



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 04:41 am BST

PDB ID : 6I5Z
Title : Papaver somniferum O-methyltransferase
Authors : Davies, G.J.; Cabry, M.P.; Offen, W.A.
Deposited on : 2018-11-15
Resolution : 3.00 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

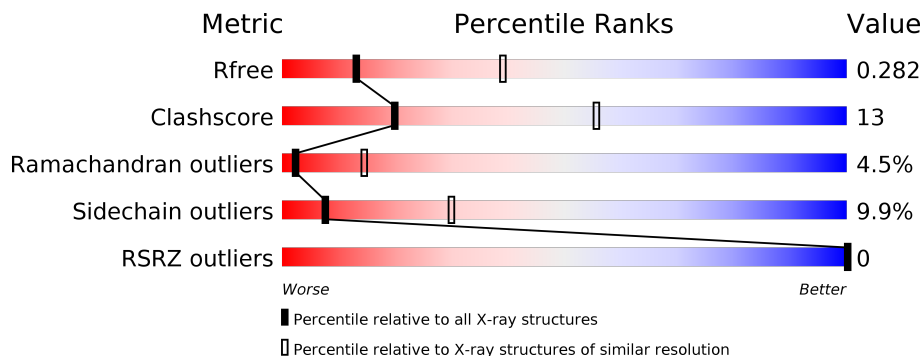
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	393	
1	B	393	
1	C	393	
1	D	393	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 10191 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.

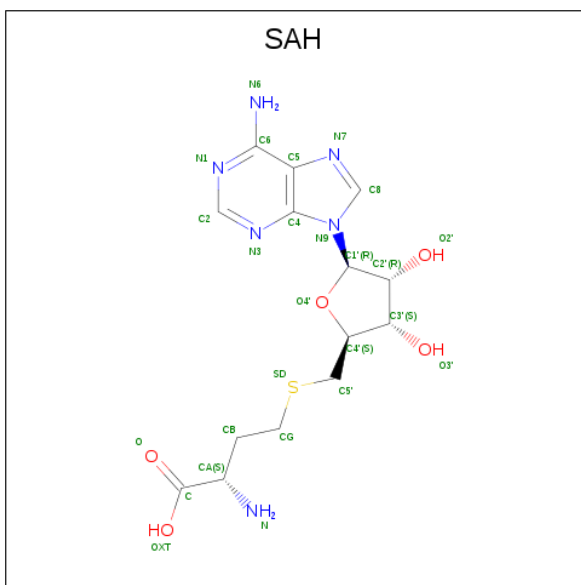
- Molecule 1 is a protein called O-methyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	342	2560	1654	419	471	16	0	0	0
1	B	349	2586	1659	430	481	16	0	0	0
1	C	342	2463	1581	409	456	17	0	0	0
1	D	347	2503	1604	411	472	16	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

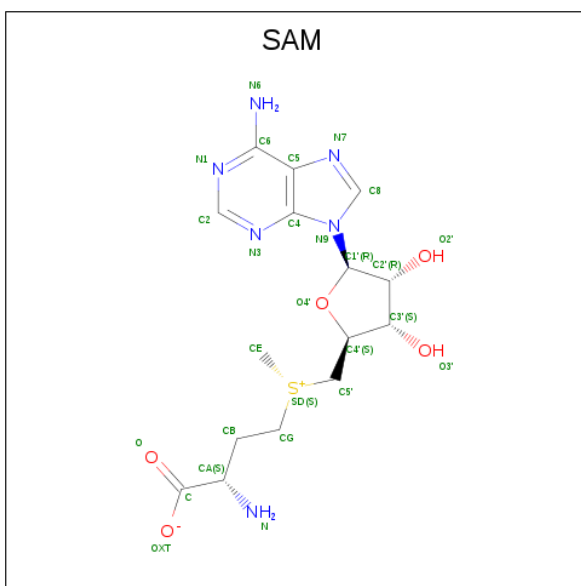
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP I3PLQ5
A	-1	PRO	-	expression tag	UNP I3PLQ5
A	0	ALA	-	expression tag	UNP I3PLQ5
B	-2	GLY	-	expression tag	UNP I3PLQ5
B	-1	PRO	-	expression tag	UNP I3PLQ5
B	0	ALA	-	expression tag	UNP I3PLQ5
C	-2	GLY	-	expression tag	UNP I3PLQ5
C	-1	PRO	-	expression tag	UNP I3PLQ5
C	0	ALA	-	expression tag	UNP I3PLQ5
D	-2	GLY	-	expression tag	UNP I3PLQ5
D	-1	PRO	-	expression tag	UNP I3PLQ5
D	0	ALA	-	expression tag	UNP I3PLQ5

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C₁₄H₂₀N₆O₅S).



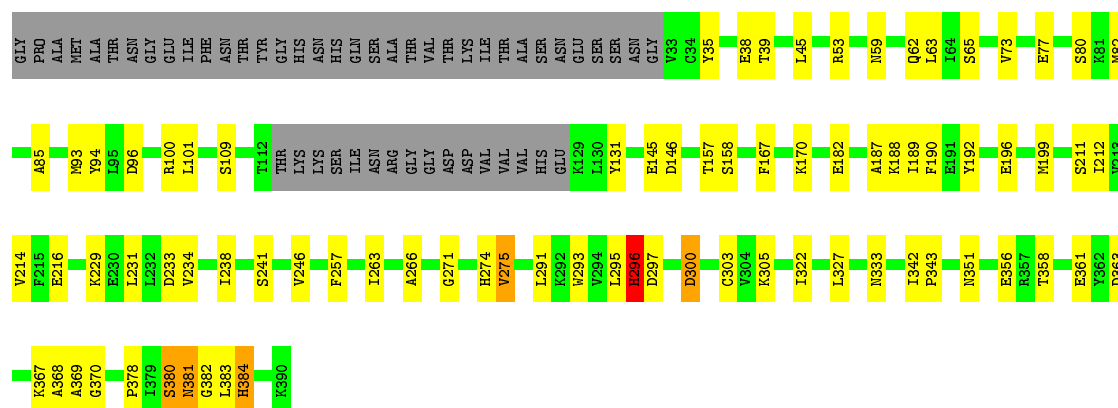
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 3 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



