.30	1.28	1.44
3	C	303	SAH	C8-N7	-3.93	1.27	1.34
3	B	302	SAH	O4'-C1'	3.84	1.46	1.41
3	D	304	SAH	C8-N7	-3.76	1.28	1.34
3	B	302	SAH	C8-N7	-3.67	1.28	1.34
4	A	401	SPF	C2-C1	-3.62	1.35	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	SAH	C8-N7	-3.48	1.28	1.34
3	A	301	SAH	C2'-C1'	-2.61	1.49	1.53
4	A	401	SPF	C7P-C6P	2.57	1.59	1.51
3	A	301	SAH	O2'-C2'	-2.42	1.37	1.43
3	C	303	SAH	O2'-C2'	-2.36	1.37	1.43
3	B	302	SAH	O2'-C2'	-2.31	1.37	1.43
4	A	401	SPF	C5P-N4P	-2.24	1.28	1.33
4	A	401	SPF	C9P-N8P	2.23	1.38	1.34
3	D	304	SAH	O2'-C2'	-2.22	1.37	1.43
4	A	401	SPF	P1A-O1A	-2.22	1.44	1.55
3	D	304	SAH	CA-N	2.21	1.52	1.47
3	B	302	SAH	CA-N	2.20	1.52	1.47
4	A	401	SPF	C8-C7	-2.18	1.27	1.33
3	A	301	SAH	C5-C4	-2.16	1.35	1.40
4	A	401	SPF	O13-C6	2.13	1.40	1.37
3	A	301	SAH	CA-N	2.01	1.51	1.47

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	401	SPF	CAP-CCP-CBP	-20.79	35.01	60.67
4	A	401	SPF	C11-O11-C2	8.97	131.07	117.53
4	A	401	SPF	C2P-C3P-N4P	-8.62	94.31	112.42
4	A	401	SPF	C4-C3-C2	6.26	128.63	120.17
4	A	401	SPF	C6P-C5P-N4P	5.80	126.18	116.42
4	A	401	SPF	O5P-C5P-C6P	-5.54	111.88	122.02
4	A	401	SPF	P1A-O5B-C5B	5.45	153.64	121.68
4	A	401	SPF	O5B-C5B-C4B	5.43	127.67	108.99
4	A	401	SPF	O3A-P2A-O6A	5.37	113.31	102.48
4	A	401	SPF	C2P-S1P-C9	5.24	106.38	99.80
4	A	401	SPF	C5-C4-C7	5.03	135.59	120.60
4	A	401	SPF	O10-C9-S1P	-4.83	111.83	122.64
4	A	401	SPF	C3P-N4P-C5P	-4.18	115.08	122.84
3	A	301	SAH	N3-C2-N1	-4.06	122.33	128.68
4	A	401	SPF	C3-C4-C7	-4.00	108.68	120.60
3	D	304	SAH	N3-C2-N1	-3.86	122.65	128.68
3	D	304	SAH	C2-N1-C6	3.82	125.29	118.75
3	C	303	SAH	C2-N1-C6	3.80	125.25	118.75
4	A	401	SPF	C7P-N8P-C9P	-3.76	115.25	122.12
3	A	301	SAH	C2-N1-C6	3.74	125.15	118.75
3	B	302	SAH	C2-N1-C6	3.73	125.14	118.75
3	B	302	SAH	N3-C2-N1	-3.68	122.93	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	303	SAH	N3-C2-N1	-3.55	123.13	128.68
3	B	302	SAH	C4-C5-N7	3.42	112.96	109.40
4	A	401	SPF	O13-C6-C1	-3.41	111.10	114.54
3	A	301	SAH	O2'-C2'-C3'	3.36	122.71	111.82
4	A	401	SPF	CEP-CBP-CDP	-3.34	109.02	112.61
3	C	303	SAH	C4-C5-N7	3.25	112.79	109.40
3	D	304	SAH	O2'-C2'-C3'	3.24	122.30	111.82
3	C	303	SAH	O2'-C2'-C3'	3.24	122.29	111.82
3	D	304	SAH	C4-C5-N7	3.19	112.72	109.40
3	B	302	SAH	O2'-C2'-C3'	3.17	122.09	111.82
4	A	401	SPF	C6P-C7P-N8P	3.17	118.29	111.90
4	A	401	SPF	C7P-C6P-C5P	-3.16	107.10	112.36
3	B	302	SAH	N6-C6-N1	3.13	125.06	118.57
4	A	401	SPF	O13-C6-C5	3.03	129.34	124.12
3	C	303	SAH	N6-C6-N1	3.00	124.80	118.57
3	A	301	SAH	O4'-C4'-C5'	2.96	116.45	108.83
3	D	304	SAH	N6-C6-N1	2.95	124.70	118.57
4	A	401	SPF	O11-C2-C1	2.95	117.52	114.54
3	A	301	SAH	C4-C5-N7	2.88	112.40	109.40
4	A	401	SPF	C5A-C6A-N6A	2.88	124.73	120.35
3	C	303	SAH	C5-C6-N1	-2.87	113.85	120.35
3	A	301	SAH	O4'-C1'-C2'	2.84	111.08	106.93
3	A	301	SAH	CB-CG-SD	2.83	119.65	113.31
3	D	304	SAH	C5-C6-N1	-2.81	113.98	120.35
3	B	302	SAH	C5-C6-N1	-2.81	113.99	120.35
3	B	302	SAH	C5'-C4'-C3'	2.80	122.05	115.06
3	A	301	SAH	C5-C6-N1	-2.74	114.14	120.35
3	A	301	SAH	N6-C6-N1	2.69	124.15	118.57
3	A	301	SAH	O4'-C4'-C3'	-2.56	100.05	105.11
3	C	303	SAH	C1'-N9-C4	2.55	131.12	126.64
3	A	301	SAH	C5'-C4'-C3'	2.54	121.40	115.06
3	D	304	SAH	O4'-C4'-C5'	2.53	115.34	108.83
3	C	303	SAH	C5'-C4'-C3'	2.52	121.35	115.06
4	A	401	SPF	C5-C4-C3	-2.50	115.73	119.12
4	A	401	SPF	O5P-C5P-N4P	-2.43	118.44	123.01
3	D	304	SAH	O2'-C2'-C1'	2.40	119.70	110.85
3	B	302	SAH	O2'-C2'-C1'	2.36	119.57	110.85
3	C	303	SAH	O2'-C2'-C1'	2.24	119.12	110.85
3	A	301	SAH	O2'-C2'-C1'	2.22	119.05	110.85
3	C	303	SAH	O4'-C4'-C3'	-2.05	101.05	105.11
3	A	301	SAH	C4'-C5'-SD	2.04	121.10	113.78
3	B	302	SAH	O4'-C4'-C3'	-2.01	101.14	105.11

