



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:48 AM UTC

PDB ID : 1YJY / pdb_00001yjy
Title : K226M Mutant Of Serine Hydroxymethyltransferase From B. Stearothermophilus, Complex With Serine
Authors : Bhavani, S.; Trivedi, V.; Jala, V.R.; Subramanya, H.S.; Kaul, P.; Purnima, K.; Prakash, V.; Appaji, R.N.; Savithri, H.S.
Deposited on : 2005-01-16
Resolution : 2.25 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

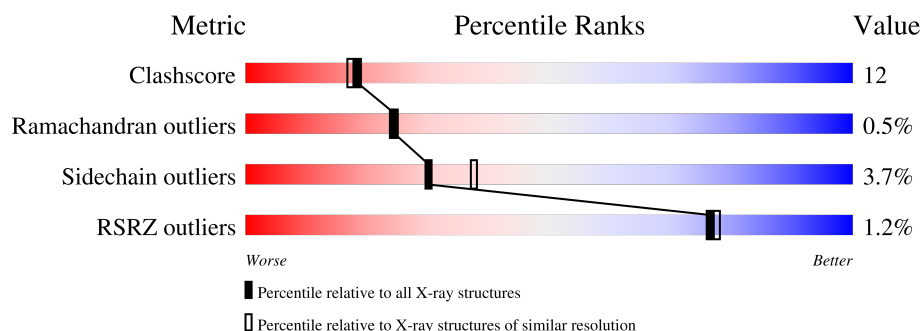
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	419	74% 17% ...

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3274 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 SERINE HYDROXYMETHYLTRANSFERASE.

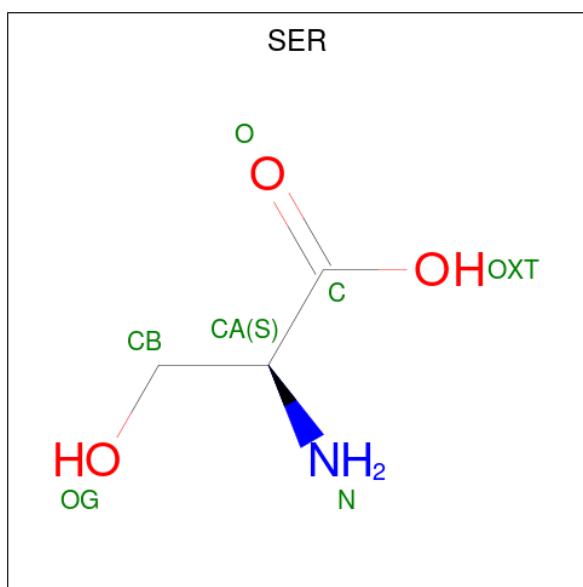
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	405	3115	1969	550	584	12	0	0	0

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	15	8	1	5	1	0	0

- Molecule 3 is SERINE (CCD ID: SER) (formula: $C_3H_7NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			7	3	1	3		

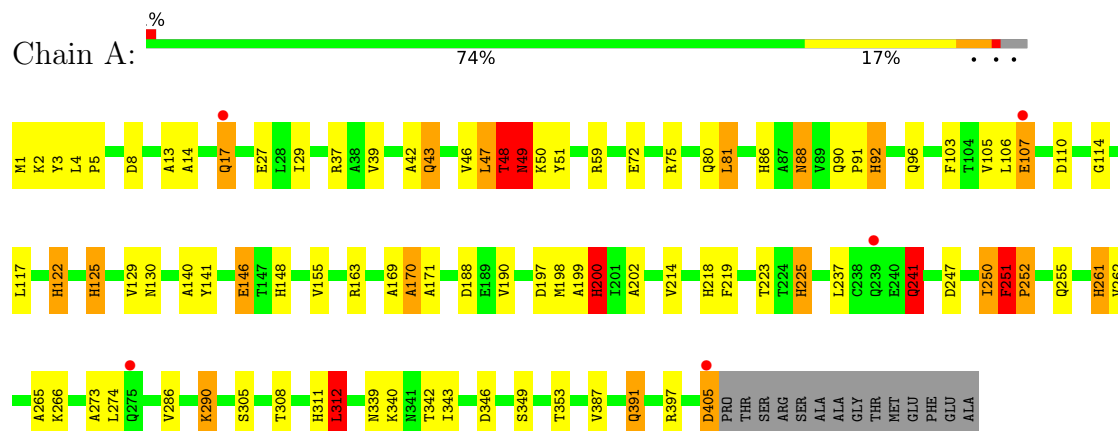
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	137	Total	O	0	0
			137	137		

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: SERINE HYDROXYMETHYLTRANSFERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	60.98Å 106.28Å 56.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.25 10.00 – 2.25	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.25) 94.5 (10.00-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.89 (at 2.22Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.190 , 0.227 0.174 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	14.5	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.51 , 58.9	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	0.94	EDS
Total number of atoms	3274	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.30% 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: PLP