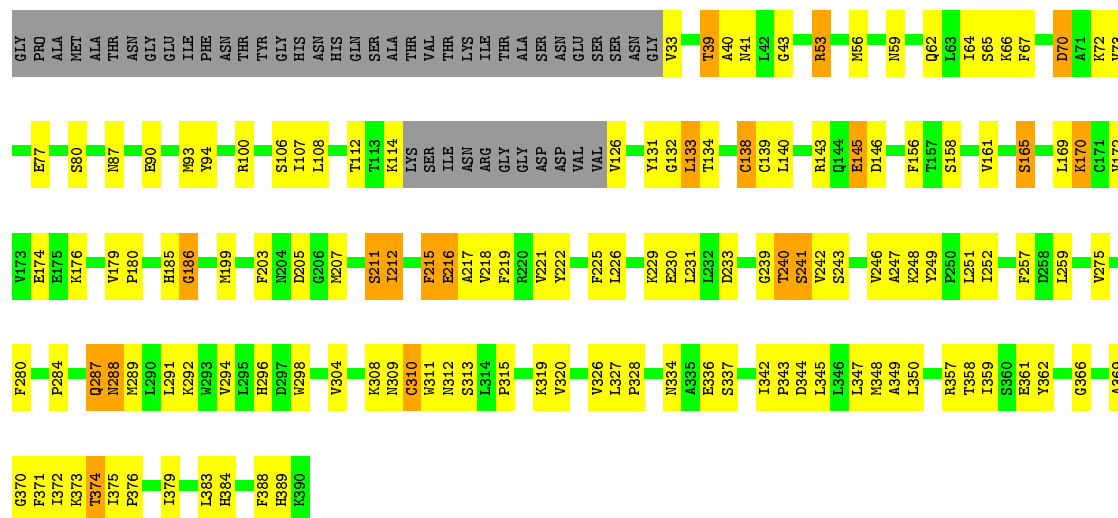
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	D	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

Chain C:  67% 19% 13%



• Molecule 1: O-methyltransferase 1

Chain D:  53% 30% 5% 12%



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	111.15Å 111.15Å 302.38Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	101.00 – 3.00 100.79 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (101.00-3.00) 100.0 (100.79-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 3.01Å)	Xtrriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.203 , 0.289 0.206 , 0.282	Depositor DCC
R_{free} test set	2123 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	94.8	Xtrriage
Anisotropy	0.083	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 80.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10191	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.11% 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: SAH, SAM

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.76	0/2613	0.94	0/3551
1	B	0.78	0/2639	0.90	0/3581
1	C	0.77	0/2511	0.91	0/3420
1	D	0.79	0/2554	0.93	0/3480
All	All	0.77	0/10317	0.92	0/14032

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	C	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	384	HIS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2560	0	2486	71	0
1	B	2586	0	2449	61	0
1	C	2463	0	2319	47	0
1	D	2503	0	2294	82	0
2	A	26	0	19	2	0
2	B	26	0	19	1	0
3	D	27	0	22	2	0
All	All	10191	0	9608	249	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 13.

