



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 19, 2026 – 05:03 AM UTC

PDB ID : 6WKB / pdb_00006wkb
Title : Human S-adenosylmethionine synthetase co-crystallized with UppNHp and Met
Authors : Tan, L.L.; Jackson, C.J.
Deposited on : 2020-04-15
Resolution : 2.55 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

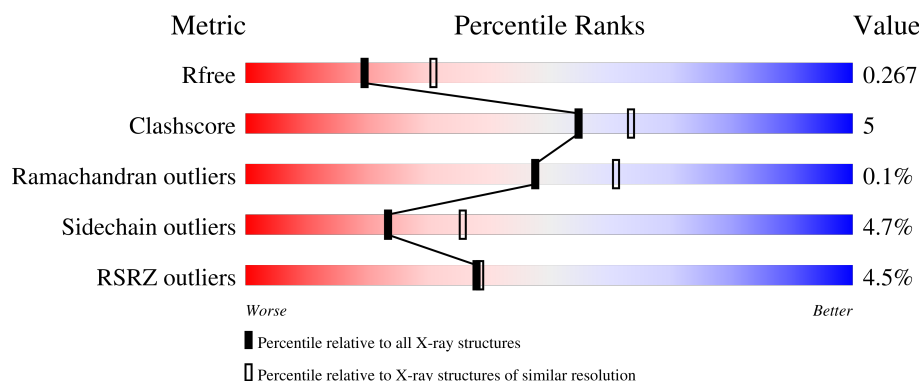
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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

Mol	Chain	Length	Quality of chain
1	A	395	2% 82% 14% ..
1	B	395	7% 83% 11% ..

2 Entry composition [i](#)

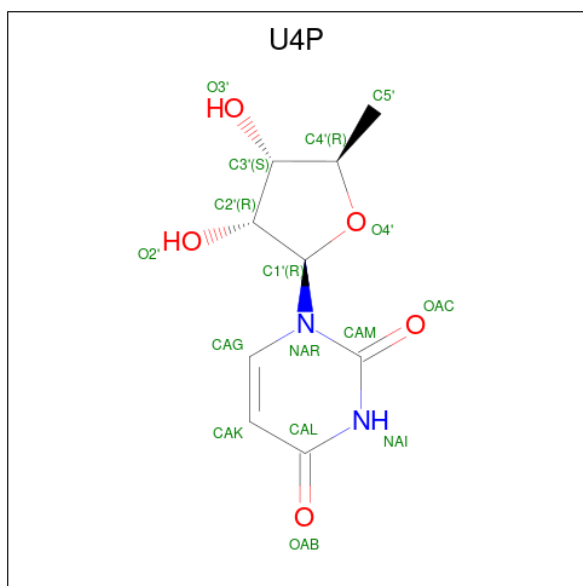
There are 6 unique types of molecules in this entry. The entry contains 6146 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 S-adenosylmethionine synthase isoform type-2.

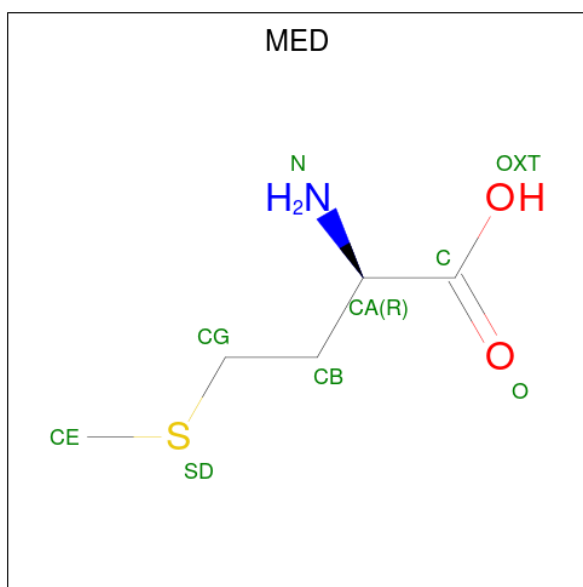
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	381	Total	C	N	O	S	0	0	0
			2963	1872	518	562	11			
1	B	380	Total	C	N	O	S	0	19	0
			3101	1956	543	590	12			

- Molecule 2 is 5'-deoxyuridine (CCD ID: U4P) (formula: $C_9H_{12}N_2O_5$).