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	0.96	3/3178 (0.1%)	1.78	58/4308 (1.3%)

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	A	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	48	THR	C-O	12.80	1.38	1.24
1	A	48	THR	CA-C	-7.59	1.42	1.52
1	A	48	THR	C-N	7.00	1.43	1.33

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	48	THR	CA-C-O	-18.88	100.70	120.90
1	A	48	THR	N-CA-C	-18.86	88.47	111.11
1	A	251	PHE	CA-C-O	-16.87	102.92	120.63
1	A	48	THR	N-CA-CB	15.01	132.31	109.94
1	A	49	ASN	N-CA-C	12.81	128.24	112.87
1	A	251	PHE	O-C-N	12.31	128.66	121.27
1	A	405	ASP	CA-CB-CG	11.48	124.08	112.60
1	A	48	THR	CA-C-N	9.68	138.99	120.99
1	A	48	THR	C-N-CA	9.68	138.99	120.99
1	A	17	GLN	CB-CA-C	-9.20	96.29	110.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	37	ARG	CD-NE-CZ	8.33	136.06	124.40
1	A	225	HIS	N-CA-C	7.31	122.22	113.16
1	A	59	ARG	CD-NE-CZ	7.13	134.38	124.40
1	A	252	PRO	CA-N-CD	-6.74	102.56	112.00
1	A	50	LYS	N-CA-C	6.66	119.76	108.90
1	A	252	PRO	N-CA-CB	6.57	110.15	103.25
1	A	80	GLN	OE1-CD-NE2	6.48	129.08	122.60
1	A	125	HIS	CA-CB-CG	6.47	120.27	113.80
1	A	340	LYS	N-CA-C	-6.37	101.53	110.50
1	A	50	LYS	N-CA-CB	-6.36	99.99	110.68
1	A	146	GLU	CB-CG-CD	6.30	123.32	112.60
1	A	339	ASN	OD1-CG-ND2	6.28	128.88	122.60
1	A	49	ASN	N-CA-CB	6.22	121.64	110.32
1	A	103	PHE	CA-C-N	6.11	128.75	120.44
1	A	103	PHE	C-N-CA	6.11	128.75	120.44
1	A	339	ASN	CB-CA-C	-6.10	97.72	109.37
1	A	171	ALA	N-CA-CB	-5.98	102.25	111.46
1	A	43	GLN	CA-C-O	-5.97	113.10	119.97
1	A	241	GLN	OE1-CD-NE2	-5.93	116.67	122.60
1	A	397	ARG	CD-NE-CZ	5.86	132.60	124.40
1	A	218	HIS	N-CA-C	-5.82	105.02	111.36
1	A	103	PHE	CA-CB-CG	5.81	119.61	113.80
1	A	171	ALA	N-CA-C	5.79	117.05	108.60
1	A	96	GLN	OE1-CD-NE2	-5.71	116.89	122.60
1	A	250	ILE	CA-C-O	-5.69	114.73	121.05
1	A	130	ASN	OD1-CG-ND2	-5.66	116.94	122.60
1	A	122	HIS	CA-C-N	5.61	128.06	120.38
1	A	122	HIS	C-N-CA	5.61	128.06	120.38
1	A	29	ILE	CB-CA-C	5.60	118.83	111.33
1	A	47	LEU	CA-C-O	5.48	126.12	119.38
1	A	169	ALA	CA-C-N	5.47	131.98	121.54
1	A	169	ALA	C-N-CA	5.47	131.98	121.54
1	A	8	ASP	CA-C-N	5.45	125.10	119.05
1	A	8	ASP	C-N-CA	5.45	125.10	119.05
1	A	202	ALA	N-CA-C	5.32	117.49	111.11
1	A	200	HIS	CA-CB-CG	-5.31	108.49	113.80
1	A	92	HIS	CA-CB-CG	5.29	119.09	113.80
1	A	397	ARG	NE-CZ-NH2	-5.24	114.49	119.20
1	A	312	LEU	N-CA-C	5.16	117.52	109.52
1	A	214	VAL	N-CA-CB	5.14	113.96	110.52
1	A	107	GLU	CB-CG-CD	5.13	121.32	112.60
1	A	387	VAL	N-CA-C	5.12	116.46	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	349	SER	CA-C-N	5.12	124.78	119.56
1	A	349	SER	C-N-CA	5.12	124.78	119.56
1	A	188	ASP	CA-CB-CG	5.10	117.70	112.60
1	A	129	VAL	N-CA-C	-5.09	107.50	112.29
1	A	42	ALA	CA-C-O	-5.04	115.20	120.55
1	A	237	LEU	CA-C-O	-5.00	115.50	121.16

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	251	PHE	Peptide,Mainchain
1	A	48	THR	Mainchain
1	A	49	ASN	Mainchain

5.2 Too-close contacts [i](#)

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	3115	0	3091	74	0
2	A	15	0	6	2	0
3	A	7	0	4	2	0
4	A	137	0	0	8	0
All	All	3274	0	3101	75	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 12.