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	401	SPF	C2B

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	304	SAH	CA-CB-CG-SD
3	A	301	SAH	O4'-C4'-C5'-SD
3	A	301	SAH	C3'-C4'-C5'-SD
3	B	302	SAH	CA-CB-CG-SD
3	B	302	SAH	O4'-C4'-C5'-SD
3	B	302	SAH	C3'-C4'-C5'-SD
4	A	401	SPF	C3B-C4B-C5B-O5B
4	A	401	SPF	O4B-C4B-C5B-O5B
4	A	401	SPF	C5B-O5B-P1A-O2A
4	A	401	SPF	C5P-C6P-C7P-N8P
4	A	401	SPF	S1P-C2P-C3P-N4P
4	A	401	SPF	C4-C7-C8-C9
4	A	401	SPF	C1-C2-O11-C11
4	A	401	SPF	C3-C2-O11-C11
4	A	401	SPF	O5P-C5P-N4P-C3P
4	A	401	SPF	C5-C6-O13-C13
4	A	401	SPF	C1-C6-O13-C13
4	A	401	SPF	C7-C8-C9-O10
4	A	401	SPF	O5P-C5P-C6P-C7P
4	A	401	SPF	CCP-O6A-P2A-O3A
4	A	401	SPF	O9P-C9P-CAP-CBP
3	A	301	SAH	CB-CG-SD-C5'
4	A	401	SPF	C3B-O3B-P3B-O7A
4	A	401	SPF	C5B-O5B-P1A-O3A
4	A	401	SPF	C5B-O5B-P1A-O1A
4	A	401	SPF	N8P-C9P-CAP-CBP
3	D	304	SAH	CB-CG-SD-C5'

There are no ring outliers.

5 monomers are involved in 39 short contacts:

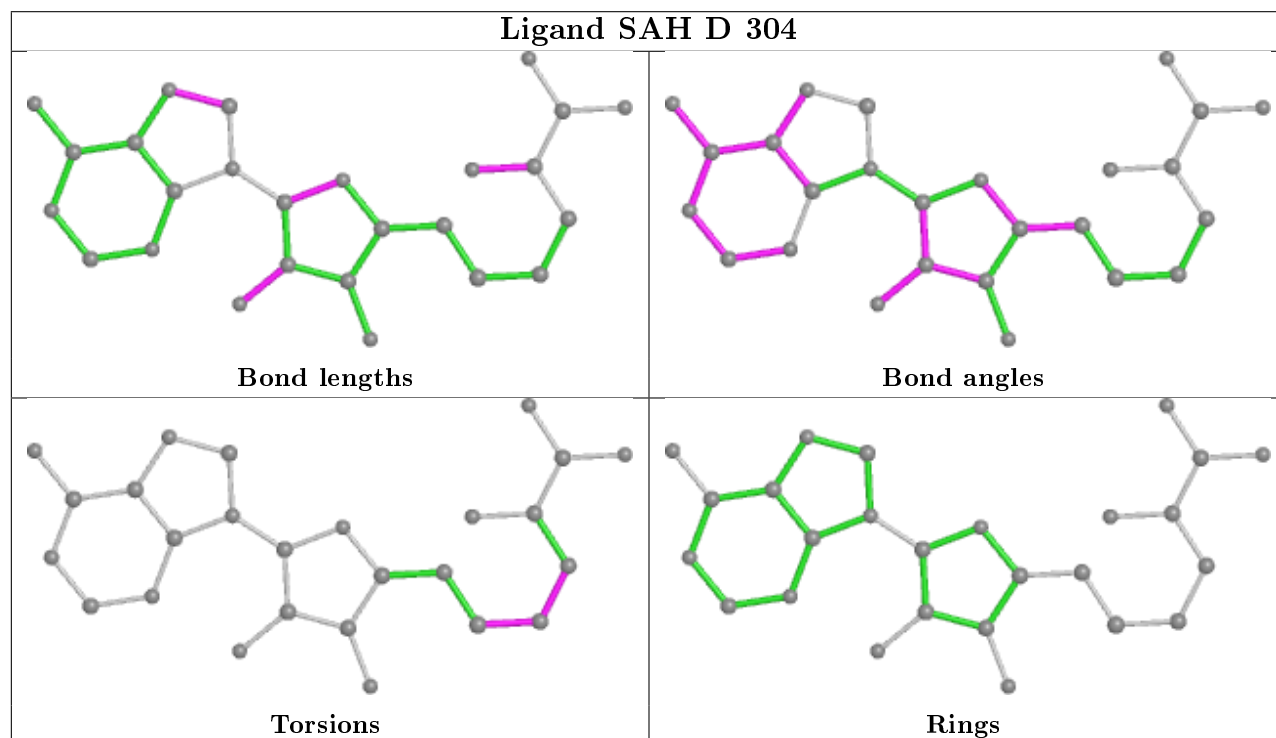
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	304	SAH	5	0
3	A	301	SAH	4	0
4	A	401	SPF	23	0
3	C	303	SAH	6	0

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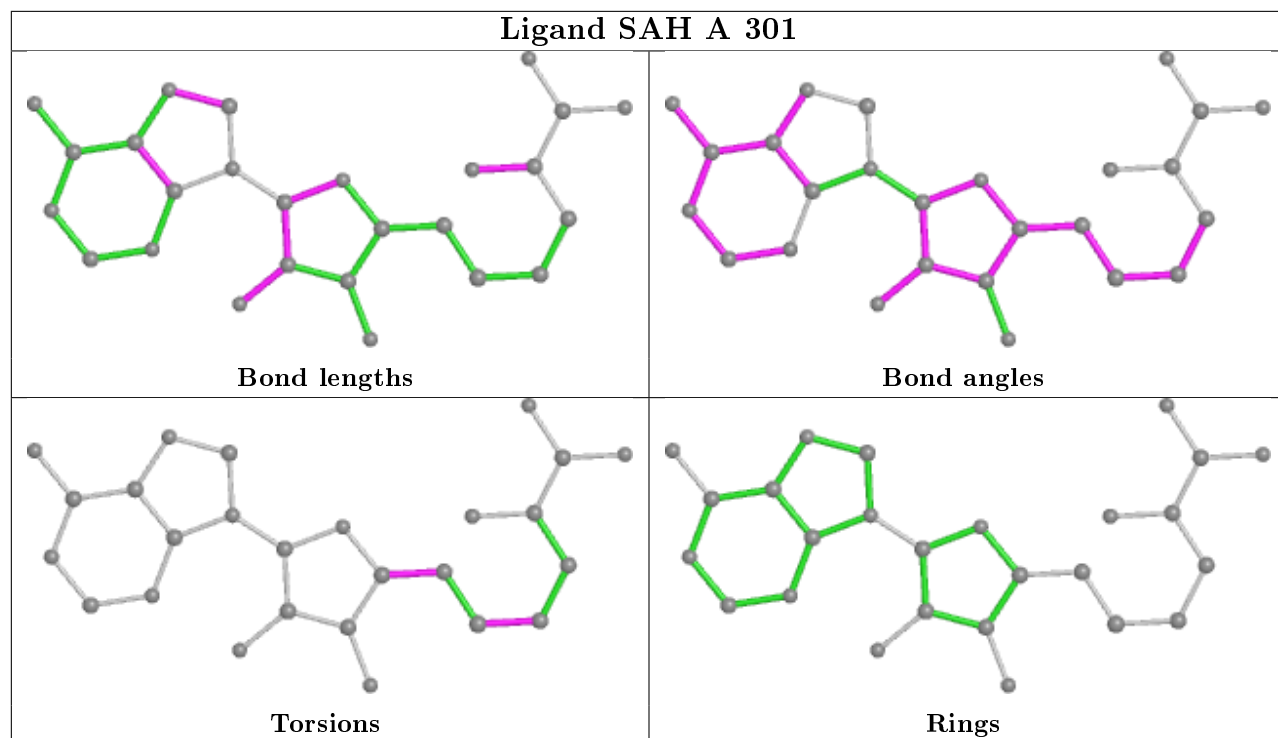
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	302	SAH	2	0