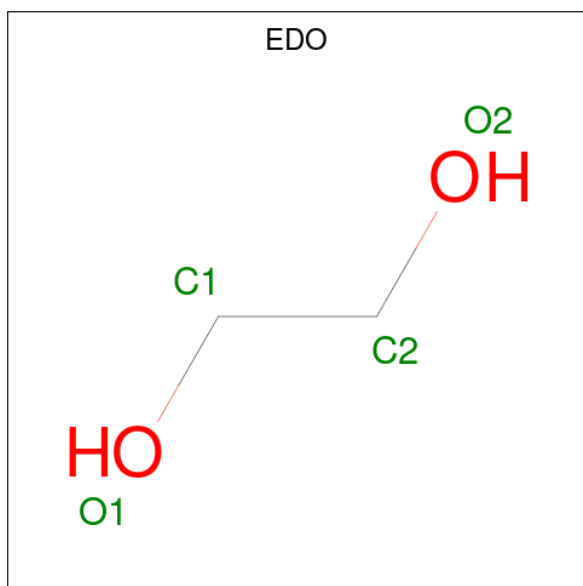
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	1
			16	9	2	5		
2	B	1	Total	C	N	O	0	0
			16	9	2	5		

- Molecule 3 is D-METHIONINE (CCD ID: MED) (formula: $C_5H_{11}NO_2S$).



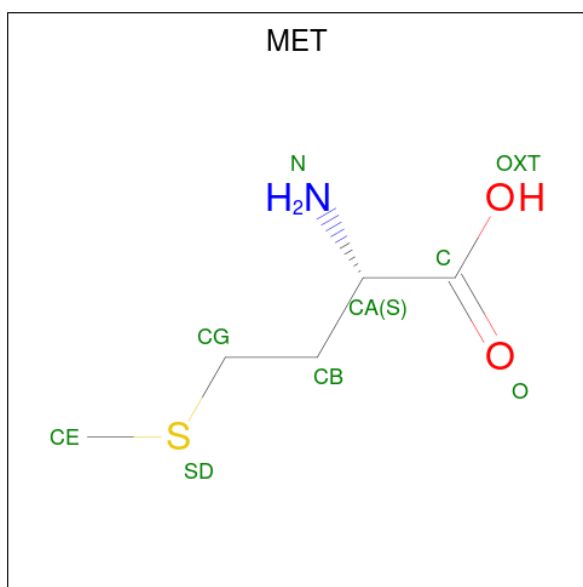
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			9	5	1	2	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	C O	0	0
			4	2 2		

- Molecule 5 is METHIONINE (CCD ID: MET) (formula: C₅H₁₁NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	S	0	1
			9	5	1	2	1		

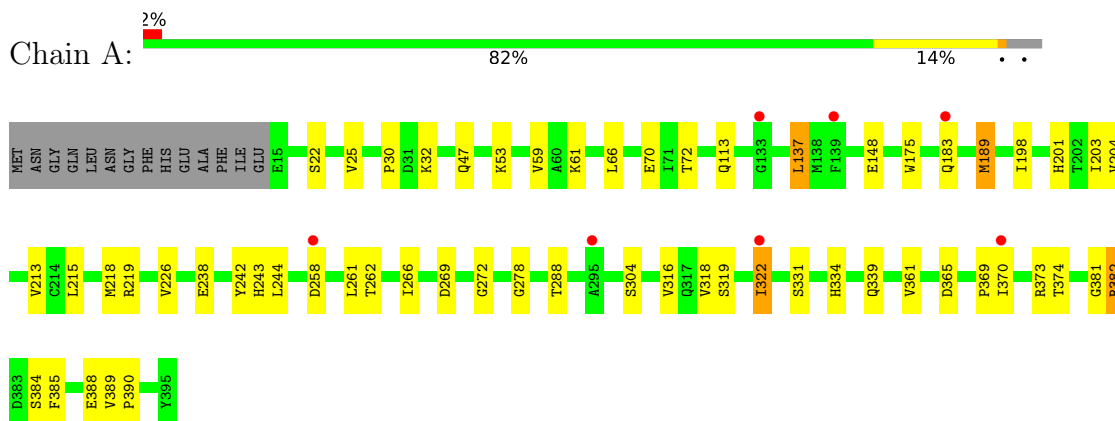
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	7	Total	O	0	0
			7	7		
6	B	21	Total	O	0	0
			21	21		