All (249) 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:198:ARG:HH11	1:B:198:ARG:CG	1.55	1.19
1:B:198:ARG:HG3	1:B:198:ARG:HH11	0.98	1.08
1:B:95:LEU:HD21	1:B:99:LEU:HD11	1.30	1.07
1:B:198:ARG:NH1	1:B:198:ARG:HG3	1.57	1.04
1:B:95:LEU:CD2	1:B:99:LEU:HD11	1.88	1.03
1:B:100:ARG:NH1	1:C:327:LEU:HD21	1.78	0.99
1:A:152:GLU:OE1	1:C:229:LYS:NZ	1.98	0.96
1:B:100:ARG:HH12	1:C:327:LEU:HD21	1.31	0.94
1:B:95:LEU:CD2	1:B:99:LEU:CD1	2.53	0.87
1:D:359:ILE:HD11	1:D:384:HIS:CE1	2.09	0.86
1:C:378:PRO:HB3	1:C:384:HIS:NE2	1.92	0.83
1:D:292:LYS:NZ	3:D:401:SAM:OXT	2.11	0.82
1:D:114:LYS:O	1:D:126:VAL:O	1.99	0.81
1:B:95:LEU:HD23	1:B:99:LEU:CD1	2.11	0.81
1:D:53:ARG:NH1	1:D:158:SER:OG	2.15	0.78
1:B:253:ARG:NH2	1:B:273:GLU:OE1	2.17	0.77
1:D:288:ASN:HD22	1:D:288:ASN:H	1.34	0.76
1:D:288:ASN:HD22	1:D:288:ASN:N	1.85	0.74
1:D:326:VAL:HG11	1:D:359:ILE:HG12	1.70	0.73
1:C:246:VAL:HG11	1:C:271:GLY:HA3	1.68	0.73
1:A:268:GLN:HA	1:A:268:GLN:OE1	1.91	0.71
1:A:100:ARG:NH2	1:D:327:LEU:HD21	2.07	0.70
1:D:374:THR:O	1:D:376:PRO:HD3	1.91	0.70
1:B:198:ARG:O	1:B:202:VAL:HG23	1.92	0.69
1:D:215:PHE:O	1:D:218:VAL:N	2.25	0.69
1:A:249:TYR:O	1:A:252:ILE:HG22	1.93	0.69
1:A:262:VAL:O	1:A:265:VAL:HG12	1.94	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:ILE:HB	1:A:386:ILE:HB	1.76	0.67
1:A:347:LEU:O	1:A:351:ASN:N	2.29	0.65
1:C:59:ASN:OD1	1:C:63:LEU:CD1	2.44	0.65
1:A:230:GLU:HG3	1:A:253:ARG:CG	2.26	0.65
1:A:62:GLN:HA	1:A:141:VAL:HG13	1.79	0.65
1:A:311:TRP:CE2	1:A:390:LYS:HD3	2.33	0.64
1:B:203:PHE:O	1:B:207:MET:HG3	1.98	0.64
1:B:285:LYS:HA	1:B:313:SER:O	1.98	0.64
1:D:249:TYR:O	1:D:251:LEU:N	2.30	0.63
1:A:77:GLU:O	1:A:80:SER:CB	2.46	0.63
1:B:198:ARG:HG2	1:B:198:ARG:HH11	1.54	0.63
1:B:214:VAL:O	1:B:218:VAL:HG23	1.99	0.63
1:C:367:LYS:O	1:C:369:ALA:N	2.32	0.63
1:D:288:ASN:ND2	1:D:288:ASN:H	1.96	0.63
1:A:223:ASP:O	1:A:225:PHE:N	2.31	0.62
1:D:185:HIS:O	1:D:186:GLY:C	2.36	0.61
1:C:367:LYS:O	1:C:370:GLY:N	2.33	0.61
1:D:143:ARG:NH2	1:D:146:ASP:OD2	2.28	0.61
1:A:97:ARG:HA	1:A:100:ARG:HD3	1.81	0.61
1:D:33:VAL:O	1:D:33:VAL:HG12	2.01	0.60
1:D:64:ILE:CG2	1:D:133:LEU:HD12	2.31	0.60
1:A:64:ILE:CB	1:A:133:LEU:HD11	2.30	0.60
1:A:256:ASN:HB3	1:A:274:HIS:ND1	2.17	0.59
1:D:126:VAL:O	1:D:126:VAL:HG12	2.01	0.59
1:C:234:VAL:HB	1:C:291:LEU:CD2	2.32	0.59
1:A:151:VAL:HG12	1:A:152:GLU:N	2.17	0.59
1:D:72:LYS:HA	1:D:131:TYR:O	2.03	0.59
1:D:161:VAL:O	1:D:165:SER:OG	2.21	0.58
1:C:263:ILE:HG23	1:C:274:HIS:HB3	1.86	0.58
1:D:359:ILE:HD11	1:D:384:HIS:ND1	2.17	0.58
1:D:225:PHE:HB2	1:D:249:TYR:CE2	2.39	0.58
1:D:345:LEU:O	1:D:348:MET:N	2.36	0.57
1:C:342:ILE:HB	1:C:343:PRO:HD3	1.87	0.57
1:D:326:VAL:HG11	1:D:359:ILE:CG1	2.34	0.57
1:D:242:VAL:O	1:D:243:SER:C	2.43	0.56
1:A:230:GLU:OE1	1:A:286:GLY:HA2	2.05	0.56
1:D:53:ARG:NH1	1:D:158:SER:O	2.38	0.56
1:A:159:ASP:OD1	1:A:198:ARG:NH2	2.38	0.56
1:C:59:ASN:OD1	1:C:63:LEU:HD13	2.03	0.56
1:D:225:PHE:HB2	1:D:249:TYR:CZ	2.40	0.56
1:C:192:TYR:CZ	1:C:196:GLU:HG3	2.41	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:359:ILE:HD11	1:D:384:HIS:HE1	1.68	0.55
1:D:294:VAL:O	1:D:298:TRP:HD1	1.90	0.55
1:D:65:SER:C	1:D:67:PHE:H	2.09	0.55
1:A:254:GLY:N	1:A:271:GLY:O	2.38	0.54
1:A:94:TYR:O	1:A:97:ARG:HB2	2.07	0.54
1:D:212:ILE:O	1:D:216:GLU:HG3	2.07	0.54
1:C:378:PRO:HB3	1:C:384:HIS:CD2	2.43	0.54
1:B:228:MET:HE1	1:B:231:LEU:HD22	1.90	0.54
1:C:77:GLU:O	1:C:80:SER:HB3	2.08	0.54
1:B:156:PHE:HE1	1:B:203:PHE:CZ	2.26	0.53
1:B:95:LEU:HD23	1:B:99:LEU:HG	1.89	0.53
1:D:179:VAL:O	1:D:180:PRO:C	2.45	0.53
1:B:228:MET:HE1	1:B:231:LEU:HD13	1.89	0.53
1:B:77:GLU:O	1:B:80:SER:CB	2.56	0.53
1:C:96:ASP:O	1:C:100:ARG:HB2	2.10	0.52
1:B:227:ASP:N	1:B:227:ASP:OD1	2.38	0.52
1:D:90:GLU:HB3	1:D:94:TYR:CD2	2.44	0.52
1:D:229:LYS:O	1:D:252:ILE:HA	2.10	0.52
1:B:95:LEU:HD23	1:B:99:LEU:CG	2.39	0.52
1:A:159:ASP:O	1:A:162:VAL:HG12	2.10	0.52
1:A:246:VAL:HG22	1:A:252:ILE:HG23	1.92	0.52
1:A:342:ILE:HB	1:A:343:PRO:HD3	1.91	0.52
1:D:64:ILE:HG21	1:D:133:LEU:HD12	1.91	0.52
1:B:35:TYR:O	1:B:39:THR:HG23	2.10	0.51
1:C:59:ASN:O	1:C:63:LEU:HD13	2.10	0.51
1:A:265:VAL:O	1:A:265:VAL:HG22	2.10	0.51
1:A:311:TRP:CE2	1:A:390:LYS:CD	2.93	0.51
1:B:179:VAL:HG23	1:B:352:PRO:CD	2.40	0.51
1:C:212:ILE:O	1:C:216:GLU:HG3	2.09	0.51
1:D:358:THR:HG23	1:D:361:GLU:H	1.76	0.51
1:D:311:TRP:C	1:D:313:SER:H	2.13	0.51
1:D:39:THR:O	1:D:41:ASN:N	2.44	0.51
1:A:345:LEU:HD12	1:A:348:MET:CE	2.41	0.51
1:B:305:LYS:O	1:B:306:LEU:C	2.49	0.51
1:A:163:VAL:O	1:A:166:PHE:HB2	2.11	0.50
1:D:342:ILE:HB	1:D:343:PRO:CD	2.42	0.50
1:D:77:GLU:O	1:D:80:SER:OG	2.15	0.50
1:B:256:ASN:HD22	1:B:274:HIS:CE1	2.29	0.50
1:B:342:ILE:N	1:B:343:PRO:HD2	2.27	0.50
1:D:288:ASN:ND2	1:D:288:ASN:N	2.53	0.50
1:A:225:PHE:HB2	1:A:249:TYR:CE2	2.47	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:VAL:O	1:A:265:VAL:CG1	2.60	0.50
1:B:198:ARG:NH1	1:B:198:ARG:CG	2.25	0.50
1:D:373:LYS:CB	1:D:389:HIS:HB2	2.41	0.50
1:B:160:LYS:HA	1:C:167:PHE:CZ	2.47	0.49
1:D:280:PHE:O	1:D:309:ASN:ND2	2.45	0.49
1:C:59:ASN:ND2	1:C:62:GLN:HB3	2.27	0.49
1:D:225:PHE:CB	1:D:249:TYR:CE2	2.95	0.49
1:D:289:MET:SD	1:D:310:CYS:SG	2.92	0.49
1:B:334:ASN:N	1:B:334:ASN:OD1	2.42	0.49
1:A:148:VAL:HG13	1:A:209:VAL:HG22	1.94	0.49
1:B:254:GLY:O	1:B:272:VAL:HA	2.13	0.49
1:C:182:GLU:HG2	1:C:187:ALA:O	2.12	0.48
1:C:234:VAL:HB	1:C:291:LEU:HD23	1.95	0.48
1:A:263:ILE:O	1:A:265:VAL:N	2.46	0.48
1:A:48:ILE:HB	1:A:49:PRO:HD3	1.95	0.48
1:B:94:TYR:O	1:B:97:ARG:N	2.44	0.48
1:A:44:LYS:O	1:A:48:ILE:HG12	2.13	0.48
1:A:64:ILE:CB	1:A:133:LEU:CD1	2.91	0.48