All (75) 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:A:49:ASN:HA	4:A:618:HOH:O	1.11	1.26
1:A:48:THR:O	4:A:618:HOH:O	1.62	1.15
1:A:48:THR:C	4:A:618:HOH:O	1.94	0.95
1:A:48:THR:HA	1:A:261:HIS:CD2	2.11	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:GLN:NE2	4:A:681:HOH:O	2.09	0.85
1:A:148:HIS:HD2	1:A:305:SER:H	1.26	0.82
1:A:47:LEU:O	1:A:48:THR:C	2.20	0.81
1:A:92:HIS:H	1:A:255:GLN:HE22	1.32	0.77
1:A:13:ALA:O	1:A:17:GLN:HG2	1.87	0.75
1:A:290:LYS:HE2	1:A:308:THR:HG23	1.69	0.75
1:A:261:HIS:CD2	1:A:261:HIS:H	2.10	0.70
1:A:286:VAL:HG13	1:A:290:LYS:NZ	2.08	0.68
1:A:14:ALA:O	1:A:17:GLN:HB2	1.97	0.65
1:A:2:LYS:HD3	1:A:3:TYR:CZ	2.33	0.64
1:A:290:LYS:CE	1:A:308:THR:HG23	2.28	0.63
1:A:311:HIS:H	1:A:311:HIS:HD1	1.46	0.61
1:A:286:VAL:HG13	1:A:290:LYS:HZ2	1.65	0.60
1:A:105:VAL:HG23	1:A:106:LEU:HG	1.84	0.60
1:A:17:GLN:HE21	1:A:17:GLN:CA	2.12	0.57
1:A:148:HIS:CD2	1:A:305:SER:H	2.17	0.56
1:A:200:HIS:HE1	3:A:601:SER:O	1.88	0.55
1:A:200:HIS:HD2	1:A:311:HIS:NE2	2.04	0.55
1:A:39:VAL:HG13	1:A:265:ALA:HB1	1.89	0.55
1:A:72:GLU:CD	1:A:75:ARG:HH21	2.15	0.54
1:A:4:LEU:HB3	1:A:5:PRO:HD3	1.91	0.53
1:A:261:HIS:H	1:A:261:HIS:HD2	1.56	0.53
1:A:290:LYS:HE2	1:A:308:THR:O	2.07	0.53
1:A:105:VAL:HG11	1:A:219:PHE:CE1	2.44	0.53
1:A:197:ASP:OD2	2:A:501:PLP:N1	2.42	0.52
1:A:17:GLN:NE2	1:A:17:GLN:CA	2.69	0.52
1:A:17:GLN:CD	4:A:681:HOH:O	2.50	0.51
1:A:343:ILE:O	1:A:346:ASP:HB2	2.10	0.51
2:A:501:PLP:O3	3:A:601:SER:N	2.43	0.51
1:A:122:HIS:H	1:A:125:HIS:CD2	2.30	0.50
1:A:223:THR:HB	1:A:225:HIS:CE1	2.47	0.50
1:A:290:LYS:HE3	1:A:290:LYS:N	2.26	0.49
1:A:92:HIS:H	1:A:255:GLN:NE2	2.07	0.49
1:A:27:GLU:HB2	4:A:609:HOH:O	2.12	0.49
1:A:88:ASN:C	1:A:88:ASN:HD22	2.21	0.48
1:A:81:LEU:HD13	1:A:274:LEU:CD2	2.43	0.48
1:A:81:LEU:HD13	1:A:274:LEU:HD23	1.96	0.48
1:A:163:ARG:HH12	1:A:190:VAL:HA	1.79	0.48
1:A:342:THR:HG22	1:A:353:THR:HG22	1.95	0.48
1:A:86:HIS:HE1	1:A:247:ASP:OD1	1.98	0.47
1:A:1:MET:SD	1:A:4:LEU:HD23	2.55	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:THR:HA	1:A:261:HIS:CG	2.49	0.46
1:A:170:ALA:HB3	1:A:197:ASP:O	2.14	0.46
1:A:46:VAL:O	1:A:49:ASN:N	2.34	0.46
1:A:251:PHE:CD2	1:A:251:PHE:C	2.94	0.46
1:A:241:GLN:H	1:A:241:GLN:CD	2.24	0.45
1:A:49:ASN:CA	4:A:618:HOH:O	1.95	0.45
1:A:198:MET:O	1:A:199:ALA:C	2.58	0.45
1:A:286:VAL:HG13	1:A:290:LYS:HZ3	1.81	0.45
1:A:43:GLN:HG2	1:A:265:ALA:HB2	2.00	0.44
1:A:262:VAL:HG12	1:A:266:LYS:HE3	1.99	0.44
1:A:141:TYR:CG	1:A:155:VAL:HG22	2.52	0.44
1:A:14:ALA:HA	1:A:17:GLN:CG	2.47	0.44
1:A:312:LEU:C	1:A:312:LEU:HD12	2.43	0.44
1:A:49:ASN:N	4:A:618:HOH:O	1.85	0.44
1:A:88:ASN:HD22	1:A:91:PRO:HD3	1.82	0.44
1:A:107:GLU:HG2	1:A:110:ASP:CG	2.43	0.43
1:A:114:GLY:O	1:A:140:ALA:HA	2.18	0.43
1:A:91:PRO:HA	1:A:255:GLN:HE22	1.82	0.43
1:A:261:HIS:CD2	1:A:261:HIS:N	2.82	0.43
1:A:88:ASN:ND2	1:A:91:PRO:HD3	2.34	0.43
1:A:107:GLU:HG2	1:A:110:ASP:OD1	2.18	0.42
1:A:14:ALA:HA	1:A:17:GLN:HG3	2.01	0.42
1:A:163:ARG:NH1	1:A:190:VAL:HB	2.35	0.42
1:A:88:ASN:ND2	1:A:90:GLN:H	2.18	0.42
1:A:17:GLN:NE2	1:A:17:GLN:HA	2.36	0.41
1:A:250:ILE:HD13	1:A:250:ILE:HA	1.98	0.41
1:A:290:LYS:HE3	1:A:290:LYS:CA	2.51	0.41
1:A:391:GLN:H	1:A:391:GLN:HG2	1.57	0.41
1:A:81:LEU:HD21	1:A:273:ALA:HB3	2.02	0.40
1:A:90:GLN:N	1:A:91:PRO:CD	2.84	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	403/419 (96%)	387 (96%)	14 (4%)	2 (0%)	24	24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	170	ALA
1	A	252	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	321/331 (97%)	309 (96%)	12 (4%)	30	37