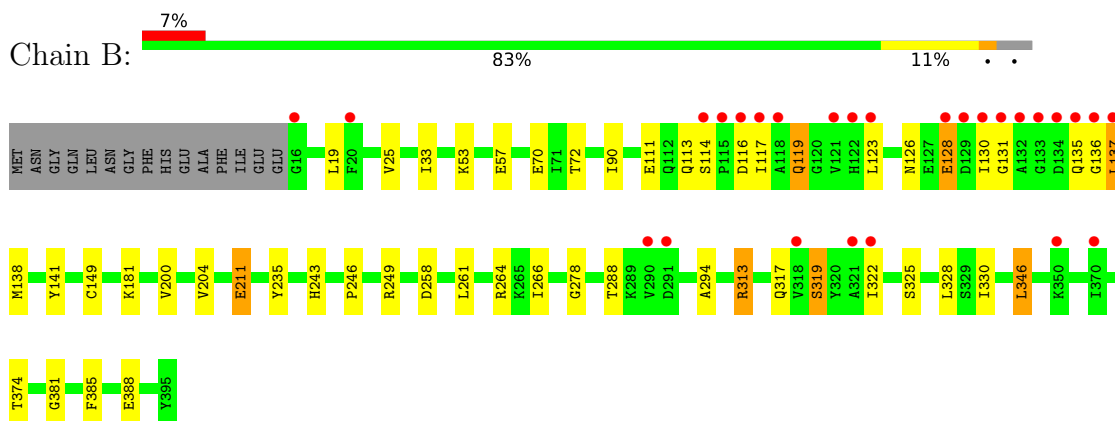
3 Residue-property plots [i](#)

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

- Molecule 1: S-adenosylmethionine synthase isoform type-2



- Molecule 1: S-adenosylmethionine synthase isoform type-2



4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	144.19Å 144.19Å 188.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.20 – 2.55 47.20 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.20-2.55) 99.9 (47.20-2.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 2.54Å)	Xtriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.220 , 0.266 0.222 , 0.267	Depositor DCC
R_{free} test set	1970 reflections (4.58%)	wwPDB-VP
Wilson B-factor (Å ²)	72.1	Xtriage
Anisotropy	0.569	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 67.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6146	wwPDB-VP
Average B, all atoms (Å ²)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% 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: MED, U4P, EDO

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	0.09	0/3022	0.29	0/4088
1	B	0.08	0/3162	0.27	0/4276
All	All	0.09	0/6184	0.28	0/8364

There are no bond length outliers.

There are no bond angle outliers.

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	2963	0	2956	30	0
1	B	3101	0	3081	36	0
2	A	16	0	0	2	0
2	B	16	0	0	0	0
3	A	9	0	10	2	0
4	B	4	0	6	0	0
5	B	9	0	8	2	0
6	A	7	0	0	0	0
6	B	21	0	0	0	0
All	All	6146	0	6061	58	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 5.