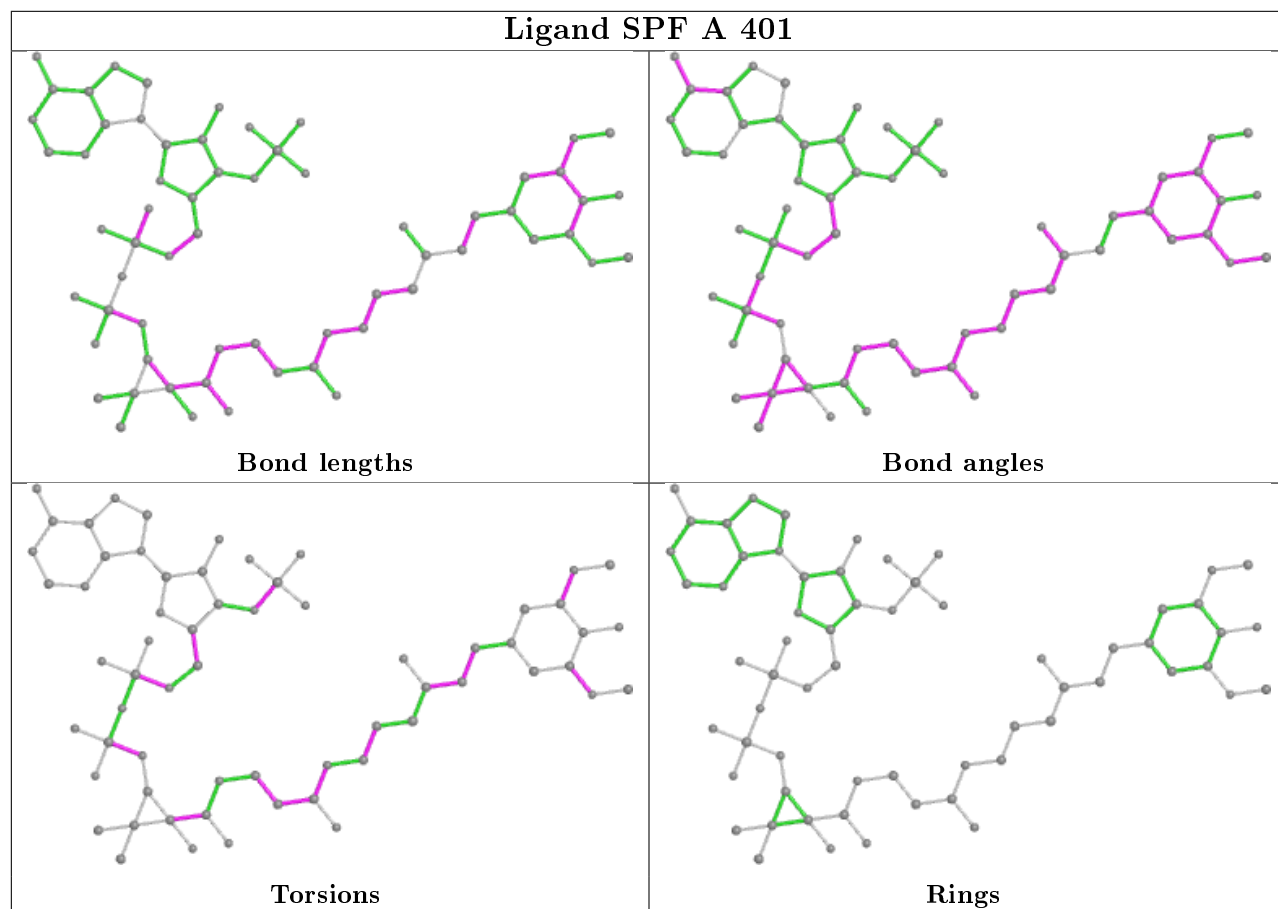
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