1:B:49:PRO:HG3	1:C:45:LEU:O	2.13	0.48
1:C:297:ASP:OD1	1:C:351:ASN:ND2	2.46	0.48
1:D:64:ILE:HG22	1:D:133:LEU:HD12	1.94	0.48
1:A:236:GLY:HA3	1:A:256:ASN:ND2	2.28	0.48
1:B:188:LYS:HB2	1:B:191:GLU:HG3	1.94	0.48
1:D:311:TRP:O	1:D:313:SER:N	2.47	0.48
1:C:380:SER:O	1:C:381:ASN:C	2.52	0.48
1:D:371:PHE:CD2	1:D:388:PHE:HB3	2.49	0.48
1:A:222:TYR:CE2	1:A:224:GLY:HA3	2.49	0.48
1:B:341:LEU:HB3	1:C:101:LEU:HD13	1.96	0.48
1:C:146:ASP:OD1	1:C:146:ASP:N	2.47	0.47
1:A:238:ILE:O	1:A:269:TYR:HE2	1.96	0.47
1:D:180:PRO:HG2	1:D:349:ALA:HA	1.94	0.47
1:C:214:VAL:HG13	1:C:383:LEU:HD21	1.95	0.47
1:B:246:VAL:HG11	1:B:271:GLY:HA3	1.96	0.47
1:B:65:SER:O	1:B:68:GLY:N	2.44	0.47
1:A:69:THR:O	1:A:70:ASP:C	2.53	0.47
1:C:59:ASN:HD21	1:C:62:GLN:CB	2.28	0.47
1:A:168:LYS:HE3	1:A:183:VAL:HG12	1.96	0.47
1:A:257:PHE:HA	1:A:275:VAL:O	2.15	0.47
1:A:59:ASN:O	1:A:60:VAL:C	2.53	0.47
1:B:331:LEU:HD22	1:B:341:LEU:HD11	1.95	0.47
1:D:239:GLY:O	1:D:241:SER:N	2.48	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:SER:O	1:B:209:VAL:HG11	2.15	0.47
1:D:215:PHE:O	1:D:217:ALA:N	2.48	0.47
1:A:267:PRO:HG2	1:A:269:TYR:CZ	2.50	0.46
1:B:215:PHE:O	1:B:218:VAL:N	2.48	0.46
1:D:231:LEU:HA	1:D:288:ASN:O	2.15	0.46
1:A:253:ARG:NH2	1:A:273:GLU:OE1	2.49	0.46
1:A:159:ASP:O	1:A:162:VAL:CG1	2.64	0.46
1:D:156:PHE:HE1	1:D:203:PHE:CZ	2.33	0.46
1:B:326:VAL:HG11	1:B:359:ILE:HG13	1.96	0.46
1:D:308:LYS:CE	1:D:369:ALA:HA	2.46	0.46
1:A:259:LEU:HD21	2:A:401:SAH:C6	2.46	0.46
1:B:331:LEU:HD13	1:C:100:ARG:HG2	1.96	0.46
1:A:222:TYR:CZ	1:A:224:GLY:HA3	2.51	0.46
1:C:380:SER:O	1:C:382:GLY:N	2.49	0.46
1:C:257:PHE:HA	1:C:275:VAL:O	2.15	0.46
1:A:257:PHE:HD1	1:A:275:VAL:O	1.99	0.45
1:C:358:THR:HG23	1:C:361:GLU:H	1.80	0.45
1:C:93:MET:HG3	1:C:94:TYR:N	2.30	0.45
1:D:145:GLU:CD	1:D:145:GLU:H	2.20	0.45
1:A:97:ARG:NH2	1:D:344:ASP:OD1	2.49	0.45
1:B:95:LEU:O	1:B:99:LEU:HG	2.17	0.45
1:B:292:LYS:O	2:B:401:SAH:N	2.49	0.45
1:D:39:THR:C	1:D:41:ASN:H	2.20	0.45
1:A:35:TYR:O	1:A:39:THR:HB	2.16	0.45
1:A:362:TYR:HA	1:A:365:LEU:HD12	1.99	0.45
1:A:292:LYS:HB3	2:A:401:SAH:HN2	1.82	0.45
1:B:232:LEU:HD23	1:B:289:MET:HG2	1.98	0.45
1:C:53:ARG:NH1	1:C:158:SER:OG	2.49	0.45
1:D:56:MET:O	1:D:59:ASN:N	2.36	0.44
1:A:345:LEU:HD12	1:A:348:MET:HE3	1.99	0.44
1:D:248:LYS:C	1:D:249:TYR:CD1	2.90	0.44
1:B:362:TYR:O	1:B:365:LEU:HB2	2.16	0.44
1:A:182:GLU:O	1:A:185:HIS:O	2.35	0.44
1:A:84:ASN:CB	1:D:174:GLU:OE2	2.66	0.44
1:D:169:LEU:O	1:D:170:LYS:C	2.55	0.44
1:A:279:MET:HG3	1:A:306:LEU:HD13	1.99	0.44
1:B:232:LEU:O	1:B:289:MET:HA	2.18	0.44
1:D:108:LEU:HD23	1:D:132:GLY:O	2.17	0.43
1:D:257:PHE:HA	1:D:275:VAL:O	2.18	0.43
1:D:233:ASP:HB2	1:D:242:VAL:CG1	2.47	0.43
1:B:286:GLY:O	1:B:315:PRO:HD3	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:259:LEU:HD21	3:D:401:SAM:C6	2.48	0.43
1:B:48:ILE:HG22	1:C:45:LEU:HD13	2.00	0.43
1:C:238:ILE:HA	1:C:266:ALA:HB2	2.01	0.43
1:A:344:ASP:OD2	1:D:100:ARG:NH2	2.51	0.43
1:D:366:GLY:HA2	1:D:388:PHE:CD2	2.54	0.43
1:A:331:LEU:HD22	1:A:341:LEU:HD11	2.01	0.43
1:D:65:SER:O	1:D:67:PHE:N	2.48	0.43
1:B:285:LYS:HB3	1:B:285:LYS:HE3	1.81	0.43
1:C:295:LEU:O	1:C:297:ASP:N	2.51	0.43
1:B:108:LEU:HA	1:B:108:LEU:HD12	1.86	0.42
1:C:295:LEU:HD12	1:C:322:ILE:CG2	2.48	0.42
1:C:73:VAL:CG1	1:C:77:GLU:CB	2.96	0.42
1:B:134:THR:O	1:B:135:ASN:C	2.56	0.42
1:B:343:PRO:O	1:B:346:LEU:HB2	2.19	0.42
1:C:233:ASP:OD2	1:C:241:SER:OG	2.35	0.42
1:C:296:HIS:ND1	1:C:356:GLU:OE2	2.52	0.42
1:D:211:SER:O	1:D:212:ILE:C	2.57	0.42
1:D:371:PHE:HD2	1:D:388:PHE:C	2.22	0.42
1:B:153:GLU:O	1:B:156:PHE:HB3	2.19	0.42
1:B:179:VAL:HG13	1:B:182:GLU:HB2	2.00	0.42
1:D:138:CYS:C	1:D:140:LEU:H	2.23	0.42
1:D:211:SER:OG	1:D:292:LYS:NZ	2.27	0.42
1:A:230:GLU:OE2	1:A:253:ARG:NH1	2.50	0.42
1:D:328:PRO:HG2	1:D:336:GLU:HG3	2.02	0.42
1:C:300:ASP:HA	1:C:303:CYS:HB2	2.02	0.42
1:A:154:LEU:C	1:A:156:PHE:N	2.72	0.42
1:A:292:LYS:HG3	1:A:323:ILE:HB	2.01	0.42
1:D:319:LYS:HD3	1:D:389:HIS:CE1	2.55	0.42
1:A:340:ALA:C	1:A:343:PRO:HD2	2.40	0.41
1:B:257:PHE:CE2	1:B:284:PRO:HD2	2.55	0.41
1:D:343:PRO:O	1:D:347:LEU:HG	2.20	0.41
1:A:48:ILE:HB	1:A:49:PRO:CD	2.50	0.41
1:A:65:SER:C	1:A:67:PHE:H	2.23	0.41
1:D:39:THR:C	1:D:41:ASN:N	2.73	0.41
1:A:358:THR:HG22	1:A:361:GLU:HG3	2.01	0.41
1:A:59:ASN:O	1:A:61:PHE:N	2.53	0.41
1:C:188:LYS:O	1:C:189:ILE:C	2.59	0.41
1:C:35:TYR:O	1:C:39:THR:HG23	2.21	0.41
1:D:287:GLN:HA	1:D:315:PRO:CG	2.51	0.41
1:D:357:ARG:HD2	1:D:362:TYR:CE1	2.55	0.41
1:A:230:GLU:HG3	1:A:253:ARG:HG3	2.00	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:286:GLY:O	1:B:314:LEU:HD12	2.20	0.41
1:C:109:SER:O	1:C:131:TYR:HA	2.20	0.41
1:A:263:ILE:C	1:A:265:VAL:H	2.24	0.41
1:A:58:LEU:O	1:A:82:MET:HE2	2.21	0.41
1:B:379:ILE:N	1:B:383:LEU:O	2.50	0.41
1:D:156:PHE:HE1	1:D:203:PHE:CE1	2.39	0.41
1:A:371:PHE:CG	1:A:388:PHE:HB3	2.56	0.41
1:D:379:ILE:HB	1:D:383:LEU:O	2.21	0.41
1:B:209:VAL:O	1:B:212:ILE:HB	2.20	0.40
1:C:82:MET:HB2	1:C:85:ALA:HB3	2.04	0.40
1:D:230:GLU:O	1:D:288:ASN:ND2	2.54	0.40
1:B:365:LEU:HD23	1:B:365:LEU:HA	1.92	0.40
1:D:240:THR:O	1:D:241:SER:C	2.60	0.40
1:A:151:VAL:O	1:A:152:GLU:C	2.59	0.40
1:A:231:LEU:HB2	1:A:252:ILE:HD11	2.03	0.40
1:B:179:VAL:HG23	1:B:352:PRO:HD3	2.03	0.40
1:D:39:THR:O	1:D:43:GLY:N	2.46	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	338/393 (86%)	288 (85%)	35 (10%)	15 (4%)	2	15
1	B	345/393 (88%)	299 (87%)	39 (11%)	7 (2%)	7	34
1	C	338/393 (86%)	286 (85%)	44 (13%)	8 (2%)	6	29
1	D	343/393 (87%)	248 (72%)	63 (18%)	32 (9%)	0	3
All	All	1364/1572 (87%)	1121 (82%)	181 (13%)	62 (4%)	2	14