All (58) 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:72:THR:HG23	1:B:113:GLN:H	1.52	0.74
1:A:72:THR:HG23	1:A:113:GLN:H	1.62	0.64
1:B:200:VAL:HG23	1:B:235:TYR:HB3	1.83	0.60
1:B:53:LYS:HE3	1:B:288:THR:HG21	1.85	0.59
1:B:330:ILE:HB	1:B:346:LEU:HD11	1.85	0.58
1:A:70:GLU:HB3	1:A:113:GLN:HA	1.86	0.57
1:B:211:GLU:OE2	1:B:249:ARG:NH2	2.38	0.57
1:B:25:VAL:HG12	1:B:181:LYS:HG2	1.88	0.55
1:B:131[A]:GLY:HA2	1:B:325:SER:HA	1.89	0.55
1:A:322:ILE:HG23	1:B:246:PRO:HG2	1.89	0.53
1:A:189:MET:HB2	1:A:198:ILE:HD11	1.89	0.52
1:B:119:GLN:HA	1:B:123[B]:LEU:HB2	1.92	0.52
1:A:204:VAL:HG21	1:B:135[A]:GLN:NE2	2.25	0.51
1:A:47:GLN:HG3	1:A:369:PRO:HG3	1.92	0.51
2:A:401[B]:U4P:NAI	1:B:117:ILE:HG12	2.25	0.51
1:A:262:THR:O	1:B:264:ARG:NH1	2.44	0.51
1:A:30:PRO:HG2	1:A:258:ASP:HB3	1.93	0.50
1:B:33:ILE:HG12	1:B:90:ILE:HD13	1.94	0.48
1:B:117:ILE:HD13	5:B:502[B]:MET:HB2	1.95	0.48
1:A:331:SER:OG	1:B:19:LEU:O	2.27	0.48
1:A:266:ILE:HD11	1:B:266:ILE:HD11	1.96	0.47
1:A:137:LEU:O	1:A:278:GLY:HA3	2.14	0.47
1:A:61:LYS:HA	1:A:61:LYS:HD2	1.60	0.46
1:B:381:GLY:H	1:B:388:GLU:CD	2.24	0.46
1:A:53:LYS:HE3	1:A:288:THR:HG21	1.97	0.46
1:B:204:VAL:HG22	1:B:243:HIS:HB2	1.98	0.46
1:B:319:SER:O	1:B:328:LEU:HB3	2.15	0.46
1:A:261:LEU:HD22	1:B:261:LEU:HD22	1.97	0.46
1:A:59:VAL:HB	1:A:66:LEU:HB3	1.98	0.45
1:A:261:LEU:HD11	1:B:57:GLU:HB3	1.98	0.45
1:B:136[A]:GLY:O	1:B:138[A]:MET:HE2	2.17	0.45
1:B:70:GLU:HB3	1:B:113:GLN:HA	1.99	0.44
1:A:215:LEU:HD21	1:A:219:ARG:CZ	2.48	0.44
1:B:126[A]:ASN:O	1:B:128[A]:GLU:N	2.51	0.44
1:A:304:SER:HA	1:A:390:PRO:HB3	2.00	0.44
1:A:215:LEU:HA	1:A:218:MET:HE2	2.00	0.44
1:A:203:ILE:HD11	1:A:242:TYR:HE1	1.83	0.43
1:B:374:THR:HG22	1:B:385:PHE:CE1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:SER:OG	1:A:272:GLY:O	2.31	0.43
1:B:138[A]:MET:HG2	1:B:294:ALA:HB3	1.99	0.43
3:A:402:MED:HE2	3:A:402:MED:HB2	1.92	0.43
1:A:32:LYS:NZ	1:A:269:ASP:OD1	2.49	0.43
1:B:135[B]:GLN:H	1:B:135[B]:GLN:HG3	1.38	0.42
2:A:401[B]:U4P:OAB	1:B:116:ASP:HB3	2.19	0.42
1:A:201:HIS:CE1	1:B:328:LEU:HD21	2.55	0.42
1:B:137[B]:LEU:HD12	1:B:278:GLY:HA2	2.01	0.41
1:A:373:ARG:O	1:A:382:ARG:NH2	2.53	0.41
1:A:381:GLY:H	1:A:388:GLU:CD	2.28	0.41
1:A:175:TRP:HB3	1:A:213:VAL:HG21	2.02	0.41
1:A:219:ARG:NE	1:A:244:LEU:O	2.53	0.41
1:A:374:THR:HG22	1:A:385:PHE:CZ	2.56	0.41
3:A:402:MED:HG3	1:B:258:ASP:CG	2.46	0.41
1:A:203:ILE:HD11	1:A:242:TYR:CE1	2.56	0.40
1:B:123[B]:LEU:HD23	1:B:123[B]:LEU:HA	1.91	0.40
1:B:141:TYR:OH	1:B:313:ARG:HD3	2.21	0.40
1:A:243:HIS:CG	1:B:322:ILE:HD12	2.56	0.40
1:B:113:GLN:NE2	5:B:502[B]:MET:O	2.53	0.40
1:B:114:SER:HB3	1:B:117:ILE:HG13	2.03	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	379/395 (96%)	357 (94%)	21 (6%)	1 (0%)	36	45
1	B	397/395 (100%)	376 (95%)	21 (5%)	0	100	100
All	All	776/790 (98%)	733 (94%)	42 (5%)	1 (0%)	48	61