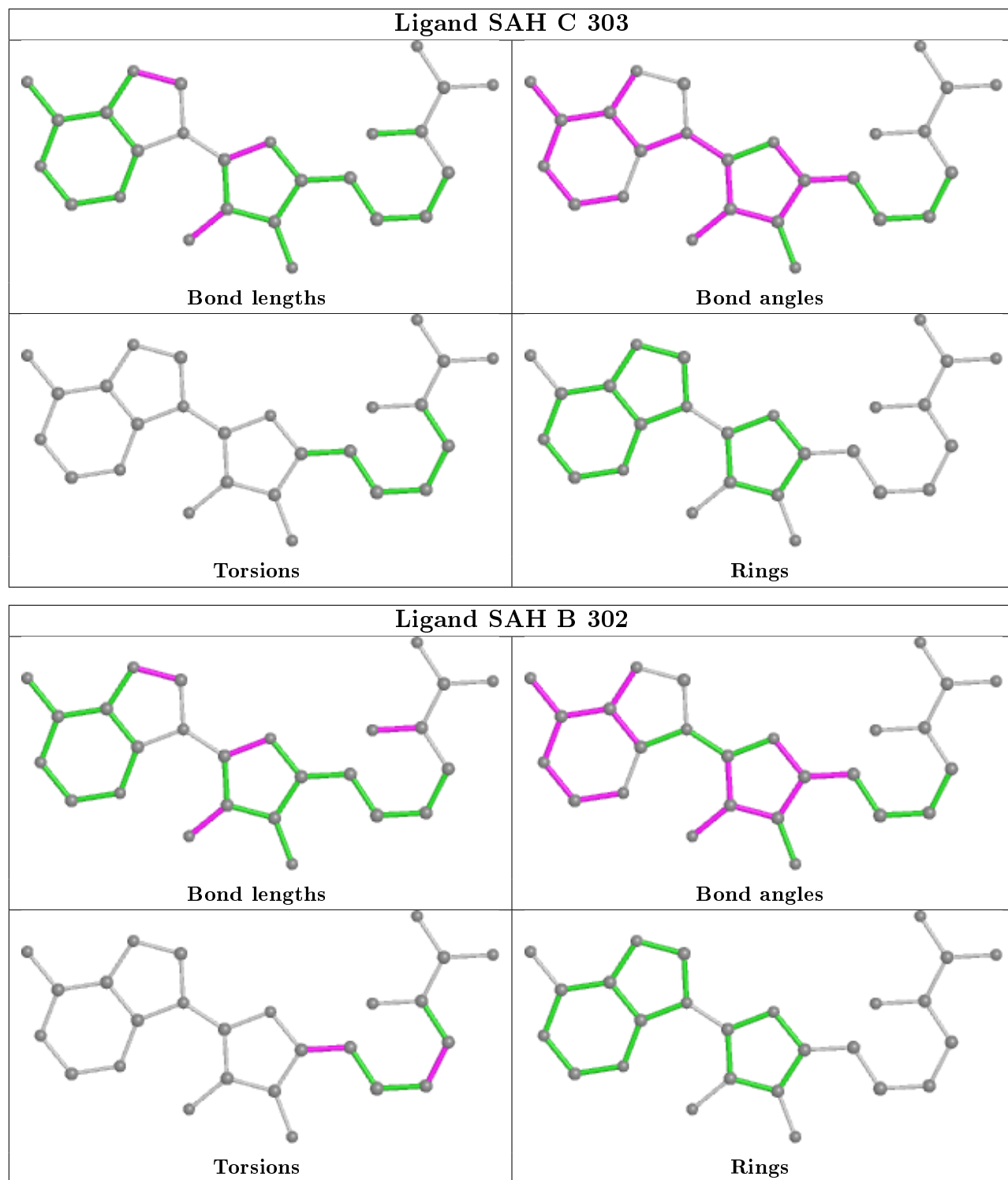


Ligand SAH A 301



Ligand SPF A 401





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	227/247 (91%)	-0.09	5 (2%) 62 63	33, 47, 70, 96	0
1	B	227/247 (91%)	0.07	11 (4%) 30 28	33, 48, 74, 94	0
1	C	227/247 (91%)	0.40	19 (8%) 11 9	44, 72, 105, 115	0
1	D	227/247 (91%)	1.06	41 (18%) 1 1	76, 110, 130, 138	0
All	All	908/988 (91%)	0.36	76 (8%) 11 9	33, 62, 124, 138	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	203	ALA	8.0
1	C	200	PRO	6.2
1	C	201	PRO	5.6
1	D	246	ILE	5.1
1	C	111	ASP	4.9
1	B	202	ASP	4.9
1	D	104	ASP	4.6
1	B	201	PRO	4.1
1	C	110	MET	4.0
1	D	152	LYS	4.0
1	B	62	THR	3.9
1	B	204	PRO	3.9
1	D	161	PHE	3.8
1	D	48	GLU	3.7
1	D	151	GLU	3.7
1	D	103	GLU	3.7
1	D	41	ARG	3.6
1	D	134	ASP	3.6
1	D	102	PRO	3.5
1	C	151	GLU	3.4
1	D	201	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	162	VAL	3.3
1	D	80	ALA	3.3
1	D	85	GLU	3.3
1	D	247	LYS	3.2
1	D	188	TYR	3.1
1	D	52	VAL	3.1
1	D	27	ASP	3.1