All (62) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	VAL
1	A	110	VAL
1	A	224	GLY
1	B	91	ALA
1	C	170	LYS
1	C	190	PHE
1	C	368	ALA
1	D	170	LYS
1	D	176	LYS
1	D	219	PHE
1	D	221	VAL
1	D	240	THR
1	D	312	ASN
1	A	70	ASP
1	A	155	LEU
1	B	60	VAL
1	B	284	PRO
1	C	381	ASN
1	D	66	LYS
1	D	139	CYS
1	D	186	GLY
1	D	207	MET
1	D	216	GLU
1	D	241	SER
1	D	247	ALA
1	D	287	GLN
1	D	334	ASN
1	D	372	ILE
1	D	374	THR
1	A	59	ASN
1	A	91	ALA
1	A	106	SER
1	A	208	ALA
1	A	264	SER
1	B	70	ASP
1	B	135	ASN
1	C	145	GLU
1	D	40	ALA
1	D	222	TYR
1	D	284	PRO
1	A	66	LYS
1	A	72	LYS
1	B	371	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	293	TRP
1	C	296	HIS
1	D	70	ASP
1	D	87	ASN
1	D	370	GLY
1	D	39	THR
1	D	107	ILE
1	D	375	ILE
1	A	89	PRO
1	A	100	ARG
1	A	151	VAL
1	B	224	GLY
1	D	106	SER
1	D	205	ASP
1	D	212	ILE
1	C	275	VAL
1	D	304	VAL
1	D	246	VAL
1	D	320	VAL