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	384	SER

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	316/327 (97%)	298 (94%)	18 (6%)	18	28
1	B	330/327 (101%)	316 (96%)	14 (4%)	26	40
All	All	646/654 (99%)	614 (95%)	32 (5%)	23	33

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	VAL
1	A	137	LEU
1	A	148	GLU
1	A	183	GLN
1	A	189	MET
1	A	226	VAL
1	A	238	GLU
1	A	316	VAL
1	A	318	VAL
1	A	319	SER
1	A	322	ILE
1	A	334	HIS
1	A	339	GLN
1	A	361	VAL
1	A	365	ASP
1	A	370	ILE
1	A	382	ARG
1	A	389	VAL
1	B	111	GLU
1	B	119	GLN
1	B	128[A]	GLU
1	B	128[B]	GLU
1	B	130[A]	ILE

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Mol	Chain	Res	Type
1	B	130[B]	ILE
1	B	137[A]	LEU
1	B	137[B]	LEU
1	B	149	CYS
1	B	211	GLU
1	B	313	ARG
1	B	317	GLN
1	B	319	SER
1	B	346	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	183	GLN
1	A	187	GLN
1	A	243	HIS
1	A	326	HIS
1	B	161	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	U4P	B	503	3	17,17,17	4.31	9 (52%)	23,25,25	2.28	10 (43%)
5	MET	B	502[B]	2	7,8,8	1.06	0	5,9,9	1.21	0
2	U4P	A	401[B]	5	17,17,17	4.30	11 (64%)	23,25,25	2.35	7 (30%)
3	MED	A	402	2	7,8,8	1.05	0	5,9,9	1.12	0
4	EDO	B	501	-	3,3,3	0.43	0	2,2,2	0.37	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
2	U4P	B	503	3	-	4/4/20/20	0/2/2/2
5	MET	B	502[B]	2	-	3/8/8/8	-
2	U4P	A	401[B]	5	-	3/4/20/20	0/2/2/2
3	MED	A	402	2	-	6/8/8/8	-
4	EDO	B	501	-	-	0/1/1/1	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	503	U4P	OAC-CAM	10.01	1.40	1.23
2	A	401[B]	U4P	OAC-CAM	10.00	1.40	1.23
2	B	503	U4P	OAB-CAL	8.56	1.41	1.24
2	A	401[B]	U4P	OAB-CAL	8.43	1.41	1.24
2	B	503	U4P	O4'-C1'	6.81	1.57	1.42
2	A	401[B]	U4P	O4'-C1'	6.51	1.57	1.42
2	B	503	U4P	CAM-NAI	4.55	1.45	1.38
2	A	401[B]	U4P	CAM-NAI	4.47	1.45	1.38
2	A	401[B]	U4P	C3'-C4'	-4.16	1.46	1.52
2	A	401[B]	U4P	C2'-C3'	-4.02	1.42	1.53
2	A	401[B]	U4P	O4'-C4'	3.83	1.55	1.44
2	B	503	U4P	C3'-C4'	-3.80	1.47	1.52
2	B	503	U4P	C2'-C3'	-3.76	1.43	1.53
2	B	503	U4P	O4'-C4'	3.71	1.55	1.44
2	B	503	U4P	O2'-C2'	2.60	1.49	1.43
2	A	401[B]	U4P	O2'-C2'	2.57	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	503	U4P	CAG-CAK	2.57	1.41	1.35
2	A	401[B]	U4P	CAG-CAK	2.52	1.40	1.35
2	A	401[B]	U4P	C1'-NAR	-2.06	1.41	1.47
2	A	401[B]	U4P	C2'-C1'	-2.01	1.47	1.53