1	C	247	LYS	3.1
1	B	63	THR	3.1
1	C	202	ASP	3.0
1	D	105	GLY	2.9
1	D	84	MET	2.9
1	D	86	ILE	2.8
1	A	161	PHE	2.8
1	B	198	VAL	2.7
1	C	61	MET	2.7
1	D	79	ASN	2.7
1	C	162	VAL	2.7
1	D	81	LYS	2.7
1	D	125	LYS	2.7
1	B	187	GLY	2.6
1	C	86	ILE	2.6
1	D	29	LEU	2.6
1	C	161	PHE	2.6
1	C	182	VAL	2.6
1	C	60	ILE	2.5
1	D	51	GLU	2.5
1	A	240	ILE	2.4
1	B	162	VAL	2.4
1	D	187	GLY	2.4
1	A	206	ARG	2.4
1	D	43	HIS	2.3
1	D	108	LEU	2.3
1	D	206	ARG	2.3
1	B	195	GLY	2.3
1	D	56	HIS	2.3
1	C	83	THR	2.3
1	C	149	LYS	2.3
1	C	160	ILE	2.2
1	D	30	TYR	2.2
1	D	150	ASP	2.2
1	A	204	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	240	ILE	2.1
1	D	181	LYS	2.1
1	D	163	ASP	2.1
1	B	149	LYS	2.1
1	C	106	LYS	2.1
1	D	208	TYR	2.1
1	C	85	GLU	2.1
1	D	44	GLU	2.1
1	D	126	LYS	2.0
1	A	202	ASP	2.0
1	D	87	GLY	2.0
1	C	81	LYS	2.0
1	D	129	VAL	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](#)

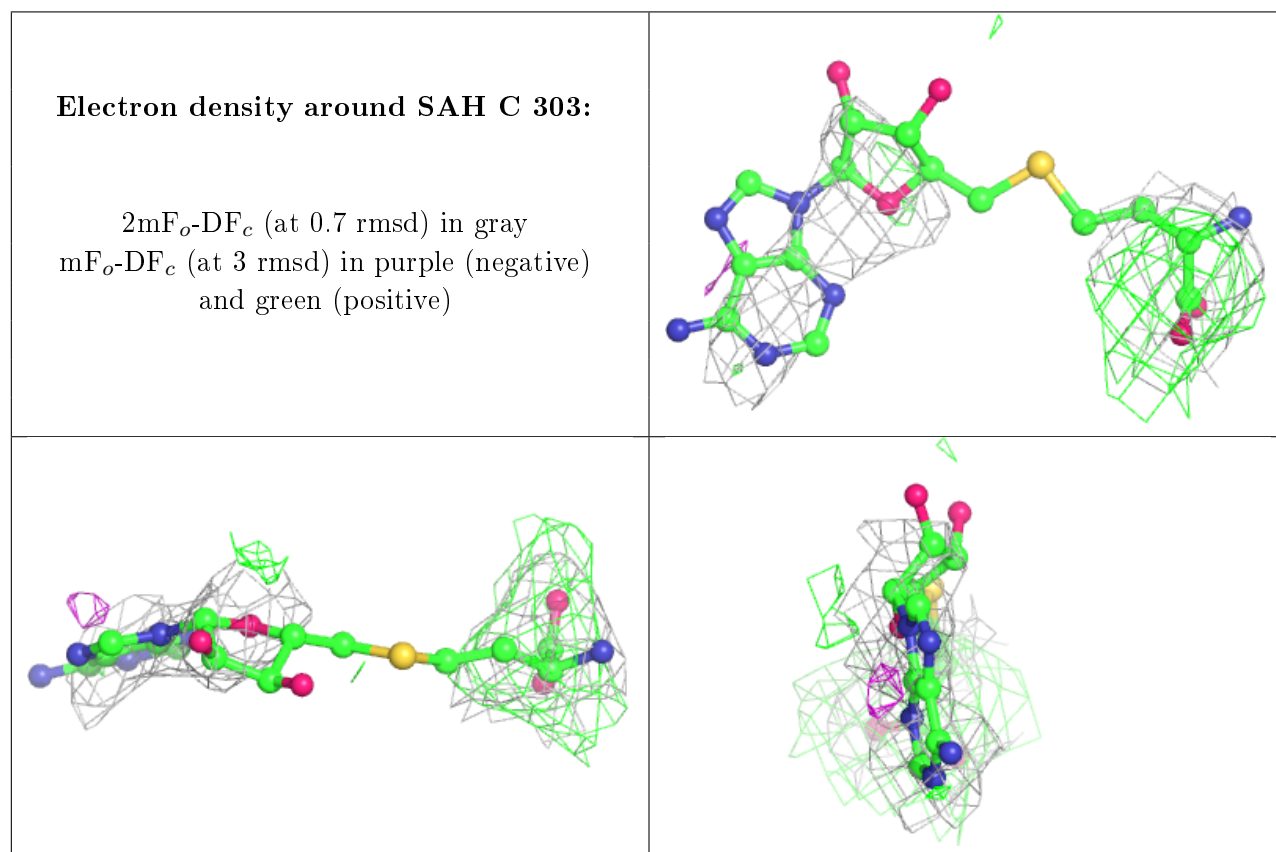
There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