5.3.2 Protein sidechains [i](#)

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	261/333 (78%)	232 (89%)	29 (11%)	6	25
1	B	255/333 (77%)	220 (86%)	35 (14%)	3	17
1	C	238/333 (72%)	226 (95%)	12 (5%)	24	60
1	D	237/333 (71%)	215 (91%)	22 (9%)	9	33
All	All	991/1332 (74%)	893 (90%)	98 (10%)	8	30

All (98) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	THR
1	A	46	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	63	LEU
1	A	70	ASP
1	A	77	GLU
1	A	89	PRO
1	A	95	LEU
1	A	101	LEU
1	A	107	ILE
1	A	112	THR
1	A	134	THR
1	A	138	CYS
1	A	157	THR
1	A	165	SER
1	A	169	LEU
1	A	172	VAL
1	A	178	SER
1	A	191	GLU
1	A	195	THR
1	A	209	VAL
1	A	215	PHE
1	A	223	ASP
1	A	240	THR
1	A	241	SER
1	A	278	ASP
1	A	282	GLU
1	A	296	HIS
1	A	336	GLU
1	A	358	THR
1	B	36	LEU
1	B	52	LEU
1	B	53	ARG
1	B	70	ASP
1	B	74	SER
1	B	76	SER
1	B	101	LEU
1	B	108	LEU
1	B	113	THR
1	B	127	HIS
1	B	133	LEU
1	B	138	CYS
1	B	144	GLN
1	B	146	ASP
1	B	151	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	162	VAL
1	B	168	LYS
1	B	172	VAL
1	B	198	ARG
1	B	199	MET
1	B	201	GLN
1	B	207	MET
1	B	215	PHE
1	B	227	ASP
1	B	240	THR
1	B	246	VAL
1	B	260	PRO
1	B	281	GLU
1	B	296	HIS
1	B	316	VAL
1	B	329	ASN
1	B	336	GLU
1	B	363	ASP
1	B	372	ILE
1	B	380	SER
1	C	38	GLU
1	C	65	SER
1	C	157	THR
1	C	199	MET
1	C	211	SER
1	C	231	LEU
1	C	296	HIS
1	C	300	ASP
1	C	305	LYS
1	C	333	ASN
1	C	363	ASP
1	C	380	SER
1	D	53	ARG
1	D	62	GLN
1	D	70	ASP
1	D	73	VAL
1	D	93	MET
1	D	112	THR
1	D	133	LEU
1	D	134	THR
1	D	138	CYS
1	D	145	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	165	SER
1	D	172	VAL
1	D	199	MET
1	D	211	SER
1	D	215	PHE
1	D	226	LEU
1	D	288	ASN
1	D	291	LEU
1	D	296	HIS
1	D	310	CYS
1	D	337	SER
1	D	350	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	41	ASN
1	D	288	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](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SAH	B	401	-	21,28,28	1.13	1 (4%)	20,40,40	1.82	7 (35%)
2	SAH	A	401	-	21,28,28	1.33	3 (14%)	20,40,40	2.22	6 (30%)
3	SAM	D	401	-	21,29,29	0.72	0	18,42,42	1.25	2 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SAH	B	401	-	-	3/7/31/31	0/3/3/3
2	SAH	A	401	-	-	5/7/31/31	0/3/3/3
3	SAM	D	401	-	-	1/8/33/33	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	SAH	C2'-C1'	-3.06	1.49	1.53
2	A	401	SAH	C5-N7	-2.67	1.30	1.39
2	A	401	SAH	C5-C4	2.22	1.46	1.40
2	B	401	SAH	C5-C4	2.13	1.46	1.40

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	SAH	C5'-SD-CG	6.40	121.46	102.27
2	B	401	SAH	C1'-N9-C4	-4.03	119.56	126.64
3	D	401	SAM	O4'-C1'-C2'	-3.40	101.96	106.93
2	A	401	SAH	C4-C5-N7	-3.32	105.94	109.40
2	B	401	SAH	C5'-SD-CG	3.10	111.57	102.27
2	A	401	SAH	O4'-C4'-C5'	-2.85	101.50	108.83
2	B	401	SAH	N3-C2-N1	-2.77	124.35	128.68
3	D	401	SAM	C5-C6-N6	2.72	124.48	120.35
2	A	401	SAH	N3-C2-N1	-2.69	124.47	128.68
2	A	401	SAH	C2-N1-C6	2.55	123.11	118.75
2	B	401	SAH	CB-CG-SD	-2.55	107.60	113.31
2	B	401	SAH	O4'-C4'-C5'	-2.34	102.80	108.83

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	SAH	C5-C6-N6	2.23	123.74	120.35
2	B	401	SAH	C2-N1-C6	2.19	122.50	118.75
2	B	401	SAH	C4-C5-N7	-2.02	107.30	109.40

There are no chirality outliers.

All (9) torsion outliers are listed below:

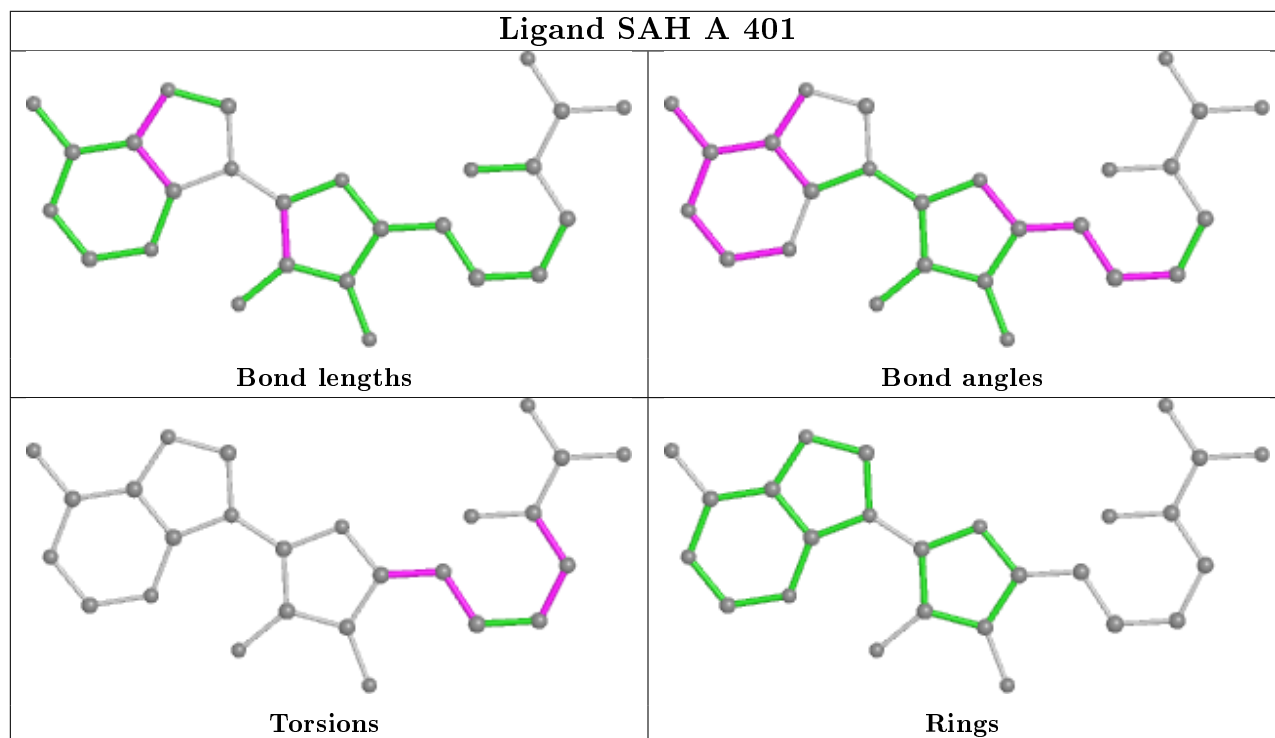
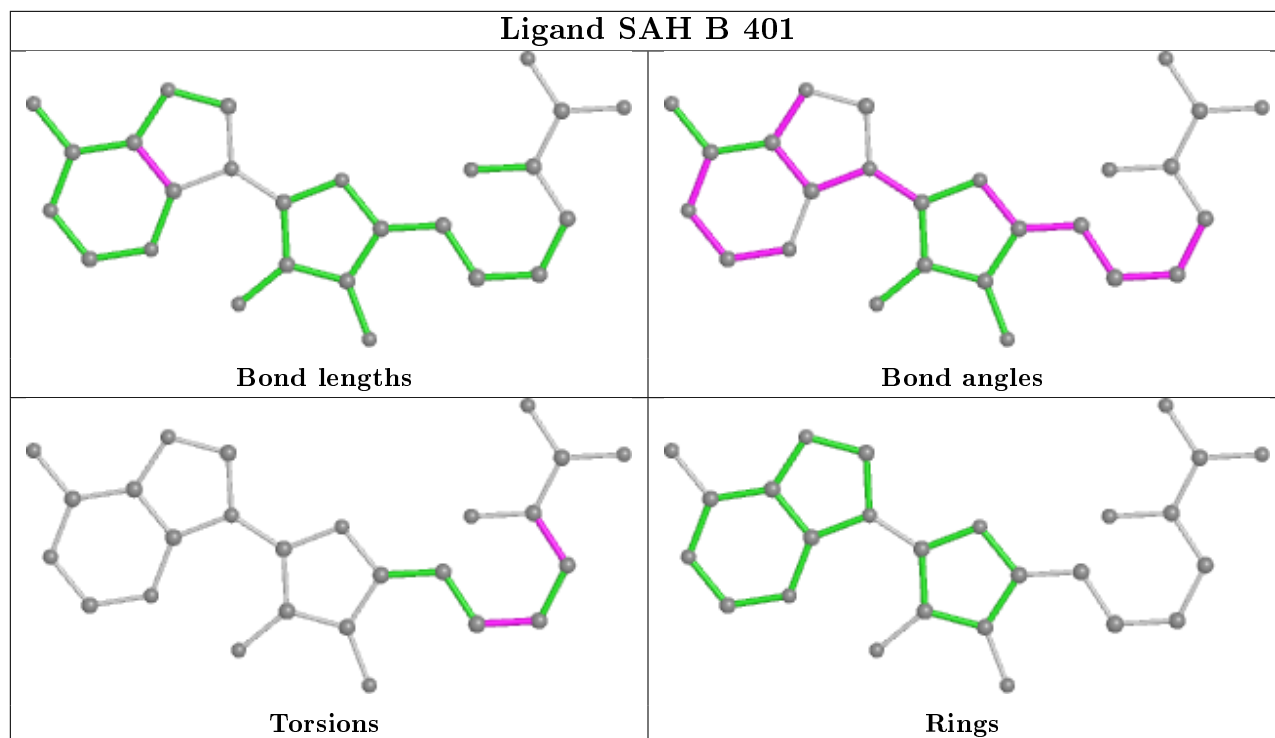
Mol	Chain	Res	Type	Atoms
2	B	401	SAH	N-CA-CB-CG
2	B	401	SAH	C-CA-CB-CG
2	A	401	SAH	C-CA-CB-CG
2	A	401	SAH	C4'-C5'-SD-CG
2	A	401	SAH	O4'-C4'-C5'-SD
2	A	401	SAH	C3'-C4'-C5'-SD
2	A	401	SAH	CA-CB-CG-SD
2	B	401	SAH	CB-CG-SD-C5'
3	D	401	SAM	N-CA-CB-CG

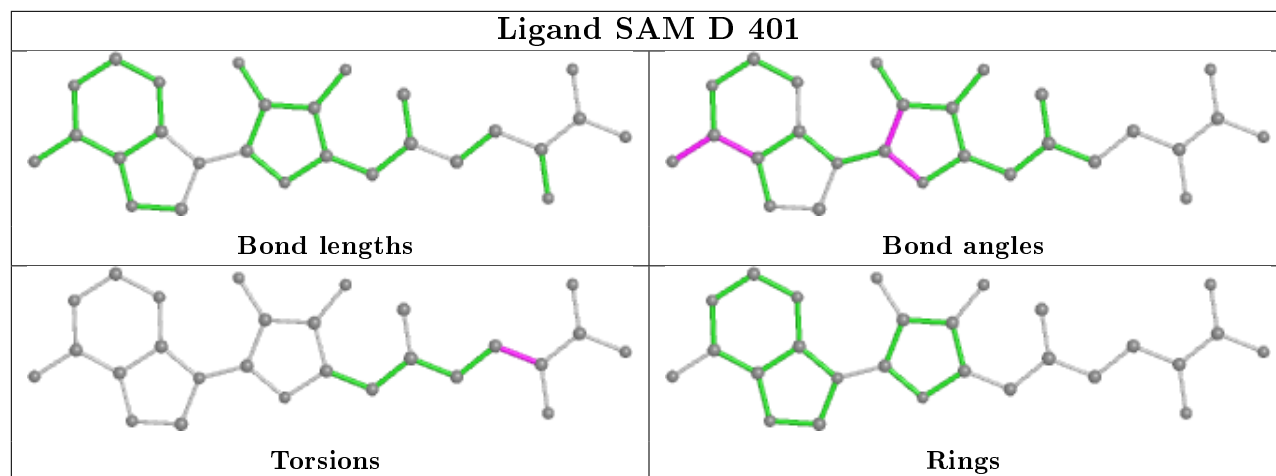
There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	SAH	1	0
2	A	401	SAH	2	0
3	D	401	SAM	2	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	342/393 (87%)	-0.27	0	100 100	48, 75, 106, 127	26 (7%)
1	B	349/393 (88%)	-0.25	0	100 100	63, 86, 121, 148	27 (7%)
1	C	342/393 (87%)	-0.23	0	100 100	58, 87, 120, 157	25 (7%)
1	D	347/393 (88%)	-0.39	0	100 100	50, 90, 126, 139	43 (12%)
All	All	1380/1572 (87%)	-0.29	0	100 100	48, 85, 120, 157	121 (8%)

There are no RSRZ outliers to report.