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401[B]	U4P	C5'-C4'-C3'	-5.66	109.76	115.70
2	A	401[B]	U4P	CAL-NAI-CAM	-4.64	120.85	126.61
2	B	503	U4P	CAL-NAI-CAM	-4.44	121.10	126.61
2	B	503	U4P	C5'-C4'-C3'	-4.12	111.37	115.70
2	B	503	U4P	C1'-NAR-CAM	3.90	124.60	117.59
2	A	401[B]	U4P	CAK-CAL-NAI	3.59	119.83	114.80
2	B	503	U4P	CAK-CAL-NAI	3.52	119.73	114.80
2	A	401[B]	U4P	OAB-CAL-CAK	-3.49	119.15	125.16
2	B	503	U4P	NAI-CAM-NAR	3.43	119.36	114.89
2	A	401[B]	U4P	NAI-CAM-NAR	3.41	119.33	114.89
2	A	401[B]	U4P	C3'-C2'-C1'	3.29	107.68	101.46
2	B	503	U4P	C3'-C2'-C1'	3.28	107.67	101.46
2	A	401[B]	U4P	C1'-NAR-CAM	3.27	123.47	117.59
2	B	503	U4P	OAB-CAL-CAK	-2.97	120.04	125.16
2	B	503	U4P	C2'-C3'-C4'	2.78	106.47	102.36
2	B	503	U4P	OAC-CAM-NAI	-2.09	117.63	121.49
2	B	503	U4P	C1'-NAR-CAG	-2.00	116.50	120.78

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	MED	O-C-CA-N
5	B	502[B]	MET	N-CA-CB-CG
3	A	402	MED	OXT-C-CA-N
3	A	402	MED	CA-CB-CG-SD
3	A	402	MED	CB-CG-SD-CE
2	B	503	U4P	C2'-C1'-NAR-CAM
3	A	402	MED	O-C-CA-CB
3	A	402	MED	OXT-C-CA-CB
5	B	502[B]	MET	CB-CG-SD-CE
5	B	502[B]	MET	C-CA-CB-CG
2	B	503	U4P	C2'-C1'-NAR-CAG
2	B	503	U4P	O4'-C1'-NAR-CAG

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Mol	Chain	Res	Type	Atoms
2	B	503	U4P	O4'-C1'-NAR-CAM
2	A	401[B]	U4P	O4'-C1'-NAR-CAG
2	A	401[B]	U4P	C2'-C1'-NAR-CAG
2	A	401[B]	U4P	O4'-C1'-NAR-CAM

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	502[B]	MET	2	0
2	A	401[B]	U4P	2	0
3	A	402	MED	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	381/395 (96%)	0.15	7 (1%) 67 68	68, 101, 149, 184	0
1	B	380/395 (96%)	0.34	27 (7%) 22 21	47, 92, 139, 211	19 (5%)
All	All	761/790 (96%)	0.24	34 (4%) 38 38	47, 97, 143, 211	19 (2%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	133[A]	GLY	8.6
1	B	135[A]	GLN	8.0
1	B	132[A]	ALA	7.7
1	B	134[A]	ASP	5.5
1	B	137[A]	LEU	4.7
1	B	131[A]	GLY	4.6
1	B	318	VAL	4.5
1	B	16	GLY	4.0
1	B	20	PHE	3.4
1	B	136[A]	GLY	3.4
1	A	322	ILE	3.4
1	B	121[A]	VAL	3.1
1	B	291	ASP	3.1
1	B	114	SER	3.0
1	A	295	ALA	3.0
1	B	370	ILE	3.0
1	B	128[A]	GLU	2.9
1	B	115	PRO	2.8
1	B	322	ILE	2.8
1	B	129[A]	ASP	2.8
1	A	370	ILE	2.6
1	B	122[A]	HIS	2.4
1	B	117	ILE	2.3
1	A	133	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	321	ALA	2.2
1	B	130[A]	ILE	2.2
1	B	118	ALA	2.2
1	A	183	GLN	2.2
1	A	258	ASP	2.2
1	B	116	ASP	2.2
1	B	290	VAL	2.2
1	B	123[A]	LEU	2.2
1	B	350	LYS	2.1
1	A	139	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	EDO	B	501	4/4	0.70	0.21	97,105,116,117	0
5	MET	B	502[B]	9/9	0.82	0.24	93,104,127,129	9
2	U4P	A	401[B]	16/16	0.87	0.20	114,119,125,127	16
2	U4P	B	503	16/16	0.88	0.14	88,99,114,118	16
3	MED	A	402	9/9	0.92	0.16	110,112,116,118	9

6.5 Other polymers [i](#)

There are no such residues in this entry.