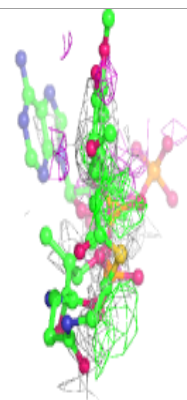
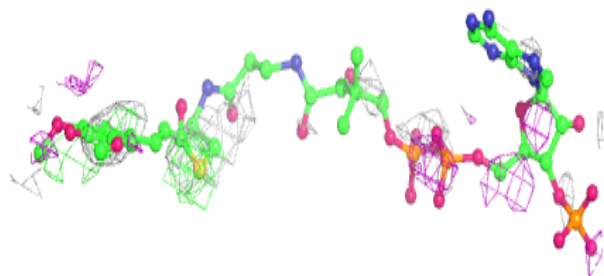
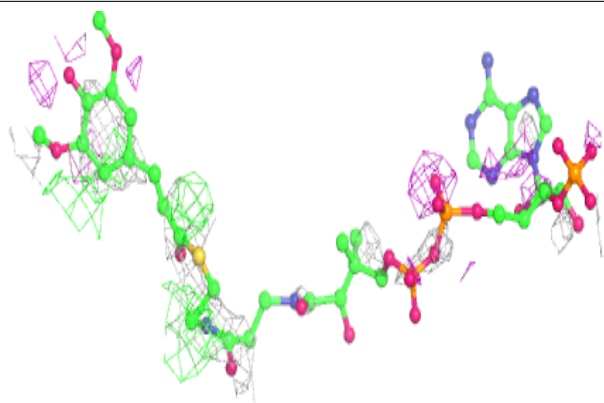
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SAH	C	303	26/26	0.19	0.77	159,170,171,171	0
4	SPF	A	401	63/63	0.35	0.80	176,192,195,200	0
3	SAH	B	302	26/26	0.61	0.42	109,119,122,122	0
3	SAH	D	304	26/26	0.68	0.32	130,135,139,139	0
3	SAH	A	301	26/26	0.93	0.23	37,47,56,57	0
2	CA	A	305	1/1	0.94	0.31	54,54,54,54	0
2	CA	B	306	1/1	0.94	0.27	121,121,121,121	0
2	CA	D	308	1/1	0.96	0.28	87,87,87,87	0
2	CA	C	307	1/1	0.97	0.16	59,59,59,59	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.

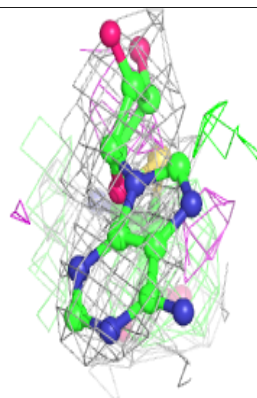
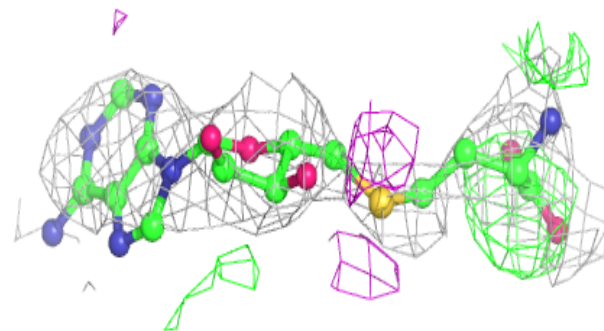
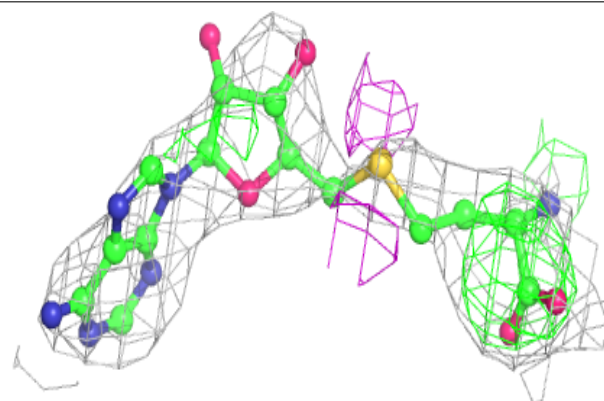