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](#)

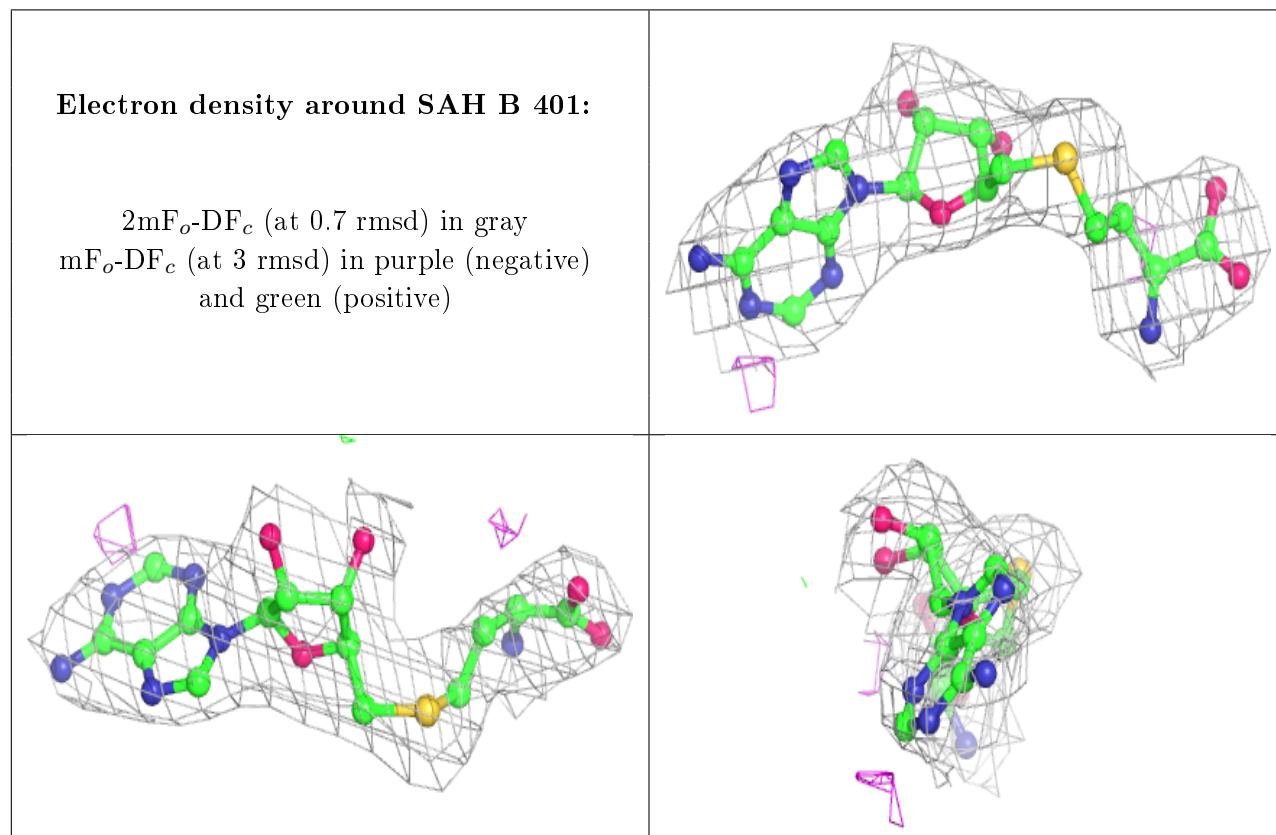
There are no carbohydrates in this entry.

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.

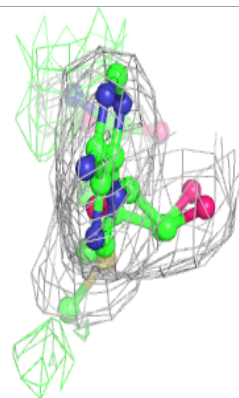
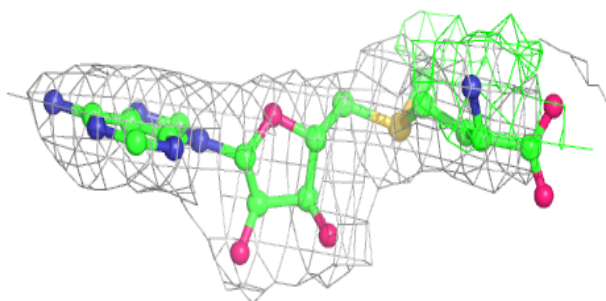
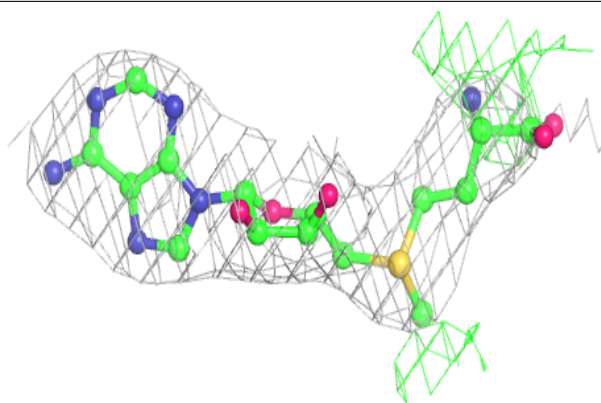
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	SAH	B	401	26/26	0.94	0.23	70,81,89,92	0
3	SAM	D	401	27/27	0.94	0.19	53,62,90,93	5
2	SAH	A	401	26/26	0.96	0.19	58,64,82,106	0

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

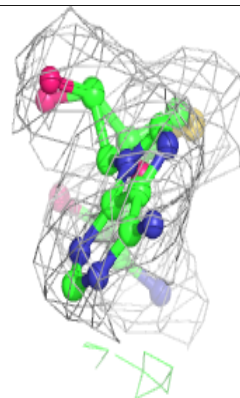
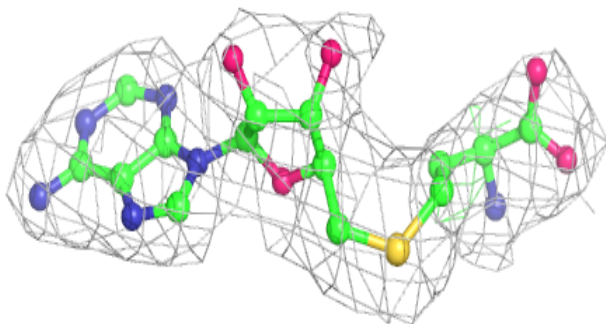
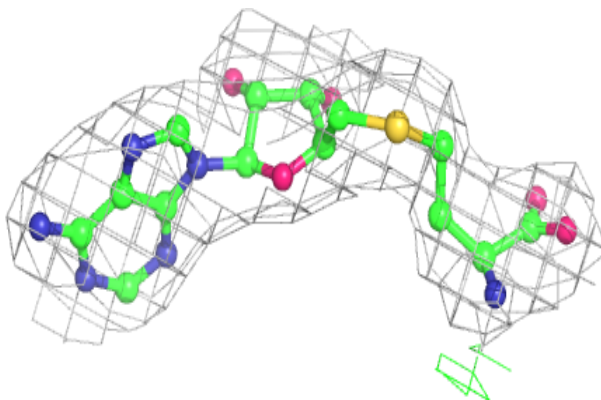


Electron density around SAM D 401:

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

**Electron density around SAH 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)



6.5 Other polymers

There are no such residues in this entry.