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	TYR
1	A	81	LEU
1	A	88	ASN
1	A	117	LEU
1	A	146	GLU
1	A	200	HIS
1	A	241	GLN
1	A	261	HIS
1	A	290	LYS
1	A	312	LEU
1	A	391	GLN
1	A	405	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	17	GLN
1	A	23	HIS
1	A	86	HIS
1	A	88	ASN
1	A	90	GLN
1	A	96	GLN
1	A	125	HIS
1	A	135	GLN
1	A	137	ASN
1	A	148	HIS
1	A	200	HIS
1	A	245	GLN
1	A	255	GLN
1	A	261	HIS
1	A	275	GLN
1	A	297	GLN

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](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SER	A	601	2	4,6,6	0.94	0	2,7,7	0.76	0
2	PLP	A	501	3	15,15,16	1.74	4 (26%)	21,22,23	2.54	8 (38%)

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	SER	A	601	2	-	1/6/6/6	-
2	PLP	A	501	3	-	0/6/6/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	PLP	C4A-C4	-3.03	1.45	1.51
2	A	501	PLP	C3-C2	3.00	1.44	1.41
2	A	501	PLP	C3-C4	2.37	1.44	1.40
2	A	501	PLP	C6-N1	2.21	1.38	1.34

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	PLP	C2A-C2-C3	6.66	128.59	120.80
2	A	501	PLP	O4P-C5A-C5	4.20	117.24	109.36
2	A	501	PLP	C6-N1-C2	4.16	126.75	119.20
2	A	501	PLP	C5-C6-N1	-3.56	118.04	123.83
2	A	501	PLP	C3-C2-N1	-3.32	116.77	120.96
2	A	501	PLP	C3-C4-C5	2.43	121.51	118.59
2	A	501	PLP	C5A-C5-C6	-2.23	115.73	119.36
2	A	501	PLP	O3P-P-O1P	2.07	118.89	110.83

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	SER	C-CA-CB-OG

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	SER	2	0
2	A	501	PLP	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 [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	405/419 (96%)	-0.49	5 (1%) 76 77	10, 17, 29, 46	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	17	GLN	2.6
1	A	239	GLN	2.5
1	A	107	GLU	2.3
1	A	405	ASP	2.2
1	A	275	GLN	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
3	SER	A	601	7/7	0.90	0.08	12,14,16,19	0
2	PLP	A	501	15/16	0.94	0.08	7,10,11,11	0

6.5 Other polymers ⓘ

There are no such residues in this entry.