Electron density around SPF A 401:

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

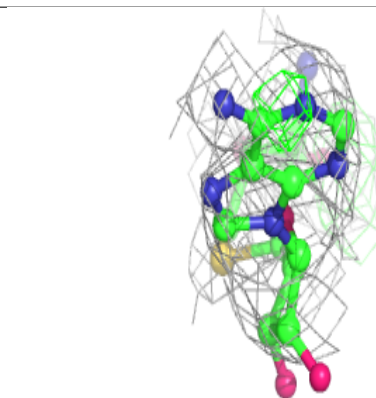
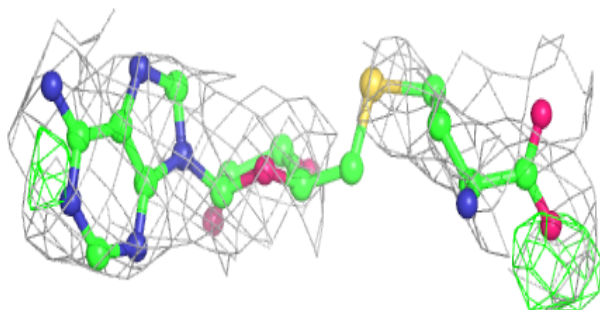
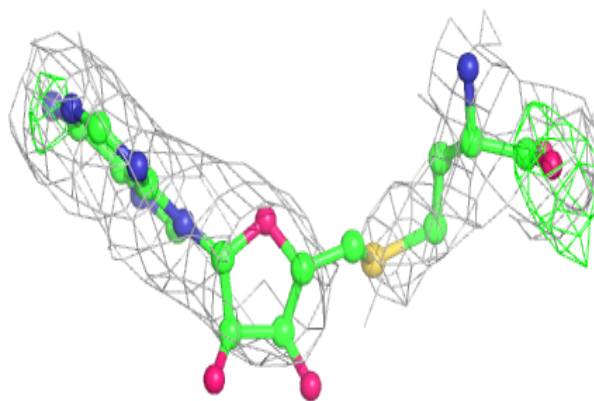
**Electron density around SAH B 302:**

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

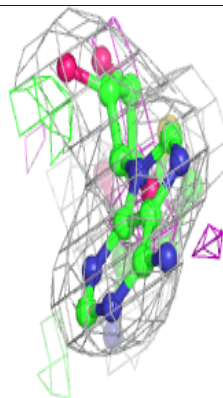
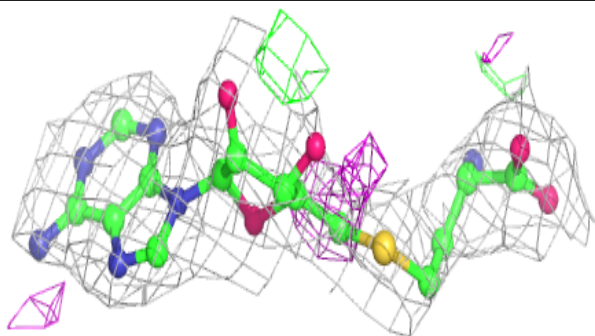
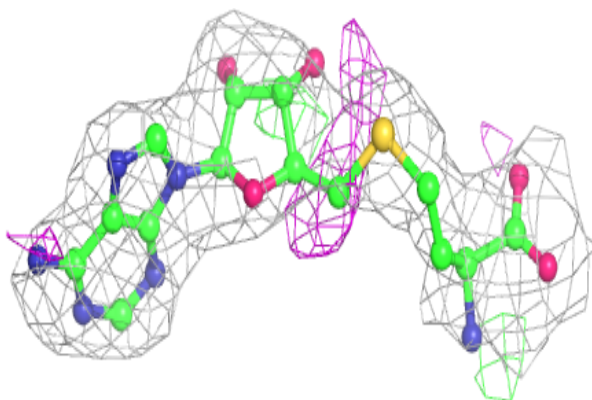


Electron density around SAH D 304:

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

**Electron density around SAH A 301:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.